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OM nucleic - nucleic search, using sw model

Run on: May 23, 2005, 09:06:05 ; Search time 544 Seconds
(without alignments)
9808.637 Million cell updates/sec

Title: US-09-373-658C-1

Perfect score: 3261

Sequence: 1 atggggaacgcggagggc.....tgcatgtgtcatnagtctn 3261

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents NA:*

1: /cgn2_6/ptodata/1/ina/5A COMB.seq.*

2: /cgn2_6/ptodata/1/ina/5B COMB.seq.*

3: /cgn2_6/ptodata/1/ina/6A COMB.seq.*

4: /cgn2_6/ptodata/1/ina/6B COMB.seq.*

5: /cgn2_6/ptodata/1/ina/PCRU COMB.seq.*

6: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3160	96.9	4676	3	US-09-130-491-1
2	3156.8	96.8	3899	4	US-09-568-559-1
3	3150.6	96.6	4858	3	US-09-392-184-1
4	2631.4	80.7	3706	3	US-09-484-9708-58
5	2131.6	65.4	2184	4	US-09-445-023A-2
6	1655	50.8	2184	4	US-09-445-023A-13
7	666.2	20.4	3638	3	US-09-369-364A-8
8	629.8	19.3	2853	4	US-10-009-332-2
9	603.4	18.5	4192	3	US-09-122-1268-1
10	603.4	18.5	4192	4	US-09-634-286A-1
11	603.4	18.5	4192	4	US-10-247-685-1
12	558.6	17.1	3250	3	US-09-122-1268-14
13	558.6	17.1	3250	4	US-09-634-286A-14
14	558.6	17.1	3250	4	US-10-247-685-14
15	544.2	16.7	3126	3	US-09-392-184-7
16	542.8	16.6	3002	3	US-09-369-364A-1
17	369.4	11.3	5804	3	US-09-369-364A-12
18	359.8	11.0	2623	3	US-09-369-364A-14
19	325	10.0	6659	4	US-09-321-987B-1
20	324	9.9	2114	3	US-09-130-491-7
21	268.6	8.2	739	3	US-09-369-364A-10
22	198.4	6.1	1520	3	US-09-369-364A-3
23	175.8	5.4	303	4	US-09-445-023A-14
24	145.6	4.5	703	3	US-09-392-184-6
25	141.8	4.3	3218	3	US-09-369-364A-6
26	140.2	4.3	5357	3	US-09-392-184-5
27	115.2	3.5	3571	4	US-09-799-451-411

28	113.6	3.5	3377	4	US-09-981-953A-3	Sequence 3, Appli
29	109.4	3.4	3675	3	US-09-930-872-3	Sequence 3, Appli
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31	109.4	3.4	3766	4	US-09-981-953A-1	Sequence 1, Appli
32	109.4	3.4	4042	3	US-09-930-872-5	Sequence 5, Appli
33	109.4	3.4	4042	4	US-10-217-774-5	Sequence 5, Appli
34	104.8	3.2	3158	4	US-09-949-016-1988	Sequence 1988, Ap
35	102.8	3.2	2274	4	US-09-963-791-23	Sequence 23, Appli
36	102.8	3.2	2727	4	US-09-963-791-1	Sequence 1, Appli
37	96.6	3.0	1061	4	US-09-270-767-995	Sequence 995, App
38	96.6	3.0	1061	4	US-09-270-767-16277	Sequence 16277, A
39	84.6	2.6	1317	4	US-09-963-791-21	Sequence 21, Appli
40	84.6	2.6	1770	4	US-09-963-791-11	Sequence 11, Appli
41	84.4	2.6	3885	3	US-09-369-364A-16	Sequence 16, Appli
42	83	2.5	1071	4	US-09-963-791-19	Sequence 19, Appli
43	83	2.5	1524	4	US-09-963-791-9	Sequence 9, Appli
44	77.4	2.4	2799	4	US-09-181-339-2	Sequence 2, Appli
45	76	2.3	944	4	US-09-461-325-105	Sequence 105, App

ALIGNMENTS

RESULT 1

US-09-130-491-1

; Sequence 1, Application US/09130491

; Patent No. 6416974

; GENERAL INFORMATION:

; APPLICANT: Holtzman, Douglas A.

; APPLICANT: Goodearl, Andrew D.J.

; TITLE OF INVENTION: TANGO-71, TANGO-73, TANGO-74, TANGO-76, AND TANGO-83

; FILE REFERENCE: 09404/041001

; CURRENT APPLICATION NUMBER: US/09/130,491

; CURRENT FILING DATE: 1998-08-07

; EARLIER APPLICATION NUMBER: US 60/058,108

; EARLIER FILING DATE: 1997-09-05

; EARLIER APPLICATION NUMBER: US 60/054,961

; EARLIER FILING DATE: 1997-08-06

; NUMBER OF SEQ ID NOS: 16

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 1

; LENGTH: 4676

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (460)...(3360)

US-09-130-491-1

Query Match 96.9%; Score 3160; DB 3; Length 4676;

Best Local Similarity 99.6%; Pred. No. 0;

Matches 3177; Conservative 0; Mismatches 11; Indels 1; Gaps 1;

Qy	1	ATGGGAAACGCGAGCGGCTCGGGGTCTCGAGCTTTGGGCGCCGACGAGCTCTG 60	
Db	511	ATGGGAAACGCGAGCGGCTCGGGGTCTCGAGCTTTGGGCGCCGACGAGCTCTG 570	
Qy	61	CTGCTCGCGCGCGGCTACTGGCCGTCTCGAGCGCACTCGGCGCCCTCCGAGGAGAC 120	
Db	571	CTGCTCGCGCGCGGCTACTGGCCGTCTCGAGCGCACTCGGCGCCCTCCGAGGAGAC 630	
Qy	121	GAGGAGCTAGTGTGTCGCGAGCTGAGCGCCCGGACACGCGGACACGCGCTCCGC 180	
Db	631	GAGGAGCTAGTGTGTCGCGAGCTGAGCGCCCGGACACGCGGACACGCGCTCCGC 690	
Qy	181	CTGACGCGCTTACCGAGCTGAGCTGAGCTGAGCTGAGCGCCCGGACACGCGCTCCGC 240	
Db	691	CTGACGCGCTTACCGAGCTGAGCTGAGCTGAGCTGAGCGCCCGGACACGCGCTCCGC 750	
Qy	241	CCCGGCTTACCGCTCCAGACGCTGGGGCGCAATCCGGTCCGAGACGCGCTTCGGAA 300	
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QY 301 ACCGACCTGGCGCACTGTTCTACTCGGCACCGGTGAATGGCGATCCAGCTCGGCTGCC 360
DB |||||
DB 811 ACCGACCTGGCGCACTGTTCTACTCGGCACCGGTGAATGGCGATCCAGCTCGGCTGCC 870
QY 361 GCCCTCAGCCTCTGGAGGCGGTGGCGCGCTTCTACTCTGCTGGGGAGCGGTATTTTC 420
DB |||||
DB 871 GCCCTCAGCCTCTGGAGGCGGTGGCGCGCTTCTACTCTGCTGGGGAGCGGTATTTTC 930
QY 421 ATCCAGCGCGCTCCCGCGCGCAGAGAGCGCTTCGCCACCGCGCGCCCGCAGGGGAGAGCGG 480
DB |||||
DB 931 ATCCAGCGCGCTCCCGCGCGCAGAGAGCGCTTCGCCACCGCGCGCCCGCAGGGGAGAGCGG 990
QY 481 CGGCAACACTACAGTTCCACCTCTCGCGCGGGAATCGGAGGCGAGCTAGCGCGCACG 540
DB |||||
DB 991 CGGCAACACTACAGTTCCACCTCTCGCGCGGGAATCGGAGGCGAGCTAGCGCGCACG 1050
QY 541 TCGCGGGTCTGGAGCAGACGAGCCCGCGCGCACTGGGAAAGCGGAGACCGGAACGAGGAC 600
DB |||||
DB 1051 TCGCGGGTCTGGAGCAGACGAGCCCGCGCGCACTGGGAAAGCGGAGACCGGAACGAGGAC 1110
QY 601 GAAGGCACTGAGGGCGAGGACGAGGGGCTCAGTGGTGGCGCGAGACCGGCACTGCAA 660
DB |||||
DB 1111 GAAGGCACTGAGGGCGAGGACGAGGGGCTCAGTGGTGGCGCGAGACCGGCACTGCAA 1170
QY 661 GCGGTAGGACAGCCACAGGAACTGGAAGCATAGAAAGAGAGCGATTTGTCTCAGTCA 720
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DB 1171 GCGGTAGGACAGCCACAGGAACTGGAAGCATAGAAAGAGAGCGATTTGTCTCAGTCA 1230
QY 721 CGCTATGTGGAAACCATGCTTGTGGCAGACCACTGATGGCGAATTCACCGCAGTGGT 780
DB |||||
DB 1231 CGCTATGTGGAAACCATGCTTGTGGCAGACCACTGATGGCGAATTCACCGCAGTGGT 1290
QY 781 CTAAGCAATTACTCTCTCAGTTGTTTTCGTTGGCGAGCCAGATTTGTACAAACACCCACG 840
DB |||||
DB 1291 CTAAGCAATTACTCTCTCAGTTGTTTTCGTTGGCGAGCCAGATTTGTACAAACACCCACG 1350
QY 841 ATTCTGTAATTAGTTAGCTGCTGTGTGTAAGATCTTGGTCACTCAGCATGAACAGAGA 900
DB |||||
DB 1351 ATTCTGTAATTAGTTAGCTGCTGTGTGTAAGATCTTGGTCACTCAGCATGAACAGAGA 1410
QY 901 GGGCGGAGTGAACCTCCAACTGCTCCCTCACTCTCGGAACTTTTGCAGCTGGCAGAG 960
DB |||||
DB 1411 GGGCGGAGTGAACCTCCAACTGCTCCCTCACTCTCGGAACTTTTGCAGCTGGCAGAG 1470
QY 961 CAGCAACCCACCCAGTGCACCGGATGAGAGCACTATGACACAGCAATCTTTTTCACC 1020
DB |||||
DB 1471 CAGCAACCCACCCAGTGCACCGGATGAGAGCACTATGACACAGCAATCTTTTTCACC 1530
QY 1021 AGACAGGACTTGTGGGTCCAGACATGTGATACTCTTGGGATGGCTGATGTGGAAT 1080
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DB 1531 AGACAGGACTTGTGGGTCCAGACATGTGATACTCTTGGGATGGCTGATGTGGAAT 1590
QY 1081 GTGTGTATCCGAGCAGAGCTGCTCCGTATAGAGATGATGGTTTCAAGCTGCCCTTC 1140
DB |||||
DB 1591 GTGTGTATCCGAGCAGAGCTGCTCCGTATAGAGATGATGGTTTCAAGCTGCCCTTC 1650
QY 1141 ACCACAGCCATGAATTAGGCACTGTTTATCATGCCATGATGATGATGATGATGATGATGAT 1200
DB |||||
DB 1651 ACCACAGCCATGAATTAGGCACTGTTTATCATGCCATGATGATGATGATGATGATGATGAT 1710
QY 1201 GCGAGCTTAAATGTTGTAACAGGATTCACATGATGGCTCAATGCTTTTCCAACTG 1260
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DB 1711 GCGAGCTTAAATGTTGTAACAGGATTCACATGATGGCTCAATGCTTTTCCAACTG 1770
QY 1261 GACACAGCCAGCTTGTGCTCTCTGAGTGCTTACATGATTTACATTTCTGATTAAT 1320
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DB 1771 GACACAGCCAGCTTGTGCTCTCTGAGTGCTTACATGATTTACATTTCTGATTAAT 1830
QY 1321 GGTCTAGGGAATGTTTGTAGCAAGCTCAGATCCATACAGCTCCAGCGCATCTC 1380
DB |||||
DB 1831 GGTCTAGGGAATGTTTGTAGCAAGCTCAGATCCATACAGCTCCAGCGCATCTC 1890
QY 1381 CCTGGCACTCTGTAAGATGCCAACCGGAGTGCAGTTTACATTTTGGGAGGACTCCAA 1440

DB 1891 CCTGGCACTCTGTAAGTCCCAACCGGCACTGCCAGTTTACATTTGGGAGGACTCCAA 1950
QY 1441 CACTGCCCTGATGAGCAGCAGACATGTAGCACTTTGTGGTGTACGGCACTCTGTGGG 1500
DB 1951 CACTGCCCTGATGAGCAGCAGACATGTAGCACTTTGTGGTGTACGGCACTCTGTGGG 2010
QY 1501 GTGCTGGTGTCTCAAAACCAACACTTCCGTTGGGGGATGGCACAGCTGTGGAGAGG 1560
DB 2011 GTGCTGGTGTCTCAAAACCAACACTTCCGTTGGGGGATGGCACAGCTGTGGAGAGG 2070
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DB 2251 TGTGAAGGCAAAACCAAGTGGCTACAGATCTCTGTAACTTGTAGGACTGTCCAGACAATAT 2310
QY 1801 GGAAGAACTTTAGAGAGGAACAATGTGAAGCACAACAAGAGTTTCAAGAGTCTCTTT 1860
DB 2311 GGAAGAACTTTAGAGAGGAACAATGTGAAGCACAACAAGAGTTTCAAGAGTCTCTTT 2370
QY 1861 GGGAGTGGGCTGGGCTGGAATGGAATCCCAAGTACGCTGGGCTCTCAACAAAGACAGG 1920
DB 2371 GGGAGTGGGCTGGGCTGGAATGGAATCCCAAGTACGCTGGGCTCTCAACAAAGACAGG 2430
QY 1921 TGCAGACTCATCTGCAAGCCAAAGGCAATGGCTACTCTTCTGTTTTCAGCCCCAAGGTT 1980
DB 2431 TGCAGACTCATCTGCAAGCCAAAGGCAATGGCTACTCTTCTGTTTTCAGCCCCAAGGTT 2490
QY 1981 GTAGATGTATCTCCATGTAGCCAGATTCACCTCTGTCTGTGTGCAAGGACAGTGTGTA 2040
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QY 2101 GGGGAAATGGATCTACTTTGTAATAAATAATACAGGATCAGTTACTAGTGCAAAAACCTGGA 2160
DB 2611 GGGGAAATGGATCTACTTTGTAATAAATAATACAGGATCAGTTACTAGTGCAAAAACCTGGA 2670
QY 2161 TATCATGATATCATCAAAATTCCTGAGCCCAACATCGAAGTGAAGAACAGCGGAAC 2220
DB 2671 TATCATGATATCATCAAAATTCCTGAGCCCAACATCGAAGTGAAGAACAGCGGAAC 2730
QY 2221 CAGAGGGATCAGGAAACAATGGCAGCTTTCTTGGCATCAAAAGCTGCTGATGGCACATAT 2280
DB 2731 CAGAGGGATCAGGAAACAATGGCAGCTTTCTTGGCATCAAAAGCTGCTGATGGCACATAT 2790
QY 2281 ATTCTTAATGGTGACTACATTTTGTCCACTTTTGAAGAGACATTAATGTACAAAGTGT 2340
DB 2791 ATTCTTAATGGTGACTACATTTTGTCCACTTTTGAAGAGACATTAATGTACAAAGTGT 2850
QY 2341 GTCTTGAAGTACAGCGCTCTCTGCGGCAATTTGGAAGAAATTCGAGCTTTAGCCCTCTC 2400
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Db 3331 ATAGACTTTTGCAATGGCAGAAATGAGTTAAGTGTGTTAAGTGTGTTAGCTTTGAGG 3390
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Qy 2940 TATCTTGGCAATCAACAGTGAAGTGTATCAGTAAGTGGGATTTAGGGGTAGATAGAA 2999
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Qy 3180 AAAAAAAA 3188
Db 3691 CTATTACAA 3699

RESULT 2
US-09-568-559-1
; Sequence 1, Application US/09568559
; Patent No. 6649377
; GENERAL INFORMATION:
; APPLICANT: Klonowski, Paul
; APPLICANT: Allard, John
; APPLICANT: Heller, Renu
; APPLICANT: Van Wart, Harold
; TITLE OF INVENTION: Human Aggreganase and Nucleic Acid
; FILE REFERENCE: ROCH-002
; CURRENT APPLICATION NUMBER: US/09/568,559
; CURRENT FILING DATE: 2000-05-09
; PRIOR APPLICATION NUMBER: 60/133,343
; PRIOR FILING DATE: 1999-05-10
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 3889
; TYPE: DNA
; ORGANISM: human

US-09-568-559-1
Query Match 96.8%; Score 3156.8; DB 4; Length 3889;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 3175; Conservative 0; Mismatches 13; Indels 1; Gaps 1;
Qy 1 ATGGGAAACCGGAGCGGGCTCCGGGCTCTCGAGGCTTTGGGCCCCGTATCCACGCTGCTG 60
Db 59 ATGGGAAACCGGAGCGGGCTCCGGGCTCTCGAGGCTTTGGGCCCCGTATCCACGCTGCTG 118
Qy 61 CTGCTCGCCGCGCGCTACTGCGCGTCTCGAGCGCACTCGGGCGCCCCCTCCGAGGAGGAC 120
Db 119 CTGCTCGCCGCGCGCTACTGCGCGTCTCGAGCGCACTCGGGCGCCCCCTCCGAGGAGGAC 178
Qy 121 GAGGAGCTAGTGTGTGCGGAGCTGAGCGCGCCCCCGGGACACGCGCCTCCGC 180
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Qy 361 GCCTCAGCTCTGCGAGGGCGTGGCGGCGCTTCTACTGCTGGGGAGGGGTATTTC 420
Db 419 GCCTCAGCTCTGCGAGGGCGTGGCGGCGCTTCTACTGCTGGGGAGGGGTATTTC 478
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Db 479 ATCCAGCGCTGCCCGCGCGCAGCGAGCGCTCCGCGCACCGCGCCCGCAGGGAGAGCGCG 538
Qy 481 CCGGCACTACTACAGTTCCACCTCTCTGCGCGGGAATCGGCGAGCGCGAGCTAGGCGGACG 540
Db 539 CCGGCACTACTACAGTTCCACCTCTCTGCGCGGGAATCGGCGAGCGCGAGCTAGGCGGACG 598
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Qy 721 CGCTATGTGAAACCATGCTTGTGGCAGACAGTCTGATGGCAGAAATTCACGCGAGTGGT 780
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Db 839 CTAAAGCATTTACCTTCTCAGTTTGTGGTGGCAGCGAGATTTGTACAAACACCCAGC 898
Qy 841 ATTCTGAATTCAGTTAGCTGGTGGTGAAGATCTTGTCTATCCAGATGAACAGAG 900
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1379 GGTATGGGGAATGTTGATGGAAGAAGCTCAGAAATCCGATACAGTCCAGGCGATCTC 1438
1381 CCTGGCACCCTCGTACGATGCCAAACCGGAGTCCAGTCTTACATTTTGGGAGGACTCCAAA 1440
1439 CCTGGCACCCTCGTACGATGCCAAACCGGAGTCCAGTCTTACATTTTGGGAGGACTCCAAA 1498
1441 CACTGCCCTGTATGACAGCAGCATGTAGCACTTTGTGGTGTACCGGCACCTCTCGTGGG 1500
1499 CACTGCCCTGTATGACAGCAGCATGTAGCACTTTGTGGTGTACCGGCACCTCTCGTGGG 1558
1501 GTGCTGTGTGTCAAAACCAACACTTCCGCTGGGCGGATGGACACAGCTGTGGAGAAGG 1560
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1621 TTTTCATGGAAGCTGGGGAATGTGGGGCCCTTGGGAGACTGTTCGAGAAACGTGCGGTGA 1680
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1801 GGAATAACCTTTAGAGAGAAACATGTGAAGCACACACAGTGTTCAAAAGCTTCCTTT 1860
1859 GGAATAACCTTTAGAGAGAAACATGTGAAGCACACACAGTGTTCAAAAGCTTCCTTT 1918
1861 GGGAGTGGCCCTGGGTGAATGGATTTCCAGTAGCTGGCGTCTCACCAAGAGCAGG 1920
1919 GGGAGTGGCCCTGGGTGAATGGATTTCCAGTAGCTGGCGTCTCACCAAGAGCAGG 1978
1921 TGCAGCTCATCTGCCAAGCCAAAGCATTTGGTCTCTCTGTTTTCAGGCCCAAGGTT 1980
1979 TGCAGCTCATCTGCCAAGCCAAAGCATTTGGTCTCTCTGTTTTCAGGCCCAAGGTT 2038
1981 GTAGATGGTACTCCATGTAGCCAGATTCACCTCTGTCTGTGTGCAAGGACAGTGTGA 2040
2039 GTAGATGGTACTCCATGTAGCCAGATTCACCTCTGTCTGTGTGCAAGGACAGTGTGA 2098
2041 AAAGCTGGTGTGATCGCATAGACTCCAAAGAAAGTTCATAAATGTGGTGTTCG 2100
2099 AAAGCTGGTGTGATCGCATAGACTCCAAAGAAAGTTCATAAATGTGGTGTTCG 2158

2101 GGGGAAATGGATCTACTTTGTAATAAAAAATATCAGATCAGTTACTAGTCGCAAAACCTGGA 2160
2159 GGGGAAATGGATCTACTTTGTAATAAAAAATATCAGATCAGTTACTAGTCGCAAAACCTGGA 2218
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2221 CAGAGGGATCCAGGAACAATGGGAGCTTTCTTGGCCATCAAGCTGCTGATGGCACATAT 2280
2279 CAGAGGGATCCAGGAACAATGGGAGCTTTCTTGGCCATCAAGCTGCTGATGGCACATAT 2338
2281 ATCTTAATGCTGACTACACATTTTGTCCACCTTAGAGCAAGACATTTATGTACAAAGTGT 2340
2339 ATCTTAATGCTGACTACACATTTTGTCCACCTTAGAGCAAGACATTTATGTACAAAGTGT 2398
2341 GTCTTAGGATCAGCGGCTCTCTCGGGCAATTTGAAAGAAATTCGAGCTTTAGCCCTCTC 2400
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2459 AAAGAGCCCTTGACCATCCAGTCTCTTACTGTGGGCAATGCCCTTCGACCTAAAAATTA 2518
2461 TACACCTACTTCGTAAGAAGAAAGAAATCTTTCAATGCTATCCCACTTTTTCAGCA 2520
2519 TACACCTACTTCGTAAGAAGAAAGAAATCTTTCAATGCTATCCCACTTTTTCAGCA 2578
2521 TGGGTCATTAAGAGTGGGGCGAATGTTCTTAAGTCAATGTAATTTGGTGGCAGAGAAGA 2580
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2581 CTGGTAGAATCCGAGACATTAATGAGACAGCTGCTTCCAGTGTGCAAGAAAGTGAAG 2640
2639 CTGGTAGAATCCGAGACATTAATGAGACAGCTGCTTCCAGTGTGCAAGAAAGTGAAG 2698
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2699 CCAGCAGCACAGACCTTTGTGCAGACCATCCCTCCGCCAGTGGCAGCTGGGGAGTGG 2758
2701 TCATCATGTTCTAAGACCTTGGGGAAGGTTACAAAAAAGAGCTTGAAGTGTCTGTCC 2760
2759 TCATCATGTTCTAAGACCTTGGGGAAGGTTACAAAAAAGAGCTTGAAGTGTCTGTCC 2818
2761 CATGATGAGGGGTGTATCTCATGAGAGCTGTGATCTTTAAAGAAACCTTAAACATTTTC 2820
2819 CATGATGAGGGGTGTATCTCATGAGAGCTGTGATCTTTAAAGAAACCTTAAACATTTTC 2878
2821 ATAGACTTTTGCACAAATGGCAGAAATGCAGTTAAGTGGTAAAGTGGTGTAGCTTTGA-G 2879
2879 ATAGACTTTTGCACAAATGGCAGAAATGCAGTTAAGTGGTAAAGTGGTGTAGCTTTGAGG 2938
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3059 AGGAGTTGAATCATCAGAGTAAACCTGCCAGTTGCAAAATTTGATAGATAGTGTAGTGAGGA 3118
3060 TTATTAACTCTGAGCAGTATATAGCAATAAANCCCCGGGCATTTATTATTATTATTT 3119
3119 TTATTAACTCTGAGCAGTATATAGCAATAAAGCCCCGGGCATTTATTATTATTATTT 3178
3120 CTTTGTGTACATCTATTACAGTTTTAGAAAAACCAAGCAATTTGTCAAAAAAATAAAAAA 3179
3179 CTTTGTGTACATCTATTACAGTTTTAGAAAAACCAAGCAATTTGTCAAAAAAATAAAAAA 3238
3180 AAAAAAAA 3188

Db 3239 CTATTACAA 3247
RESULT 3
US-09-392-184-1
; Sequence 1, Application US/09392184
; Patent No. 6395889
; GENERAL INFORMATION:
; APPLICANT: Robison, Keith E.
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN
; FILE REFERENCE: 5800-55
; CURRENT APPLICATION NUMBER: US/09/392,184
; CURRENT FILING DATE: 1999-09-09
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 4858
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)...(4858)
; OTHER INFORMATION: reprotolysin (ADAM family of metalloprotease)
; NAME/KEY: misc.feature
; LOCATION: (1)...(4858)
; OTHER INFORMATION: n = A, T, C or G
US-09-392-184-1
Query Match 96.6%; Score 3150.6; DB 3; Length 4858;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 3178; Conservative 0; Mismatches 10; Indels 2; Gaps 2;
QY 1 ATGGGAAACCGGAGCGGGCTCGGGTCTCGAGCTTTGGGCGCGTACCCAGCTGCTG 60
Db 505 ATGGGAAACCGGAGCGGGCTCGGGTCTCGAGCTTTGGGCGCGTACCCAGCTGCTG 564
QY 61 CTGCTCGCGCGCGCTACTGCGCGTGTGCGAGCGCACTCGGGCGCGCCCTCCGAGGAGGAC 120
Db 565 CTGCTCGCGCGCGCTACTGCGCGTGTGCGAGCGCACTCGGGCGCGCCCTCCGAGGAGGAC 624
QY 121 GAGGAGCTAGTGTGCGGAGCTGAGAGCGCGCCCGGGAACAACCGCGCTCCGC 180
Db 625 GAGGAGCTAGTGTGCGGAGCTGAGAGCGCGCCCGGGAACAACCGCGCTCCGC 684
QY 181 CTGACGCGCTTTGACGAGCGAGCTGAGATCTGAGCTGCGGCGCGCCGACAGCAGCTTTTGGCG 240
Db 685 CTGACGCGCTTTGACGAGCGAGCTGAGATCTGAGCTGCGGCGCGCCGACAGCAGCTTTTGGCG 744
QY 241 CCCGGCTTACGCTCCAGAACGTGGGCGCAAAATCCGGGTCCGAGAGCGCGCTTCCGGAA 300
Db 745 CCCGGCTTACGCTTCCAGAACGTGGGCGCAAAATCCGGGTCCGAGAGCGCGCTTCCGGAA 804
QY 301 ACCGACCTGCGGCACTGCTTCTACTCCGGCACCGTGAATGGCGATCCAGCTCGGCTGCC 360
Db 805 ACCGACCTGCGGCACTGCTTCTACTCCGGCACCGTGAATGGCGATCCAGCTCGGCTGCC 864
QY 361 GCCTCAGCGCTTGGAGGCGGTGCGGCGCGCTTCTACTGCTGGGGAGGCGTATTTC 420
Db 865 GCCTCAGCGCTTGGAGGCGGTGCGGCGCGCTTCTACTGCTGGGGAGGCGTATTTC 924
QY 421 ATCCAGCGCTGCGGCGCGGAGCGCTGCGCACCGCGCCCGCGGAGAGAGCGCG 480
Db 925 ATCCAGCGCTGCGGCGCGGAGCGCTGCGCACCGCGCCCGCGGAGAGAGCGCG 984
QY 481 CCGGCACTACAGTTTCCACCTCTGCGGCGGAATCGGAGGCGGCGAGCTAGGCGGCAAG 540
Db 985 CCGGCACTACAGTTTCCACCTCTGCGGCGGAATCGGAGGCGGCGAGCTAGGCGGCAAG 1044
QY 541 TGGGGGTCTGAGCGAGAGCGCGCGCGCTGCGGGAAGCGGAGCGAGAGCGAGGAC 600
Db 1045 TGGGGGTCTGAGCGAGAGCGCGCGCGCTGCGGGAAGCGGAGCGAGAGCGAGGAC 1104

QY 601 GAAGGCACTGAGGGCGAGGACGAAGGGCTCAGTGGTCCCGCAGGACCCGGCACTGCAA 660
Db 1105 GAAGGCACTGAGGGCGAGGACGAAGGGCTCAGTGGTCCCGCAGGACCCGGCACTGCAA 1164
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QY 721 CGCTATGTGAAACCAATGCTTGTGGCAGACCACTGATGCGAGAAATTCACAGCGAGTGT 780
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QY 781 CTAAAGCATTAACCTTCTC-ACGTTGTTTGGTGGCAGCAGATTTGAACAAACCCCGAG 839
Db 1285 CTAAAGCATTAACCTTCTC-ACGTTGTTTGGTGGCAGCAGATTTGAACAAACCCCGAG 1344
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Db 1405 GGGGCGGAAAGTGAACCTCCAAATGCTGCCCTCACTCTGCGGAACTTTTGCAACTGGCAGAA 1464
QY 960 GCAGCAACCCCAACCCAGTGAACCGGATGCGAGCACTATGACACAGCAATTTCTTTTAC 1019
Db 1465 GCAGCAACCCCAACCCAGTGAACCGGATGCGAGCACTATGACACAGCAATTTCTTTTAC 1524
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QY 1380 CCCTGCGACCTCGTACGATGCGGAGGCTGCGAGTGTGATGATGATGATGATGATGATGATG 1439
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QY 1440 ACAGTGCCTGATGAGCAGCAGCAGCAGTGTAGTGTGCTGCTGCTGCTGCTGCTGCTGCTG 1499
Db 1945 ACAGTGCCTGATGAGCAGCAGCAGCAGTGTAGTGTGCTGCTGCTGCTGCTGCTGCTGCTG 2004
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Db 2065 GAAATGCTGTATCAACCGGAGTGTGTGAACAAACCGACAGAAAGCATTTTGTATGCGCC 2124
QY 1620 TTTTTCATGGAAGCTGGGGAATGTGGGGCTTGGGGAGACTGTTTCGAGAAAGCTGCGGTGG 1679
Db 2125 TTTTTCATGGAAGCTGGGGAATGTGGGGCTTGGGGAGACTGTTTCGAGAAAGCTGCGGTGG 2184

1680 AGGAGTCCAGTACAGATGAGGGAATGTGACAAACCCAGTCCCAAGAAATGGAGGGAAGTA 1739
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1740 CTGTGAAGGCAACAGAGTCCGCTACAGATCCCTGTAACTTGAAGGACTGTCCAGACAATAA 1799
1741 |||||
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2246 |||||
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1861 |||||
2365 TGGAGAGTGGGCTGGGTGGAATGGAATCCCAAGTACGCTGCGCTCCCAAGAGAGAG 2424
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2160 ATATCATGATATCATCAATTCATTCAGTGGACCAACATCGAAGTGAACACGGGAA 2219
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2220 CCAGAGGGGATCCAGGAAATGGAGCTTTCTTCCATCAAGCTGCTGTGAGGACACATA 2279
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2280 TATTTCTTAATGGTACTACACTTTGTCCACCTTAGCAAGACATTTATGTACAAAGGTGT 2339
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2905 CAAAGAGCCCTTGACCATCCAGGTTCTTACTGTGGCAATGCCCTTCGACCTTAAATTA 2964
2906 |||||
2460 ATACACCTACTTCTGTAAGAAGAGAAATCTTTCAATGCTATCCCCACTTTTTCAGC 2519
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2520 ATGGGTCTATTGAAGTGGGGGAAATGTTCTAAGTCAATGTAATGGGTGGCAGAGAG 2579
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3086 |||||
2640 GCCAGCCAGCACAGACTTTGTGCAACCATCTCTGCCCAAGTGGCAGCTGGGGAGTG 2699
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3146 |||||
2700 GTCATCATGTTCTAAGACCTTGGGAGGTTTACAAAAAAGAGCTTTGAAGTGTCTGTC 2759
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2760 CCATGATGAGGGGTGTTATCTCATGAGAGCTGTGATCTCTTTAAAGAAACCTTAAACATTT 2819
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2821 |||||
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3326 |||||
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3626 |||||
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3180 |||||
3685 ACTATTACAA 3694
3686 |||||

RESULT 4
US-09-484-970B-58
; Sequence 58, Application US/09484970B
; Patent No. 6426186
; GENERAL INFORMATION:
; APPLICANT: Jones, Karen A.
; APPLICANT: Volkmutch, Wayne
; TITLE OF INVENTION: BONE REMODELING GENES
; FILE REFERENCE: PB-0014 US
; CURRENT APPLICATION NUMBER: US/09/484,970B
; CURRENT FILING DATE: 2000-01-18
; NUMBER OF SEQ ID NOS: 172
; SOFTWARE: PERL Program
; SEQ ID NO 58
; LENGTH: 3706
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6426186 007074.1
; NAME/KEY: unsure
; LOCATION: 3634, 3638-3639, 3642-3643, 3647-3648, 3652, 3654-3658, 3664, 3674, 3681
; OTHER INFORMATION: a, t, c, g, or other
US-09-484-970B-58

Query Match 80.7%; Score 2631.4; DB 3; Length 3706;
Best Local Similarity 99.5%; Pred. No. 0;
Matches 2660; Conservative 0; Mismatches 12; Indels 2; Gaps 2;

518 GGCAGGGCGAGTGTAGCGGCGAGTGTGGGCGTGTGGAGCAGCAGCCCGGCGACTGGGA 577
519 |||||
578 AAGCCGAGACCCGAGACGAGGAGGAGCTGAGGGCGAGGACGAGGAGGCGCTCAGTGTGT 637
579 |||||
61 AAGCCGAGACCCGAGACGAGGAGGAGTGTGGGCGAGGAGCAGGAGGCGCTCAGTGTGT 120
62 |||||
638 GGCAGGAGACCCGCGACTGTGAGGCGGTAGGACGCCCAAGGAACTGGAAGCATAGAA 697
639 |||||
121 CGCCGAGAGACCCGCGACTGTGAGGCGGTAGGACGCCCAAGGAACTGGAAGCATAGAA 180
122 |||||

Qy	698	AGAAGCGATTTTGTGTCAGTCAACCGCTATGCTGGAACCAATGCTTGTGGCAGACCACTCGA	757
Dd	181	AGAAGCGATTTTGTGTCAGTCAACCGCTATGCTGGAACCAATGCTTGTGGCAGACCACTCGA	240
Qy	758	TGGCAGAAATTCACCGCAGTGGTCTAAAGCAATTAACCTTCTCAAGTGTGTTTTCGGTGGCAG	817
Dd	241	TGGCAGAAATTCACCGCAGTGGTCTAAAGCAATTAACCTTCTCAAGTGTGTTTTCGGTGGCAG	300
Qy	818	CCAGATTTGTAACAAACACCCAGCAATTCGTAATTCAGTTAGCTCTGGTGGTGAAGATCT	877
Dd	301	CCAGATTTGTAACAAACACCCAGCAATTCGTAATTCAGTTAGCTCTGGTGGTGAAGATCT	360
Qy	878	TGGTCTATCCACGATGAACAGAGGGGCGGAAGTGACCTCCAATGCTGCCCTCACTCTGC	937
Dd	361	TGGTCTATCCACGATGAACAGAGGGGCGGAAGTGACCTCCAATGCTGCCCTCACTCTGC	420
Qy	938	GGAACTTTTGCACCTGSCAGAGCAGCAACACCCACCACTGACCGGATGCGAGACAT	997
Dd	421	GGAACTTTTGCACCTGSCAGAGCAGCAACACCCACCACTGACCGGATGCGAGACAT	480
Qy	998	ATGACACAGCAATTTCTTTTACACAGACAGCACTTGTGTGGTCCAGACATGTGATCTC	1057
Dd	481	ATGACACAGCAATTTCTTTTACACAGACAGCACTTGTGTGGTCCAGACATGTGATCTC	540
Qy	1058	TTGGGATGGCTGATGTTGGAACTGTGTGATCCGACAGCAAGCTGCTCCGTCATAGAAG	1117
Dd	541	TTGGGATGGCTGATGTTGGAACTGTGTGATCCGACAGCAAGCTGCTCCGTCATAGAAG	600
Qy	1118	ATGATGGTTTTACAGCTGCTTCCACACAGCCCAATGAATAGGCCAGCTGTTTAAACATGC	1177
Dd	601	ATGATGGTTTTACAGCTGCTTCCACACAGCCCAATGAATAGGCCAGCTGTTTAAACATGC	660
Qy	1178	CACATGATGACAAAGCAGTGGCCAGCTTAAATGCTGTGAACAGGATTTCCACATGA	1237
Dd	661	CACATGATGACAAAGCAGTGGCCAGCTTAAATGCTGTGAACAGGATTTCCACATGA	720
Qy	1238	TGGGCTCAATGCTTCCAACTGACACACAGCCAGCTTGGTCTCTTCGAGTGCCTTACA	1297
Dd	721	TGGGCTCAATGCTTCCAACTGACACACAGCCAGCTTGGTCTCTTCGAGTGCCTTACA	780
Qy	1298	TGATTAATCATTTCTGGATAATGGTCAATGGGGAATGTTTGTAGGACCAAGCCTCAGAAATC	1357
Dd	781	TGATTAATCATTTCTGGATAATGGTCAATGGGGAATGTTTGTAGGACCAAGCCTCAGAAATC	840
Qy	1358	CCATACAGCTCCACAGCGATCTCCCTGGCAGCTCTGTACGATGCCAAACCGGAGTGGCCAGT	1417
Dd	841	CCATACAGCTCCACAGCGATCTCCCTGGCAGCTCTGTACGATGCCAAACCGGAGTGGCCAGT	900
Qy	1418	TTACATTTGGGGAGGACTCCAAACACTGCTGATGACGACGACATGTAGCACCTTGT	1477
Dd	901	TTACATTTGGGGAGGACTCCAAACACTGCTGATGACGACGACATGTAGCACCTTGT	960
Qy	1478	GGTGTACCGGCACCTCTGGTGGGTGCTGTGTGTCAAAACCAACACTTCCCGTGGGCGG	1537
Dd	961	GGTGTACCGGCACCTCTGGTGGGTGCTGTGTGTCAAAACCAACACTTCCCGTGGGCGG	1020
Qy	1538	ATGGCACAGCTGTGGAGAGGGAATGGTGTATCAACGGCAAGTGTGAGCAAAACCG	1597
Dd	1021	ATGGCACAGCTGTGGAGAGGGAATGGTGTATCAACGGCAAGTGTGAGCAAAACCG	1080
Qy	1598	ACAGAAAGCATTTTGTATACGCTTTTCAATGGAAGCTGGGGAATGTGGGGGCTTTGGGAG	1657
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Qy	1658	ACTGTTCCAGAACCTGGCGTGGAGGAGTCCAGTACACGATGAGGGAATGTGACAAACCCAG	1717
Dd	1141	ACTGTTCCAGAACCTGGCGTGGAGGAGTCCAGTACACGATGAGGGAATGTGACAAACCCAG	1200
Qy	1718	TCCAAAGAAATGGAGGGAAGTACTGTGAGGCAACCGATGCGCTACAGATCTCTGTAACC	1777
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Qy	1778	TTGAGGACTGTCCAGACAATAATGGAAAAACCTTTTAGAGAGGAACAATGTGAAGCACACA	1837
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Qy	1838	ACGAGTTTTCAAAAGCTTCTCTTTGGGAGTGGGCTCGCGTGGGAATGGATTTCCCAAGTACG	1897
Dd	1321	ACGAGTTTTCAAAAGCTTCTCTTTGGGAGTGGGCTCGCGTGGGAATGGATTTCCCAAGTACG	1380
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Dd	1381	CTGGCCTCTCACCAAGGACAGGTGCAAGCTCATCTGCCAAGCCAAGGCAATTTGGGTACT	1440
Qy	1958	TCCTGTTTTGACGCCCAAGTTGTAGATGGTACTCATGTAGTCCAGATTTCCACCTCTG	2017
Dd	1441	TCCTGTTTTGACGCCCAAGTTGTAGATGGTACTCATGTAGTCCAGATTTCCACCTCTG	1500
Qy	2018	TCCTGTCGAAGGACAGTGTGTAAGAGCTGTTGTATCGCATCATAGACTCCAAAAGA	2077
Dd	1501	TCCTGTCGAAGGACAGTGTGTAAGAGCTGTTGTATCGCATCATAGACTCCAAAAGA	1560
Qy	2078	AGTTTGTATAAATGCTGGTGTGTTGGGGGGAATGGATCTACTTGTAAAAAATATCAGGAT	2137
Dd	1561	AGTTTGTATAAATGCTGGTGTGTTGGGGGGAATGGATCTACTTGTAAAAAATATCAGGAT	1620
Qy	2138	CAGTTACTAGTGCAAAACCTGGATATCATGATATCATCAATTCCAACTGGAGCCACCA	2197
Dd	1621	CAGTTACTAGTGCAAAACCTGGATATCATGATATCATCAATTCCAACTGGAGCCACCA	1680
Qy	2198	ACATCGAAGTGAACAGCGGAAACAGAGGGGATCCAGGAACAAT-GGCAGCTTCTTTGCC	2256
Dd	1681	ACATCGAAGTGAACAGCGGAAACAGAGGGGATCCAGGAACAAT-GGCAGCTTCTTTGCC	1740
Qy	2257	ATCAAAAGCTCTCATGGCACATATATTTCTTAATGGTGACTACACTTTTGTCCACTTAGAG	2316
Dd	1741	ATCAAAAGCTCTCATGGCACATATATTTCTTAATGGTGACTACACTTTTGTCCACTTAGAG	1800
Qy	2317	CAAGACATTTATGTACAAAGGTGTGTTGAGGTACAGCGGCTCTCTGGGGCAATGGAA	2376
Dd	1801	CAAGACATTTATGTACAAAGGTGTGTTGAGGTACAGCGGCTCTCTGGGGCAATGGAA	1860
Qy	2377	AGAACTCGAGCTTTAGCCCTCTCAAGAGCCCTTGACCATCCAGGTTCTTACTGTGGGC	2436
Dd	1861	AGAACTCGAGCTTTAGCCCTCTCAAGAGCCCTTGACCATCCAGGTTCTTACTGTGGGC	1920
Qy	2437	AATGCCCTTCGACTTAAATTAACACCTACTTCTGTAAGAGGAAGAAGGAATCTTTC	2496
Dd	1921	AATGCCCTTCGACTTAAATTAACACCTACTTCTGTAAGAGGAAGAAGGAATCTTTC	1980
Qy	2497	AATGCTATCCCACTTTTTCAGCATGGGTCAATGAAGTGGGGCGAATGTTCTTAAGTCA	2556
Dd	1981	AATGCTATCCCACTTTTTCAGCATGGGTCAATGAAGTGGGGCGAATGTTCTTAAGTCA	2040
Qy	2557	TGTGAATTTGGTGGCAGAGAGACTGTTAGATGCCGAGACATTAATGGACAGCTGCT	2616
Dd	2041	TGTGAATTTGGTGGCAGAGAGACTGTTAGATGCCGAGACATTAATGGACAGCTGCT	2100
Qy	2617	TCCGAGTGTGCAAAAGGAAGTGAAGCCAGCAGCAGACCTTGTGAGACCATCTTTC	2676
Dd	2101	TCCGAGTGTGCAAAAGGAAGTGAAGCCAGCAGCAGACCTTGTGAGACCATCTTTC	2160
Qy	2677	CCCCAGTGGCAGCTGGGGGAGTGGTCAATGTTCTTAAGACTCTGTGGGAAGGGTTACAA	2736
Dd	2161	CCCCAGTGGCAGCTGGGGGAGTGGTCAATGTTCTTAAGACTCTGTGGGAAGGGTTACAA	2220
Qy	2737	AAAAGAGCTTGAAGTCTCTGCTCCCATGATGGGGGTGTTATCTCATGAGCTGTGAT	2796
Dd	2221	AAAAGAGCTTGAAGTCTCTGCTCCCATGATGGGGGTGTTATCTCATGAGCTGTGAT	2280
Qy	2797	CCTTTAAAGAAACCTTAAACATTTTCATAGACTTTTTCACAATGGCAGGAATGAGTTAAGTG	2856
Dd	2281	CCTTTAAAGAAACCTTAAACATTTTCATAGACTTTTTCACAATGGCAGGAATGAGTTAAGTG	2340
Qy	2857	GTTTTAAGTGGTGTAGCTTTGA-GGCAAGGCAAAAGTGAAGGAGGCTGCTGCAGGGAAG	2915

Db 2341 GTTAAAGTGGTGTAGCTTTGAGGCAAGCGCAAGTGGAGGGCTGGTCAGGGAAAG 2400
QY 2916 CAAAGAGGCTGGAGGATCCAGGATATCTTGCAGTAACACAGTGAGGTGTATCAGTAAGG 2975
Db 2401 CAAAGAGGCTGGAGGATCCAGGATATCTTGCAGTAACACAGTGAGGTGTATCAGTAAGG 2460
QY 2976 TGGGATTATGGGGGTAGATAGAAAAGGCTTGAATCATCAGAGTAACCTGCCAGTTGCAA 3035
Db 2461 TGGGATTATGGGGGTAGATAGAAAAGGCTTGAATCATCAGAGTAACCTGCCAGTTGCAA 2520
QY 3036 ATTTGATAGGATAGTTAGTGAGGATTTATTAACCTCTGAGCAGTGATATAGCATATAAAN 3095
Db 2521 ATTTGATAGGATAGTTAGTGAGGATTTATTAACCTCTGAGCAGTGATATAGCATATAAAG 2580
QY 3096 CCCCGGCAATATATATATATATTTCTTTTGGTTACATCTATTAACAAGTTAGAAAAACAA 3155
Db 2581 CCCCGGCAATATATATATATATTTCTTTTGGTTACATCTATTAACAAGTTAGAAAAACAA 2640
QY 3156 AGCAATTGTCAAAAAAGGCTTGAATCATCAGAGTAACCTGCCAGTTGCAA 3189
Db 2641 AGCAATTGTCAAAAAAGGCTTGAATCATCAGAGTAACCTGCCAGTTGCAA 2674

RESULT 5

US-09-445-023A-2
; Sequence 2, Application US/09445023A
; Patent No. 658588
; GENERAL INFORMATION:
; APPLICANT: Hirose, Kunitaka
; APPLICANT: Inoguchi, Biiji
; APPLICANT: Hakezaki, Michinori
; APPLICANT: Ishioka, Keiko
; APPLICANT: Ishida, Yukako
; APPLICANT: Matsushima, Kouji
; APPLICANT: Kuno, Kouji
; TITLE OF INVENTION: Human ADAMTS-1 protein, gene encoding the same, pharmaceutical
; FILE OF INVENTION: composition and method of immunologically analyzing human ADAMTS
; FILE REFERENCE: Q57092
; CURRENT APPLICATION NUMBER: US/09/445,023A
; CURRENT FILING DATE: 1999-12-03
; PRIOR APPLICATION NUMBER: JP 9-160422
; PRIOR FILING DATE: 1997-06-03
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 2184
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: exon
; LOCATION: (1)..(2184)
US-09-445-023A-2

Query Match 65.4%; Score 2131.6; DB 4; Length 2184;
Best Local Similarity 99.1%; Pred. No. 0;
Matches 2143; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

QY 692 TAAGAAAGACGATTTGTGTCCAGTCAACCGCTATGTGAAACCAATGCTTGTGGCAGACC 751
Db 23 TTAGGAAGAAGCGATTTGTGTCCAGCCCGCTATGTGAAACCAATGCTTGTGGCAGACC 82
QY 752 AGTCGATGCGAGATTTCCAGCGGAGTGGTCTAAGGATTTACCTTCTCAGCTTTGTTTCGG 811
Db 83 AGTCGATGCGAGATTTCCAGCGGAGTGGTCTAAGGATTTACCTTCTCAGCTTTGTTTCGG 142
QY 812 TGGCAGCCAGATTTGTACAAACACCCAGCATTTCTGTAATTCAGTTAGCTTGGTGGTGA 871
Db 143 TGGCAGCCAGATTTGTACAAACACCCAGCATTTCTGTAATTCAGTTAGCTTGGTGGTGA 202
QY 872 AGATCTTGTCATCCACGATGAACAGAGGGGCGGAAGTGACCTCCAATGTCGCCCTCA 931
Db 203 AGATCTTGTCATCCACGATGAACAGAGGGGCGGAAGTGACCTCCAATGTCGCCCTCA 262

QY 932 CTCTCGGNACTTTTGGCACTGGCAGAGCAGCAAAACCCAGTGCACCGGGATGCAG 991
Db 263 CTCTCGGNACTTTTGGCACTGGCAGAGCAGCAAAACCCAGTGCACCGGGATGCAG 322
QY 992 AGCACTATGACACAGCAATTTCTTTTCCACAGACAGGACTTGTGTGGGTCCCAGACATGTG 1051
Db 323 AGCACTATGACACAGCAATTTCTTTTCCACAGACAGGACTTGTGTGGGTCCCAGACATGTG 382
QY 1052 ATACTCTTGGGATGGCTGATGTGGAACTGTGTGTGATCCGAGCAGAGCTGCTCCGTCA 1111
Db 383 ATACTCTTGGGATGGCTGATGTGGAACTGTGTGTGATCCGAGCAGAGCTGCTCCGTCA 442
QY 1112 TAGAAGATGATGGTTTACAGCTGCTTCCACACAGCCCATCAATTTAGGCCACGTGTTTA 1171
Db 443 TAGAAGATGATGGTTTACAGCTGCTTCCACACAGCCCATCAATTTAGGCCACGTGTTTA 502
QY 1172 ACATGCCACATGATGATGCAAAAGCAGTGTGCCAGGCTTTAATGTTGTGAACACAGGATTC 1231
Db 503 ACATGCCACATGATGATGCAAAAGCAGTGTGCCAGGCTTTAATGTTGTGAACACAGGATTC 562
QY 1232 ACATGATGCGTCAATGTCTTCCAACTGTGGAACACAGCAGCCTTGGTCTCTTGTGAGTG 1291
Db 563 ACATGATGCGTCAATGTCTTCCAACTGTGGAACACAGCAGCCTTGGTCTCTTGTGAGTG 622
QY 1292 CCTACATGATACATCATTTCTGGATTAATGTCATGGGGAATGTTTGTGGCAACAGCCTC 1351
Db 623 CCTACATGATTAATCATTTCTGGATTAATGTCATGGGGAATGTTTGTGGCAACAGCCTC 682
QY 1352 AGAATCCCATACAGCTCCAGGCGATCTCCCTGGCACCTCTGTCAGATGCAACCGGCACT 1411
Db 683 AGAATCCCATACAGCTCCAGGCGATCTCCCTGGCACCTTGTACGATGCCAACCGGCACT 742
QY 1412 GCCAGTTTACATTTGGGGAGGACTCTCAAACTGCTGCTGATGAGCCAGCAGCATGTAGCA 1471
Db 743 GCCAGTTTACATTTGGGGAGGACTCTCAAACTGCTGCTGATGAGCCAGCAGCATGTAGCA 802
QY 1472 CCTGTGTGTACCGGCACTCTCTGTGGGTGCTGTGTGTCAGAACCAAACTTCCCTT 1531
Db 803 CCTGTGTGTACCGGCACTCTCTGTGGGTGCTGTGTGTCAGAACCAAACTTCCCTT 862
QY 1532 GGGCGGATGGCACACAGCTGTGGAGAGGGAATGTTGTATCAACCGCAAGTGTGTGAACA 1591
Db 863 GGGCGGATGGCACACAGCTGTGGAGAGGGAATGTTGTATCAACCGCAAGTGTGTGAACA 922
QY 1592 AAACCGACAGAAAGCATTTTGTAGCCCTTTTCATGGAAGCTGGGGAATGTGGGGCCTT 1651
Db 923 AAACCGACAGAAAGCATTTTGTAGCCCTTTTCATGGAAGCTGGGGAATGTGGGGCCTT 982
QY 1652 GGGGAGACTGTTTCGAGAACGTCGGTGGAGGAGTCCAGTACACGATGAGGGAATGTGACA 1711
Db 983 GGGGAGACTGTTTCGAGAACGTCGGTGGAGGAGTCCAGTACACGATGAGGGAATGTGACA 1042
QY 1712 ACCCAGTCCCAGAAATGGAGGAAAGTACTGTGAAGGCAAAACAGTGTGCTACAGATCT 1771
Db 1043 ACCCAGTCCCAGAAATGGAGGAAAGTACTGTGAAGGCAAAACAGTGTGCTACAGATCT 1102
QY 1772 GTAACTTGGAGACTGTCCAGACATTAATGGAAGAAACCTTTAGAGAGGAAACATGTGAAG 1831
Db 1103 GTAACTTGGAGACTGTCCAGACATTAATGGAAGAAACCTTTAGAGAGGAAACATGTGAAG 1162
QY 1832 CACACAAAGGATTTTCAAAAGCTTCTTCTTGGGAGTGGGCTCGGTGGGAATGGATTTCCA 1891
Db 1163 CACACAAAGGATTTTCAAAAGCTTCTTCTTGGGAGTGGGCTCGGTGGGAATGGATTTCCA 1222
QY 1892 AGTACGCTGGCTCTCAACAAAGGACAGGTCAAGCTCACTGTGCCAAGCAAGGCAATG 1951
Db 1223 AGTACGCTGGCTCTCAACAAAGGACAGGTCAAGCTCACTGTGCCAAGCAAGGCAATG 1282
QY 1952 GCTACTTCTTCTGTTTGGAGCCCAAGGTTGTAGATGTTACTCCATGTAGCCAGATTTCCA 2011
Db 1283 GCTACTTCTTCTGTTTGGAGCCCAAGGTTGTAGATGTTACTCCATGTAGCCAGATTTCCA 1342

QY 2012 CCTCTGTCTGTGTCAGGACAGTGTGTAAAGCTGGTGTGATCGCATCATAGACTCCA 2071
Db 1343 CCTCTGTCTGTGTCAGGACAGTGTGTAAAGCTGGTGTGATCGCATCATAGACTCCA 1402
QY 2072 AAAAGAAATTTGATAATGTGGTGTTCGGGGGAAATGATCTACTTGTAAAAAATAT 2131
Db 1403 AAAAGAAATTTGATAATGTGGTGTTCGGGGGAAATGATCTACTTGTAAAAAATAT 1462
QY 2132 CAGGATCAGTACTTAGTGCAAAACCTGGATATCATGATATCATCACAATTTCCAACTGGAG 2191
Db 1463 CAGGATCAGTACTTAGTGCAAAACCTGGATATCATGATATCATCACAATTTCCAACTGGAG 1522
QY 2192 CCACCAATCGAAGTGAACACAGCGGAACAGAGGGGATCCAGGAACAATGGCAGCTTTC 2251
Db 1523 CCACCAATCGAAGTGAACACAGCGGAACAGAGGGGATCCAGGAACAATGGCAGCTTTC 1582
QY 2252 TTGGCATCAAGCTGTGATGGGCACATATATTTCTTAATGGTGACTACACTTTGTCCACCT 2311
Db 1583 TTGGCATCAAGCTGTGATGGGCACATATATTTCTTAATGGTGACTACACTTTGTCCACCT 1642
QY 2312 TAGAGCAAGACATTTATGTACAAAGGTGTGTCTTTGAGGTACAGCGGCTCTCTCGCGCAT 2371
Db 1643 TAGAGCAAGACATTTATGTACAAAGGTGTGTCTTTGAGGTACAGCGGCTCTCTCGCGCAT 1702
QY 2372 TGGAAAGAAATTCGAGCTTTAGCCCTCTCAAAGAGCCCTTTGACCATCCAGGTTCTTACTG 2431
Db 1703 TGGAAAGAAATTCGAGCTTTAGCCCTCTCAAAGAGCCCTTTGACCATCCAGGTTCTTACTG 1762
QY 2432 TGGGCAATGCCCTTCGACCTTAAATTAATTAACACCTACTTCTGTTAAGAAAGAGGAAT 2491
Db 1763 TGGGCAATGCCCTTCGACCTTAAATTAATTAACACCTACTTCTGTTAAGAAAGAGGAAT 1822
QY 2492 CTTTCAATGTATCCCACTTTTTCAGCATGGGTCAATTGAAGAGTGGGGGAAATGTTCTA 2551
Db 1823 CTTTCAATGTATCCCACTTTTTCAGCATGGGTCAATTGAAGAGTGGGGGAAATGTTCTA 1882
QY 2552 AGTCATGTGAATTTGGGTTGGCAGAGAAGTGTGTAGAAATGCCAGACATTAATGGACAGC 2611
Db 1883 AGTCATGTGAATTTGGGTTGGCAGAGAAGTGTGTAGAAATGCCAGACATTAATGGACAGC 1942
QY 2612 CTGCTCCGAGTGTGAAAGAAAGTGAAGCCAGCCAGCAGACAGACTTGTGCGAGACCATC 2671
Db 1943 CTGCTCCGAGTGTGAAAGAAAGTGAAGCCAGCCAGCAGACAGACTTGTGCGAGACCATC 2002
QY 2672 CCTGCCCCAGTGCAGCTGGGGAGTGTGTCATCATGTTCTTAAGACCTGTGGGAAGGTT 2731
Db 2003 CCTGCCCCAGTGCAGCTGGGGAGTGTGTCATCATGTTCTTAAGACCTGTGGGAAGGTT 2062
QY 2732 AAAAAAAGAGCTTGAAGTGTCTGTCCCATGATGGAGGGGTGTTATCTCATGAGAGCT 2791
Db 2063 AAAAAAAGAGCTTGAAGTGTCTGTCCCATGATGGAGGGGTGTTATCTCATGAGAGCT 2122
QY 2792 GTGATCCTTTAAAGAAACCTTAAACATTTATAGACTTTTGGCAATGGCGAATGCAAGTT 2851
Db 2123 GTGATCCTTTAAAGAAACCTTAAACATTTATAGACTTTTGGCAATGGCGAATGCAAGTT 2182
QY 2852 AA 2853
Db 2183 AA 2184

RESULT 6
US-09-445-023A-13
; Sequence 13, Application US/09445023A
; Patent No. 6565858
; GENERAL INFORMATION:
; APPLICANT: Hirose, Kunitaka
; APPLICANT: Inoguchi, Eiji
; APPLICANT: Hakozaki, Michinori
; APPLICANT: Ishioka, Keiko
; APPLICANT: Matsushima, Kouji
; APPLICANT: Kuno, Kouji

; TITLE OF INVENTION: Human ADAMTS-1 protein, gene encoding the same, pharmaceutical
; FILE REFERENCE: 057092
; CURRENT APPLICATION NUMBER: US/09/445,023A
; CURRENT FILING DATE: 1999-12-03
; PRIOR FILING DATE: 1999-12-03
; PRIOR FILING DATE: 1997-06-03
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 13
; LENGTH: 2184
; TYPE: DNA
; ORGANISM: Mus sp.
; FEATURE:
; NAME/KEY: exon
; LOCATION: (1)..(2184)
US-09-445-023A-13

Query Match 50.8%; Score 1655; DB 4; Length 2184;
Best Local Similarity 84.9%; Pred. No. 0;
Matches 1853; Conservative 0; Mismatches 330; Indels 0; Gaps 0;
QY 671 AGCCCAAGCACTGGAGCATATGAAGAGCGATTTGTGTCCAGTCCCGCTATCTGG 730
Db 2 AGCCATCAGGACCCAGGAAGCATTAAGGAAGCGATTTGTGTCCAGCCCGCTATCTGG 61
QY 731 AAACCATGCTGTGGCAGACCACTCGATGGCAGAAATTCACGCGCAGTGGTCTTAAGCAAT 790
Db 62 AAACCATGCTGTGTGACCTCATGCGCCGACTTCCAGCGCAGCGGTCTTAAGCAAT 121
QY 791 ACCTTCTCAGCTTTGTTTGGTGGCAGCCAGATTTGTATCAAAACACCCAGCATTCGTAAAT 850
Db 122 ACCTTCTCAGCTTTGTTTGGTGGCAGCCAGATTTGTATCAAAACACCCAGCATTCGTAAAT 181
QY 851 CAGTTAGCCTGGTGGTGAAGATCTTGTGTATCCAGCATGACAGAGGGCCGAG 910
Db 182 CAATTAGCCTGGTGGTGAAGATCTTGTGTATATACAGGAGCAGAGGACAGAG 241
QY 911 TGACCTTCAATGTGCGCTCACTCTGCGGAATCTTTTGCAACTGGCAGAGCAGCAAC 970
Db 242 TTACCTTCAATGAGCTCTCACCTTTCGGAATTTCTGCAGCTGGCAGAAACACACA 301
QY 971 CACCCAGTGAACCGGATGACAGACATATGACAGCAATTTCTTTTCCAGACAGACT 1030
Db 302 GCCCAGTGAACCGGATCCAGAGCACTATGACATGCAATTTCTGTTCCAGACAGACT 361
QY 1031 TGTGTGGTCCAGACATGTGATCTTGGGATGGCTGTGGAATCTTGGAACTGTGTGATC 1090
Db 362 TATGTGGCTCCCAACAGTGTGACACTCTCGGAATGGCAGATTTTGGAACTGTGTGACC 421
QY 1091 CGAGCAGAGCTGCTCGTCTATAGAAGATGATGTTTACAAGCTGCCTTCCACACAGCCC 1150
Db 422 CAGCAGGAGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 481
QY 1151 ATGAATTTAGGCCACGTGTTTAAATGCAATGCAATGCAATGCAATGCAATGCAATGCAAT 1210
Db 482 ATGAATTTAGGCCACGTGTTTAAATGCAATGCAATGCAATGCAATGCAATGCAATGCAAT 541
QY 1211 ATGCTGTGAACAGGATTTCCACATGATGGCTCAATGCTTCCAACTGGACACAGCC 1270
Db 542 ATGCTGTGAGTGGCGATTTCTCATGTATGGCTCGATGCTCTCCAGCTTATAGCATAGCC 601
QY 1271 AGCTTGGTCTCTTGGAGTGGCTTACATGATTAATCATTTCTGGATAAATGGTCAATGGGG 1330
Db 602 AGCTTGGTCACTTGGAGTGGCTTACATGATGATGATGATGATGATGATGATGATGATGAT 661
QY 1331 AATGTTTGTAGTGAACAGCTTCCAGATCCCATGATGCTCCAGCGGATCTCCCTGGCACT 1390
Db 662 AATGTTTGTAGTGAACAGCTTCCAGATCCCATGATGCTCCCTTCTGATCTTCCCGGTACCT 721
QY 1391 CGTACGATGCAACCGGAGTGGCAATTTACATTTGGGGAGGACTCCAAACACTGCGCTG 1450
Db 722 TGTACGATGCAACCGGAGTGGCAATTTACATTTCCGAGAGGAAATCCAAAGCACTGCGCTG 781

1451 ATGCAGCCAGCACATGTAGCACCTTGTGTGTACCGGCACCTCTGGTGGGGTCTGTGTGT 1510
Db |||||
782 ATGCAGCCAGCACATGTACTACCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 841
1511 GTCAAAACCAAAACATTTCCCGTGGGGGATGGGCACAGCTGTGTGTGTGTGTGTGTGTGTGT 1570
Db |||||
842 GCCAAACCAAAACATTTCCCTTGGGCAGATGGGCACAGCTGTGTGTGTGTGTGTGTGTGTGT 901
1571 TCAGCGGCAAGT 1630
Db |||||
902 TCAGTGGCAAGT 961
1631 GCTGGGGAATGTGGGGCTTGGGAGACTGTTCGAGACCTGTGGGAGAGTGTGGGAGTGTGGG 1690
Db |||||
962 GCTGGGGAATGTGGGGCTTGGGAGACTGTTCGAGACCTGTGGGAGAGTGTGGGAGTGTGGG 1021
1691 ACAGATGAGGGAATGT 1750
Db |||||
1022 ACACATGAGGAATGT 1081
1751 AACGATGGGCTACAGATCTGT 1810
Db |||||
1082 AACGATGGGCTACAGATCTGT 1141
1811 TTAGAGGGAACATGT 1870
Db |||||
1142 TCAGAGAGGAGAGT 1201
1871 CTGGGCTGGAATGT 1930
Db |||||
1202 CCACTGTAGT 1261
1931 TGTGCAAGCCAAAGGATGT 1990
Db |||||
1262 CTTGTGAAGCCAAAGGATGT 1321
1991 CTCCATGTAGCCAGATTTCCACTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2050
Db |||||
1322 CTCCCTGTAGT 1381
2051 GTGATCGCATATAGATCTCAAAAGAGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2110
Db |||||
1382 GTGATCGCATATAGATCTCAAAAGAGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1441
2111 GATCTACTGT 2170
Db |||||
1442 GTTCCACATGTGAAGAGATGT 1501
2171 TCATCACAATTCCTGT 2230
Db |||||
1502 TTGTCAATTCCTGT 1561
2231 CCAGGAACATGT 2290
Db |||||
1562 CCAGGAACATGT 1621
2291 GTGACTACTGT 2350
Db |||||
1622 GAACTTCACTGT 1681
2351 ACAGCGGCTCTGT 2410
Db |||||
1682 ACAGT 1741
2411 TGACCATCAGGTTCTTACTGTGGGCAATGCCCTTGCAGCTAAATTAATAACACTACT 2470
Db |||||
1742 TAAACCATCAGGTTCTTACTGTGGGCAATGCCCTTGCAGCTAAATTAATAACACTACT 1801
2471 TCGTAAAGAGAGAGGATCTTCAATGTCTATCCCACTTTTTCAGCATGGGTCTATG 2530
Db |||||
1802 TTATGAAGAGAGAGAGATCTTCAATGTCTATCCCACTTTTTCAGCATGGGTCTATG 1861

2531 AAGATGGGGGGAATGTTCTAAGTCTATGTGAATTTGGGTTGGCAGAGAGACTGGTAGAAT 2590
Db |||||
1862 AAGATGGGGGGAATGTTCTAAGTCTATGTGAATTTGGGTTGGCAGAGAGACTGGTAGAAT 1921
2591 GCCGAGACATTAATGGACAGCCTGCTTCGAGTGTGCAAAAGAGTGAAGCCAGCCAGCA 2650
Db |||||
1922 GCAGAGACATTAAGCGACACCTGCTTCGATGTGCAAAAGAGTGAAGCCAGCCAGTA 1981
2651 CCAGACCTTGTGCAGACCATCTCTGCCAGTGTGCAAAAGAGTGAAGCCAGCCAGTA 2710
Db |||||
1982 CCAGACCTTGTGCAGACCATCTCTGCCAGTGTGCAAAAGAGTGAAGCCAGCCAGTA 2041
2711 CTAACACCTGTGGGAGGTTTACAAAAGAGTGTGCAAAAGAGTGAAGCCAGCCAGTA 2770
Db |||||
2042 CCAAACTTGGGGAAGGTTTACAAAGAGTGTGCAAAAGAGTGAAGCCAGCCAGTA 2101
2771 GGGTGTATCTCATGAGAGTGTGATCTCTTTTAAAGAACTTAAACATTTTATAGACTTTT 2830
Db |||||
2102 GCTGTGTATCAATGAGAGTGTGATCTCTTTTGAAGAGCAAAAGCATTACATTGACTTTT 2161
2831 GCACATGGCAGATGCCAGTTAA 2853
Db |||||
2162 GCACATGGCAGATGCCAGTTAA 2184

RESULT 7
US-09-369-364A-8
; Sequence 8, Application US/09369364A
; Patent No. 6391610
; GENERAL INFORMATION:
; APPLICANT: Apte, Suneel
; APPLICANT: Hurskainen, Tiina L.
; APPLICANT: Hirohata, Satoshi
; TITLE OF INVENTION: Nucleic Acids Encoding Zinc Metalloproteases
; FILE REFERENCE: 26473/4007/10-30-00
; CURRENT APPLICATION NUMBER: US/09/369,364A
; CURRENT FILING DATE: 1999-08-06
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 3638
; TYPE: DNA
; ORGANISM: Mus musculus ADAMTS-8
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (278)..(2992)
; NAME/KEY: misc.feature
; LOCATION: (3636)
; OTHER INFORMATION: n = T
US-09-369-364A-8

Query Match 20.4%; Score 666.2; DB 3; Length 3638;
Best Local Similarity 56.1%; Pred. No. 1.6e-145;
Matches 1544; Conservative 0; Mismatches 1123; Indels 84; Gaps 12;

56 TGCTGCTGTCTGCCGCGCGCTACTTGGCGTGTGCGACGCACTCGGGGCGCCCTCCGAGG 115
Db |||||
330 TGCAGCTGCCGCGCGCACTCGTCTGCGAGCCCCCGGGCGCGGAACCGGGGCGC 389
116 AGGACGAGAGT 175
Db |||||
390 AGGCTCGAGCTAGT 446
176 TCGGCTCGACCTTTTGCAGCAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 235
Db |||||
447 TCCACTGTCTGCCCTTCGGCCAGGGGTTCTGTCTGGCTTGGCGCTGTGACGCCAGCTTCC 506
236 TGGCGCCCGGCTTTCAGCTTCCAGAACTGTGGGGCGCAAAATCCGGGTCCGAGACGCCCTTC 295
507 TGGCGCCGGAATTCAGATCGAGCGCTTCGGGG-----CTCGAGCGCGGGCGGG 560
296 CGGAACCGACTGTGGGCACTGTCTTCTACTCGGCACCGTGAATGGCGATCCAGCTCGG 355

Db 561 GGAGCCGGGAGCTGCGTGGCTGCTTCTCTGSCACAGTGAATGAGAAACGGGAGTCGC 620
Qy 356 CTGCCGCTCTACGCTCTCGAGGGGCTGCGGGCGCTTCTACCTGCTGGGGAGCGCT 415
Db 621 TGGCGCGATAGCTGTGTCGGGGCTGGAGCGGCTCGTCTTGTCTGGCAGGGGAGGT 680
Qy 416 ATTTCATCAGCGCGCTCGCGCGCAGCGAGCGCTCGCCACCGCGCCGCCAAGGGGAGA 475
Db 681 TCACCATCAGCCACAG--GGCGCTGGGAGCTCCCTGGACACGCTCATCGCTCGAGC 737
Qy 476 AGCGCGGACACACTACAGTTTCCACTCTCGGGCGGAATCGGAGGGGAGCTAGGCG 535
Db 738 GCTGGGGCGGGACAGCGCGCGAAGACCCGGGCTCGCTCGCGCAAGTTTCCCC 797
Qy 536 GCAGCTGCGGGTCTGTGGACGAGCGCCCGCGGACTGGGAAGCGGAGACCGAAGACG 595
Db 798 TCCTCAAGACTGGAGTGGAGGTGGAGTGGGTAAATGGGACGGACAGGAGAGGTG 857
Qy 596 AGGACGAAGGACTGAGGGCGAGGACGAAGGGCTCAGTGGTCCGCGCAGGACCCGGCAC 655
Db 858 ACAACGAAGAGGACAAGAGCAGGACAAGG-----AGGGTTGCTCAAGAGACAGAAG 911
Qy 656 TGCAGCGTAGACAGACGCCACAGGAACCTGGAAGCATAGAAAGACCGAATTTGTCTCCA 715
Db 912 ACTCCCGCAAGTGCCACACCTCTCGGATCCAAACTAGAACCAAGAGGTTTGTCTCG 971
Qy 716 GTCACCGCTATGTGGAACCATCTGTGGCAGACCGATCGATGGCAGGAATTCACGGCA 775
Db 972 AGGCTCGTTCTGTGGAAACACTTCTGGTGGCTGATGGTCCATGGCTCTCTATGGGA 1031
Qy 776 GTGGTCTAAGACATTAACCTTCTCACGTTGTTTTCGGTGGCAGCCAGATTGTACAAACCC 835
Db 1032 CGACCTCGAGAACCATCTCACGGTGTATGTCATGGCAGCCCGAATCTCAAGCAC 1091
Qy 836 CAGCATTCGTAAATTCGTTAGCTGTGTGTGTGAAGATCTTGGTCAATCCAGATGAAC 895
Db 1092 CGAGCATCAGAACTCCGTCAACCTTGTGGTGGTGAAGTGTAAATGTGGAAGAA 1151
Qy 896 AGAAGGGCGGGAAGTGAACCTCAATGCTCCCTCACTCTGCGGAACCTTTGCACTGGC 955
Db 1152 GATGGGGCGGGAAGTGTCCGAACCGGGGGTCACTGCGCACTTCTGCACTGGC 1211
Qy 956 AGAAGCAGCAACACCCACGATGACCGGATGACAGCACTATGACAGCAATCTTT 1015
Db 1212 AACGGCTTTCAACAGCCAGTGACCGCCACCGGAGCACTATGACACTGCCATCTGT 1271
Qy 1016 TCACAGACAGGACTTGTGTGG--GTCCAGACATGTGTATCTCTTGGATGGCTGATG 1072
Db 1272 TCACAGACAGAACTTCTGTGGGAAGGAGAGCAGTGTGACCCCTGGGGATGGCAGAC 1331
Qy 1073 TTGGAATGTGTGATCCGAGCAGAGCTGCTCCGTCATAGAGATGATGGTTTACAAG 1132
Db 1332 TTGGACCACTGTGTACCCCGACAAGAGCTGCTCAGTGATCAAGATGAGGACTGCGAG 1391
Qy 1133 CTGCTTTACCAAGCCCATGAATTAGGCCACGCTGTTTAACTGCCACATGATGATGCAA 1192
Db 1392 CAGCTACACCTGGCCCATGAGTAGGGCAGGTTCTCAGCACTGCCCATGATGATCTTA 1451
Qy 1193 AGCAGTGTCCAGCTTAATGTGTGTGAACAGGATTCCHCATGATGGCGTCAATGCTTT 1252
Db 1452 AGCCCTGTGTGAGATTGTTTGGGCCCATGGGCAAGTACCAATGATGGGCCCATTTCTCA 1511
Qy 1253 CCAACCTGGACCAAGCAGCTGTGTCTCTTGGAGTCTCTATGATTTACATCATTTTC 1312
Db 1512 TCACGTGAACAAGACGCTGCCCTGGTCTCTCTGAGTGTGTCTACTCTCAGAGCTCC 1571
Qy 1313 TGGATAATGTGTATGGGAATGTTTGTATGGAACAGCTTCAGAAATCCCAATCAGCTCCAG 1372
Db 1572 TGGATGATGTTCAGGAGATTGTTCTCTGTGATGCCCCACCTCGCTTCTGCCCTCCCA 1631
Qy 1373 GCGATCTCCCTG-----GCACCTGTGATGATGCAACCGGAGTGCAGTTTACATTG 1426
Db 1632 CAGGCTTCCGGGCCACAGCACCTCTACGAGCTGGACAGAGTGAAGCAGATCTTTG 1691

Qy 1427 GGGAGGACTCCAAACACTGCCCTCTGA-----TGACCCACGACATGTAGCACCTTGTGGT 1480
Db 1692 GGCTGATTTCCGACACTGCCCCCAACACCTCTGTGGAGGACATCTGTCTCAGCTCTGTG 1751
Qy 1481 GTACCGGCACTCTGTGTGGGTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1534
Db 1752 CCGCTCATCGGGATAGTGTAGCCCATTTGGCCACACAAAGAAATGTGTAGCTCTCTCTGG 1811
Qy 1535 CGGATGGCACAGCTGTGTGAGAAAGGAAATGTGTATCAACGGCAAGTGTGTGAACAAA 1594
Db 1812 CTGATGGTACACCTGTGTGGCTTGGGCACTGTGTCTGTGTGTGTGTGTGTGTGTGTGTGT 1871
Qy 1595 CCGACAGAAGCAATTTGTATACGCCCTTTTCAATGAAAGCTGGGAAATGTGTGGGCTTGGG 1654
Db 1872 AGGATGTGAGAAATCCAAAGGCTGTGTAGATGAGACTGGGCTCCCTGGAGACCTCTGGG 1931
Qy 1655 GAGACTTTCGAGAACGTGTGGTGGAGGAGTCCAGTACACGATGAGGAATGTGACAAC 1714
Db 1932 GACAAATGTTTCTCGCACCTGTGTGGAGGGATACAAATCTCGAACCGTGAATGTGATATC 1991
Qy 1715 CAGTCCCAAAGAAATGAGGGAAGTACTGTGAAGGCAAAACGAGTGCCTACAGATCTCTGTA 1774
Db 1992 CAATGCTCAGATGAGGAGATTTTGGCTGGGTGAAGAGTCAAGTACCAATCATGCA 2051
Qy 1775 ACCTTGAGGACTGTCCAGACAAATATGGAAGAACCTTTTGTAGAGGAAACAAATGTGAAGCAC 1834
Db 2052 ACACAGGAAATGTCCA---CCAAACGGAAGAAAGCTTCCGGGAGCAGCAGTGTGAGAAAT 2108
Qy 1835 ACACAGATTTTCAAAGCTTCTTTGGGAGTGGGCTCGGTGGGAATGGAATTTCCCAAGT 1894
Db 2109 ATAATGCCCTACACCACTGACCT---GGATGGAAATTTCTGCACTGGGTCCCCAAGT 2165
Qy 1895 ACCTGGGCTCTCACCAGGACAGGTGCAAGCTCATCTGCCAAGCCAAAGCAATTTGGCT 1954
Db 2166 ATTACAGATGTTCCCGGAGCCGATGCAAGCTGTTTTCAGAGCCCGTGGGAGGATG 2225
Qy 1955 ACTTCTTCTGTTTTCAGAGCCCAAGTTGTAGATGGTATCTCATGTAGCCCAAGATTTCCACT 2014
Db 2226 AGTTCAAAGTGTTTGAAGCTTAAGTGTATCGATGGCACTCTGTGTGGACCGGATACTCTGT 2285
Qy 2015 CTGTCTGTGTGCAAGACAGTGTGTAAAGCTGGTTGTGATCGCATCATAGATCTCCAAA 2074
Db 2286 CCACTCTCGTCCGGGGCAATGTGTTAAGCTGGCTGTGACCATGTGGTGAACCTCACCTA 2345
Qy 2075 AGAAGTTTGTATAATGTGTGTTTGGGGGAAATGATCTACTTGTAAAAAATAATATCAG 2134
Db 2346 AGAAGCTGGAACAATGTGGGTGTGTGGGGCAAGGCACTGTCTGTAGGAGATCTCCG 2405
Qy 2135 GATCAGTTACTAGTGCAAAACCTGGATATCATGATATCATCAATTTCCAACTGGAGCCA 2194
Db 2406 GTTCTTTTCACTTTCAGTTATGGCTATGCTACATGACATTTGTCACTCCAGCTGGTCCCA 2465
Qy 2195 CCAACATCGAAGTGAACAGCGGAAACGAGGGGATCCAGGAACAAATGGCAGCTTTCTTG 2254
Db 2466 CAAACATGTATGTGAACAGCGGAGTCAACCGGGGTGAGAAACGAGGAGCTTACCTGG 2525
Qy 2255 CCATCAAGCTGTGTATGGCACAATATTTCTTAATGTGTACTACACTTTTGTCCACCTTAG 2314
Db 2526 CGCTGAAGACAGCAATGGCAGTACTGTCTCAATGTGTAACTGGCCATCTCTGCCATAG 2585
Qy 2315 AGCAAGACATTTATGTACAAAGGTGTGTCTGTAGGATACAGCGGTCTCTCTGGGGCATGG 2374
Db 2586 AGCAAGACATTTTGGTGAAGGGACCATCTCTGAAGTACAGTGGCTCCATGGCTACCTCTGG 2645
Qy 2375 AAAGAATTCGAGCTTTAGCCCTCTCAAGAGCCCTTGACCATCCAGGCTTCTTACTGTG- 2433
Db 2646 AGCGGCTGCAGAGCTTCCAGGCCCTGCTGAGCCTCTTACAGTACAGCTCTGACTGTGT 2705
Qy 2434 --GGCAATGCCCTTCGACCTTAAATAATACACTTCTCGTAAAGAGAGAGGAAT 2491
Db 2706 CTGTGAGGTCTTCCCTCCAAAGTCAATATACCTTCTTTGTGTCCTCCCAATGACATGGACT 2765

QY 2492 -----CTTTCAATGCTATCCCACTTTT 2515
Db 2766 TCAGCGTCAGAAATAGCAAGGAAGCAACCAACATCATTCAGTCACCTGCTCTG 2825
QY 2516 CAGCATGGGTCAATGAAGAGTGGGCGAATGTTCTAAAGTCATGTGAATTTGGGTGGCAGA 2575
Db 2826 CGGAGTGGGTCTGGGAGACTGGTCTGAATGTCGAGACAGTGCAGAGGTAGCTGGCAGC 2885
QY 2576 GAAGACTGTAGATGCCAGACATTAATGGACAGCTCTCCGAGTGTGCAAGGAAG 2635
Db 2886 GCGGACTGTGAATGCAAGGACCCCTCAGGTCAAGCTCTGACACTGTGATGAGGCTC 2945
QY 2636 TGAAGCCAGCAGCACACACTTGTGACAGACATCCCTGCCCCAGTGGCAGCTGGGG 2695
Db 2946 TGAACCTGAGATGCCAAGCCCTGTGGAAGCAGCCGTGTCCCTCTGATCCCTTGGT 3005
QY 2696 AGTGTGTCATGTTCTAAGACTGTGGGAAGGTTTCAAAAAAGAAAGCT 2746
Db 3006 GGAATCTCTTAGGCTTATGGATTGGGCTACTGGTGTAAACAGACAAAGGT 3056

RESULT 8
US-10-009-332-2
; Sequence 2, Application US/10009332
; Patent No. 6716613
; GENERAL INFORMATION:
; APPLICANT: Yamanouchi Pharmaceutical Co., Ltd.
; APPLICANT: Kazusa DNA Research Institute
; TITLE OF INVENTION: NOVEL METALLOPROTEASE HAVING AGGRECANASE ACTIVITY
; FILE REFERENCE: Q67541
; CURRENT APPLICATION NUMBER: US/10/009,332
; CURRENT FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: JPA Hei 11-321740
; PRIOR FILING DATE: 1999-11-11
; PRIOR APPLICATION NUMBER: JPA 2000-144020
; PRIOR FILING DATE: 2000-05-16
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 2853
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-009-332-2

Query Match 19.3%; Score 629.8; DB 4; Length 2853;
Best Local Similarity 57.1%; Pred. No. 4.8e-137;
Matches 1306; Conservative 0; Mismatches 912; Indels 69; Gaps 6;

QY 187 GCCTTTGACAGCAGCTGGATCTGGAGCTGCGGCCCGACAGCAGCTTTTGGGCGCCGCG 246
Db 175 GCATTTGAGGAGCTTTTACCTACACCTGACCGCCGGATGCTCAGTTCTTGGCTCCGCGC 234
QY 247 TTCAGCTCCAGAACGTGGGGGCGCAATCCGGGTCCGAGACGCGCTTCCGGAACCGAC 306
Db 235 TTCTCCACTGAGCATCTGGGCGTCCCTCCAGGGGCTCACCGGGGGCTC---TTCAGAC 291
QY 307 CTGGCGCACTGCTTACTCCGCGACCGTGAATGGGATCCAGCTCGGCTCGGCGCCCTC 366
Db 292 CTGGCAGCTGCTTCTATTCTGGGACGTGAACCGCGAGCCGAGCTCGTTCGCTGCTG 351
QY 367 AGCCTCTGGAGGGGCTGCGCGCGCTTCTACTGCTGGGGGAGCGGTATTTTCATCCAC 426
Db 352 AGCCTCTGGGGGGCTTCCGCGAGCTTTGGCTACCGAGGCGCGAGTATGTCAATTAGC 411
QY 427 CCGCTGCCCGCCAGCAGCGCTCTGCCACCGCGCCCGCCAGGGGAGAGCGCGCGCA 486
Db 412 CCGCTGCCCAATGTAGCGCGC-CGGCGGCGCAGCGCAACAGCCAGGGGCGCACACCTTCT 470
QY 487 CCACCTACAGTCCACCTCTCGCGGGGGAATCCGCGAGGCGAGCTAGCGCGCACGTCGCG 546
Db 471 CCAGCGCCGGGGTGTTCGGGGCGGGCTTCCGAGACCCCACTCTCTCGCTCGGGGTGCG 530
QY 547 GTCTGGACGACGAGCGCCCGCGCACTGGGAAAGCGGAGACCGAGACGAGGACGAAGGG 606

Db 531 CTCGGGCTGGAACCCCGCCATCTCAGCGGCCCTTGACCCCTTACAGCCGCGCGCGCG 590
QY 607 ACTGAGGGGAGGAGCAAGAGGCTCAGTGGTCCGCGCAGGACCCCGGCACTGCAAGCGGTA 666
Db 591 CTTGCGGGAGAGTCTAGCCGCGCAGGTCTGGGCGC----- 627
QY 667 GGACAGCCCAAGGAACTGGAAGCATAGAAAGAACGATTTGTGTCAGTCAACCGCTAT 726
Db 628 -----GCCAGCGTTTCGTGTCTATCCCGCGGTAC 657
QY 727 GTGGAAACCATCTTGTGGCAGACCATCGATGGCAGAAATCCACGGCAGTGGTCTTAAAG 786
Db 658 GTGGAGACGCTGGTGGTCCGCGACGAGTCAATGTCAGTTCACCGGCGCGACCTGGAA 717
QY 787 CATTACCTTCTCAGCTTGTGTTTCGGTGGCAGCAGATGTACAAACACCCAGCATTCGT 846
Db 718 CATTATCTGCTGACGCTGTGCAACGCGCGCGGACTCTACCGCATCCAGCATCTCTC 777
QY 847 AATTCAAGTTAGCTGTGTGGTGAAGATCTTGTGTCATCCAGATGAACAGAAAGGGCG 906
Db 778 AACCCCATCAATCGTTGTGGTCAAGGTGCTGCTTCTTAGAGATCGTGACTCCGGGCCC 837
QY 907 GAAGTGACCTCCAATGCTGCCCTCACTCTGCGGAACTTTTGAACCTGGCAGAGCAGAC 966
Db 838 AAGGTCAACCGCAATGCGGCCCTGACGCTGCGCAACTTCTGTGCTGGCAGAAAGCTG 897
QY 967 AACCCACCGATGACCGGGATGACAGACACTATGACAGCAATTTCTTTACCAGACAG 1026
Db 898 AACAAAGTGAGTGACAAGCACCCCGAGTACTGGGACACTGCCATCTCTTTCACAGGCG 957
QY 1027 GACTTGTGTGGTCCAGACATGTGATCTCTTGGATGGTGGTGTGGAATGTGTGT 1086
Db 958 GACCTGTGTGGAGCACACACTGTGACACCTTGGGATGGCTGATGTGGGTACCATGTGT 1017
QY 1087 GATCCGAGCAGAAGCTGCTCCGTCTATAGAAGATGATGTTTCAAGCTGCCCTTACCACA 1146
Db 1018 GACCCCAAGAGAAGCTGCTCTGCTATGAGGACGATGGGCTTCCATCAGCCTTCACT 1077
QY 1147 GCCATGAATTAGGCAAGCTGTTTAACTGCCACATGATGATGCAAGCAGTGTGCCAGC 1206
Db 1078 GCCACGAGCTGGGCGCAGTGTTCACATGCCCCATGCAACATGTGAAAGTCTGTGAGGAG 1137
QY 1207 CTTAATGTTGTAACACAGGATTTCCACATGATGGGTCAATGCTTCCAACTGGAGCCAC 1266
Db 1138 GTGTTTGGAGACTCGAGCCAAACACATGATGTCCCAGACCTCATCCAGATCGACCTG 1197
QY 1267 AGCCAGCTTGTCTCTCTTGGAGTGCCTACATGATTAATCATTTCTGATGAATGTGTAT 1326
Db 1198 GCCAACCCCTGCTCAGCCTGCGAGTGTGCTCATCATCCGACTTCTGTCAGCAGCGGCAC 1257
QY 1327 GGGGAATGTTGATGGACAGGCTCAGATCCATACAGTCCAGGCGCATCTCCCTGGC 1386
Db 1258 GGTGATGCTCTCTGGAACCAACCGAGCAAGCCCATCTCCCTGCCGAGAGTCTGCCGGGC 1317
QY 1387 ACCTGCTAGCATGATGCAACCGGAGTGCCTGTTTACATTTGGGGAGGACTTCCAAACACTGC 1446
Db 1318 GCCAGTACACCTGAGCCAGCAGTGGAGCTGGCTTTTGGCGTGGCTTCCAGACCTGT 1377
QY 1447 CCTGATGACGACGACATGATAGCACTTGTGGTGTACCGGCACTCTCTGGTGGGGTGTG 1506
Db 1378 CCTTACATGCAGTAC---TGCAACCAAGCTGTGGTGCACCGGGAAGGCCAAGGACAGATG 1434
QY 1507 GTGTGTCAACCAACACTTCCCGTGGCGGATGCAACAGCTGTGGAGAAAGGAATGG 1566
Db 1435 GTGTGCGAGACCGGCCTTCCCTTGGGCGGATGGACAGCTGTGGCGAGGCAAGCTC 1494
QY 1567 TGTATCAACCGCAAGTGTGTGAACAAACCGACAGAAAGCATTTTGTATAGCCTTTTCAT 1626
Db 1495 TGCTTCAAGGGGCTGCTGTGGAGACACAACTCAA-----CAAGCACAGGTTGGAT 1548
QY 1627 GGAAGCTGGGGAATGTGGGGGCTTGGGGAGACTGTTCAGAACGTCGCGTGGAGAGTC 1686

1549 GGTTCCTGGGCCAAATGGGATCCTATATGGCCCTGCTCGCGCACATGTGTGGGGCGTG 1608
1687 CAGTACACGATGAGGGAATGTGACACCCAGTCCCAAGATGAGGAGTACTGTGAA 1746
1609 CAGCTGGCCAGGAGGAGTGCACCAACCCACCCCTGCCAACCGGGGCAAGTACTGGAG 1668
1747 GGCACAAACGAGTGGCTACAGATCCTGTAACTCTTGAGGACTGTCCAGAC---AATAATGGA 1803
1669 GGAGTGAAGGTGAATACCACTCTGCAACCTGGAGCCCTGCCAGCTCAGCTCCGGA 1728
1804 AAAACCTTTAGAGGAGGAACAAATGTGAAGACACAAAGAGTTTCAAAGCTTCTCTTTGGG 1863
1729 AAGAGCTTCCGGGAGGAGAGTGTGAGGCTTTCAAACCGCTTACAAACACACAGCAGCAACCGG 1788
1864 AGTGGGCTCGGTGGGAGTTCACCAAGTACGTGGGCTTCACCAAGGACAGGTGC 1923
1789 CTCACTCTCGCCGCTGGGATGGGTCGCCAAGTACTCGCGCGTGTCTCCCGGGGCAAGTGC 1848
1924 AAGCTCATCTGCCAAGCACAAGGCAATGGCTACTTCTTCCGTTTTCAGCCCAAGGTTGTA 1983
1849 AAGCTCATCTGCCGAGCAATGGCACTGGCTACTTCTATGTGTGGCACCACCAAGGTGGT 1908
1984 GATGGTACTCCATGTAGCCAGATTTCCACTCTGTCTGTGTGCAAGGACAGTGTGTAATA 2043
1909 GACGGCAGCTGTGCTCTCTGACTCCACCTCGTCTGTGTGCAAGGCAAGTGCATCAAG 1968
2044 GCTGGTGTGATCGCATATAGACTCCAAAGAGTTTGTAAATGTGGTGTGTGGG 2103
1969 GCTGGCTGTGATGGGAACCTGGGCTCCAAAGAGATTCGACAAAGTGTGGG 2028
2104 GGAATGGATCTACTTGTAAATAAATATCAGGATCAGTTACTAGTGCAAAACCTGGATAT 2163
2029 GGAGACAAATAGAGCTGCAAGAGGTGACTGGACTCTTACCAAGCCATGCAATGGCTAC 2088
2164 CATGATATCATCAATTTCAAATCGAGGCCACCAACATCGAAGTGAAGACAGCGGAACAG 2223
2089 AATTTCTGGTGGCCATCCCGCAGGCGCTCAAGCATCGACATCCCGCAGCGCGGTTAC 2148
2224 AGGGATCCAGGACATGCGAGCTTCTTGGCCATCAAGCTGTGATGGCACATATTT 2283
2149 AAAGGGCTGATCGGGGATGCAACTACTCTGCTCTGAAGAACAGCCAAAGGCAAGTACTG 2208
2284 CTTAATGGTACTACACTTTGTTCACCTTAGAGCAAGCAATATGTACAAAGGTGTGTGTC 2343
2209 CTCAACGGGCAATTTCTGGTGTGGCGGTGGAGCGGACCTGTGTGGTGAAGGGCAGTCTG 2268
2344 TTGAGGTACAGCGGCTCTCTGCGGCATGTGAAGAAATTCGACGTTTTCAGCCCTCTCAAA 2403
2269 CTGGGTACAGCGGCACGGGCACAGCGGTGGAGAGCCTGCAAGGCTTCCCGGCCCATCTG 2328
2404 GAGCCCTTGACCATCCAGGTTCTTACTGTGGGCAATGCCCTTTCGACCTAAATTAATATC 2463
2329 GAGCCGCTGACCGGTGGAGGCTCTCTCCGTGGGGAAGATGACACCGCGCCCGGCTCCGCTAC 2388
2464 ACCTACT 2470
2389 TCCTTCT 2395

RESULT 9

US-09-122-126B-1

; Sequence 1, Application US/09122126B

; Patent No. 6451575

; GENERAL INFORMATION:

; APPLICANT: Bristol-Myers Squibb Company

; TITLE OF INVENTION: AGGRECAN DEGRADING METALLO PROTEASES

; FILE REFERENCE: DM6909

; CURRENT APPLICATION NUMBER: US/09/122.126B

; CURRENT FILING DATE: 1998-07-24

; NUMBER OF SEQ ID NOS: 21

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 1

; LENGTH: 4192

TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (406)..(2916)
US-09-122-126B-1

Query Match 18.5%; Score 603.4; DB 3; Length 4192;

Best Local Similarity 59.7%; Pred. No. 8.3e-131;

Matches 1072; Conservative 0; Mismatches 711; Indels 12; Gaps 3;

686 GAAGCATAGAAGAAAGACGATTTGTGTCCAGTCCAGCTATGTGGAACCATGTTGTGG 745
1022 GACCCGAAGAGCAAGCGCTTTGCTTCACTGATAGATTGTGTGAGACACTGGTGTGG 1081
746 CAGACAGTCGATGGGCAAGTTCACGGCAGTGTCTTAAAGCATTAACCTTCTCACGTTGT 805
1082 CAGATGACAAAGATGGCGCATTCACGGTGGGGGTAAAGCGCTACTCTCTAACAGTGA 1141
806 TTTTCGGTGGCAGCCAGATTTGTACAAACACCCAGCATTCGTAAATTCAGTTAGCTGTGG 865
1142 TGGCAGCAGCAGCCAAAGGCTTCAAGCACCCCAAGCATCCGCAATTCCTGTCAAGCTGGTGG 1201
866 TGGTGAAGATCTTTGGTCAATCCACGATGAACAGAAAGGGGCCGGAAGTGAACCTCCATGCTG 925
1202 TGACTCGGCTAGTGTATCTGGGGTCAAGCGAGGAGGGGCCCAAGTGGGGCCCAAGTGTCTG 1261
926 CCCTCACTCTGGGAACTTTTGCAACTGGCAGAAGCAGACAAACCCACAGTGACCCGGG 985
1262 CCAGACCTCTGGCAGCTTCTGTGCTGGCAGGGGCTCAACACCCCTGAGGACTCGG 1321
986 ATGCAGAGCACTATGACACAGCAATTTCTTTTACCAGACAGGACTTGTGTGGTCCAGGA 1045
1322 ACCTGACCACTTTGACACAGCCATTTCTTTTACCCTGAGGACCTGTGTGGAGTCTCCA 1381
1046 CATGTGATCTCTTGGGATGGCTGATGTTGGAACTGTGTGATCCGAGCAGAGCTGCT 1105
1382 CTTTGGACACGCTGGGTATGGCTGATGTGGGCAACCGTCTGTGACCCGGCTCGGAGCTGTG 1441
1106 CCGTCTAGAGATGATGTTTACAAAGCTGCTTTACCAAGCCCATGAATAGGCCACG 1165
1442 CCATTTGGAGGATGATGGGCTCAAGTCAAGCTTCTGCTCATGAACTGGGTCTATG 1501
1166 TGTTTAACTGCCACATGATGATGCAAAAGCAGTGTGCAGCCTTAATGG---TGTGAACC 1222
1502 TCTTCAACATGCTCCATGACAACTCCAAAGCATGATCATGTTGAAATGGGCTTTGAGCA 1561
1223 AGGATTCACCATGATGGCGTCAATGCTTTCCAACTTGGACCAACAGCCAGGCTTGGTCTC 1282
1562 CCTCTCGCCATGTATGGGCCCTGTGATGGCTCATGTGGATCTCTGAGGAGGCCCTGGTCCC 1621
1283 CTTTGCAGTGTCTACATGATTAACATCATTTCTGGATATGTTGATGGGAATGTTTGTATGG 1342
1622 CTTGCACTGCGGCTTCTCATCACTGACTTCTTGGACAATGGCTATGGGCACTGTCTCTTAG 1681
1343 ACAAGCTCAGAAATCCCATACAGCTCCCGAGCGCATCTCCCTGGCACCCTCGTACGATGCCA 1402
1682 ACAACAGAGGCTCCATTGCACTGTGCTGTGACTTTCCCTGGCAAGGACTATGATGCTG 1741
1403 ACCGGCAGTCCAGTGTTAATTTGGGGAGGACTCCAAACACTGCGCTGTATGACGCCAGCA 1462
1742 ACCGCCAGTGCAGCTGACCTTCGGGCGCGACTCACGCCATTTGTCCACAGCTGCGCGCGC 1801
1463 CATGTAGCAGCTTGTGGTGTACCGGCACTCTGGTGGGCTGTGGTGTGTCAAACCAAAAC 1522
1802 CCTGTGCTGCCCTCTGGTGTCTTGGCCACCTCAATGGCCCATGCCATGTGCCAGACCAAAAC 1861
1523 ACTTCCCGTGGGCGGATGGCAACAGCTGTGTGAGAGAGGGAATGTGTATCAACCGCAAGT 1582
1862 ACTCGCCTTGGGCGATGGCACACCTTCGCGGCCCGGCACAGGCTGTCATGGGTGGTCTGCT 1921
1583 GTGTGAACAAACCGACAGAAAGCATTTTGTGATAGCCCTTTTTCATGGAAGCTTGGGGAATGT 1642

Db 1922 GCCTCCACATGACCCAGCTCCAGGACTTCAATATATCCACAGGCTGGTGGGTCTCTT 1981
Qy 1643 GGGGGCTTTGGGAGACTGTTTCAGAAAGTGGGGTGGAGGAGTCCAGTACAGATGAGGG 1702
Db 1982 GGGGACCAATGGGGTGAAGTCTTCGGAGCTGTGGGGTGGTGTCCAGTTCCTCCCGAG 2041
Qy 1703 AATGTGACAAACCCAGTCCCAAGAAATGGAGGAAATGACTGTGTAAGGCAAAACAGTGGCT 1762
Db 2042 ACTGCAGAGGCTGTCCCGGAATGGTGGCAAGTACTGTGAGGGCCGCCGTACCCGT 2101
Qy 1763 ACAGATCTCTGTAACCTTGAGGACTGTCCAGACAAATAATGGAAAAACCTTTAGAGGAAAC 1822
Db 2102 TCCGCTCTCTCAACACTGAGGACTGCCAACTGGCTCAGCCCTGACCTTCCCGGAGGAGC 2161
Qy 1823 AATGTGAAACACACACAGAGTTCCTCAAGAGCTTCCTTTGGAGTGGGCTGGGTGGAT 1882
Db 2162 AGTGTGCTGCTTACAAACCCGACCGACTCTTCAAGAGCTTCCAGGGCCCAATGGACT 2221
Qy 1883 GGAATTCCTCAAGTACGCTGGCGTCTCACCAGAGGACAGGTGCAAGCTCATCTGCCAAGCCA 1942
Db 2222 GGGTTCCTCGCTACACAGGCTGGCCGCCAGGACCAAGTGCAAACTCAGCTGCCAGGCC 2281
Qy 1943 AAGCAATGGCTTACTTCTTCGTTTTCAGCCCAAGTGTGATGATCTCATGTAGCC 2002
Db 2282 GGGCACTGGGCTTACTATGTGCTGGAGCCAGGCTGGTAGATGGGACCCCTGTTCCT 2341
Qy 2003 CAGATTCACCTCTGCTGTGCGAGGACAGTGTAAAGCTGGTGTGATCGCATCA 2062
Db 2342 CGGACAGCTCTCTGGTCTGTGCGAGGCGGATGATCCTGCTGGCTGTGATCGCATCA 2401
Qy 2063 TAGACTCCAAAAAGATTTGATAATGTGTGTTTGGGGGAAATGATCTACTTTGA 2122
Db 2402 TTGGCTCCAAAGAGAGTTTGACAGTGCATGTGTGCGAGGGACGGTCTGGTTGCA 2461
Qy 2123 AAAAAATATCAGGATCAGTTACTGTGCAAAACCTGGGATATCATGATATCATCAATTC 2182
Db 2462 GCAAGCAGTCAGGCTCTTTCAGGAAATTCAGGTAACGATACAAATGTGTCACTATCC 2521
Qy 2183 CAACTGGAGCCACCAACATCGAAGTGAACAGCGGAAACAGAGGGGATCCAGGAACATG 2242
Db 2522 CCGCGGGGCCACCACTTCTTGT-----CCGGCAGCAGGGAACCTCGGCCACCGA 2575
Qy 2243 GCAGCTTTCTTGCCATCAAAGCTGTGTGTCAGCATATATCTTAATGGTGACTACATT 2302
Db 2576 GCATCTACTTGGCCCTGAGCTGCCAGATGGCTCTCTATGCCCTCAATGGTGAATACAGC 2635
Qy 2303 TGTCCACCTTAGAGCAGACATATGTACAAAGTGTGT-----CTTGAGGTACAGGGCT 2359
Db 2636 TGATGCCCTTCCGCCACAGATGTGTACTGCTGGGGCAGTCAGCTTGGCTACAGCGGG 2695
Qy 2360 CCTCTGGCGCATTTGGAAGAAATTCGAGCTTTAGCCCTCTCAAGAGCCCTTGACCATCC 2419
Db 2696 CCACTGCAGCTCAGAGACACTGTCAAGGCATGGGCCACTGGCCAGCCCTTTGACACTGC 2755
Qy 2420 AGGTTCTTACTGTGGCAATGCCCTTCGACCTTAAATTAATATACACTTCTTCTGT 2474
Db 2756 AAGTCTAGTGGCTGSCAACCCCGCAGGACACAGCCCTCCGATACAGCTTCTTCGT 2810

RESULT 10
US-09-634-286A-1
; Sequence 1, Application US/09634286A
; Patent No. 6521436
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: AGGRECAN DEGRADING METALLO PROTEASES
; FILE REFERENCE: DM6909A
; CURRENT APPLICATION NUMBER: US/09/634,286A
; CURRENT FILING DATE: 2000-08-09
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 4192

; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (406)..(2916)
US-09-634-286A-1

Query Match 18.5%; Score 603.4; DB 4; Length 4192;
Best Local Similarity 59.7%; Pred. No. 8,3e-131;
Matches 1072; Conservative 0; Mismatches 711; Indels 12; Gaps 3;

Qy 686 GAAGCATAGAAGAACGATTTGTGTCAAGGAGTGGTCTTAAGCATTAACCTTCTCAAGTGT 805
Db 1022 GACCCCGAAGAGCCAAAGCGCTTTGCTTCACTAGTAGATTTTGTGAGACACTGTGTGGTGG 1081
Qy 746 CAGACAGTCCGATGCGAGAAATTCACGCGAGTGGTCTTAAGCATTAACCTTCTCAAGTGT 805
Db 1082 CAGATGACAGATGGCCGATTTCCACGGTGGGGCTAAAGCGCTACCTGCTAAACAGTGA 1141
Qy 806 TTTCCGTCGACGACCAAGATTTGTACAAACACCCAGCATTTCTGTAATTCAGTTAGCTTGGTGG 865
Db 1142 TGGCAGCAGCAGCCAAAGCGCTTCAAGCACCACCAAGCATCCGCAATCTGTTCAGTGTGGTGG 1201
Qy 866 TGGTGAAGATCTTGTGTATCCACGATGAACAGAAAGGGCCGGAGTGAAGTCAATCTCAATGCTG 925
Db 1202 TGACTCGGCTAGTGTATCTTGGGGTCAGGCGAGGAGGGGCCCAAGTGGGGGCCAGTGTCTG 1261
Qy 926 CCCTCACTCTCGGAACTTTTGCACACTGGCAGAGCAGCAGCAACCCACAGTGAACCCGG 985
Db 1262 CCCAGACCTTGGCAGCTTCTGTGCTTGGCAGCGGGGCTCAACACCCCTGAGGACTCGG 1321
Qy 986 ATGCAGAGCACTATGACACAGCAATTTCTTTTCCACAGACAGGACTTTGTGTGGTCCCAGA 1045
Db 1322 ACCCTGACCACTTTGACACAGCCATTTCTGTTTACCGTCAGGACCTGTGTGGAGTCTCCA 1381
Qy 1046 CATGTGATCTCTTGGGATGGCTGATGTTGGAACCTGTGTGTGATCCGAGCAGAGTGTCT 1105
Db 1382 CTTGCGACACGCTGGGTATGCTGATGTGGGCACCGTCTGTGACCGCGCTCGAGAGTGTG 1441
Qy 1106 CGTCTATAGATGATGTTTACAGCTGCTTCCACACAGCCCATGAATTTAGGCAAG 1165
Db 1442 CCAITGTGAGGATGATGGCTCCAGTCAAGCTTCACTGCTCTCATGAACTGGGTCTATG 1501
Qy 1166 TGTTTAAACATGCACATGATGATGCAAAAGCAGTGTGCCAGCCTTAATGG---TGTGAACC 1222
Db 1502 TCTTCAACATGCTCCAATGACAACTCCAAAGCCATGATCATGATTTGAATGGGCTTTGAGCA 1561
Qy 1223 AGGATTTCCACATGATGGGCTCAATGCTTTCCAACTGGACACACAGCCAGCCTTGGTCTC 1282
Db 1562 CCTCTCGCCATGTCATGGCCCTGTGATGGCTCATGTGATGCTCTGAGGAGCCCTGTGTCCC 1621
Qy 1283 CTTGCAAGTCCATGATGATATCATATTTCTGGATAATGGTTCATGGGGAATGTTTGAATGG 1342
Db 1622 CTTGCAAGTCCCGCTTCTCATCTGATCTTCTGGAACATGGGCTATGGGCACTGTCTCTTAG 1681
Qy 1343 ACAAGCCTCAGAAATCCCATACAGCTCCAGGGCGATCTCCCTGGCAGCCTCGTACGATGCCA 1402
Db 1682 ACAAAACAGAGGCTCCATTTGCAATCTGCTGTGACTTTTCCCTGGCAAGGACTATGATGCTG 1741
Qy 1403 ACCGGCAGTCCGATTTTACATTTTGGGGAGGACTCCAAACACTGCTGCTGATGAGCCAGCA 1462
Db 1742 ACCGCCAGTGGCAGCTGACCTTTCGGGCCCGAGCTCAAGCCATTTGTCCAGAGTCCGCCCGC 1801
Qy 1463 CATGTAGCACTTGTGTGTACCGGCACCTCTGTGTGGGGTGTGTTGTCTCAAAACCAAAAC 1522
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Qy 1523 ACTTCCGCTGGCGGATGGCAGCAGCTGTGGAGAAAGGAAATGGTGTATCAACGGCAAGT 1582
Db 1862 ACTCGCCCTGGGCCGATGGCAGACCTCTGGGGCCCGCCACAGGCGCTGCATGGGTGTGCT 1921
Qy 1583 GTGTGAACAAACCCGACAGAAAGCATTTTGTATACGCTTTTTCATGGAAGCTGGGAATGT 1642

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Db 1982 GGGGACATGGGGTGAAGTCTCTCGGACCTGTGGGGTGTGTCCAGTCTCTCCCGAG 2041
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Db 2042 ACTGCAGGAGCCTGTCCCCCGGAATGGTGGCAAGTACTGTGAGGCGCGCGTACCCT 2101
Qy 1763 ACAGATCTCTTAACCTTGAGGACTGTCCAGACAAATATGAAACAACTTTAGAGAGAAC 1822
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Qy 1823 AATGTGAAGCACAAACGAGTCTTCAAAAGCTTCTTTGGAGTGGGCTTGGCGTGGAAAT 1882
Db 2162 AGTGTGCTGCTAAACCCAGCAGCAGCTCTTCAAGAGCTTCCAGGGCCCATGAGT 2221
Qy 1883 GGAATCCCAAGTACGCTGGGCTCTCAACAAAGACAGGTCAAGCTCATCTGCCAAGCCA 1942
Db 2222 GGGTTCCTCGCTACACAGGCGTGGCCCCCAGGACCAAGTGCAAACTCACCTGCGAGGCC 2281
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Qy 2420 AGGTCTTACTGTGGGCAATGCCCCCTTCGACTTAAATTAATATACACTTCTGT 2474
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RESULT 11

US-10-247-685-1

; Sequence 1, Application US/10247685

; Patent No. 6753176

; GENERAL INFORMATION:

; APPLICANT: Bristol-Myers Squibb Company

; TITLE OF INVENTION: AGGRECAN DEGRADING METALLO PROTEASES

; FILE REFERENCE: DM6909D

; CURRENT APPLICATION NUMBER: US/10/247,685

; CURRENT FILING DATE: 2002-09-19

; NUMBER OF SEQ ID NOS: 21

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 1

; LENGTH: 4192

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; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (406)..(2916)
US-10-247-685-1
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Query Match 18.5%; Score 603.4; DB 4; Length 4192;
Best Local Similarity 59.7%; Pred. No. 8.3e-131;
Matches 1072; Conservative 0; Mismatches 711; Indels 12; Gaps 3;

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Qy 746 CAGACAGTTCGATGGGCAGAAATCCAGCGAGTGGTCTAAAGCATTAACCTTCTCACGTTGT 805
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Qy 1583 GTGTGAACAAAACCGACAGAAAGCATTTTGTATAGGCTTTTTCATGGAAGCTTGGGGAATGT 1642
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RESULT 12

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US-09-122-126B-14
; Sequence 14, Application US/09122126B
; Patent No. 6451575
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: AGGRECAN DEGRADING METALLO PROTEASES
; FILE REFERENCE: DM6909
; CURRENT APPLICATION NUMBER: US/09/122,126B
; CURRENT FILING DATE: 1998-07-24
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 14
; LENGTH: 3250
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; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (121)..(2910)
US-09-122-126B-14
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Query Match 17.1%; Score 558.6; DB 3; Length 3250;
Best Local Similarity 55.2%; Pred. No. 2.2e-120;
Matches 1155; Conservative 0; Mismatches 924; Indels 12; Gaps 3;
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Qy 1529 GTGGGCGGATGGACAGCTGTGAGAGAGGAAATGTTGTATCAACGGCAAGTGTGTGA 1588
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RESULT 13
US-09-634-286A-14
; Sequence 14, Application US/09634286A
; Patent No. 6521436
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: AGGRECAN DEGRADING METALLO PROTEASES
; FILE REFERENCE: DM6909A
; CURRENT APPLICATION NUMBER: US/09/634,286A
; CURRENT FILING DATE: 2000-08-09
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 14
; LENGTH: 3250
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (121)..(2910)
US-09-634-286A-14

Query Match 17.1%; Score 558.6; DB 4; Length 3250;
Best Local Similarity 55.2%; Pred. No. 2.2e-120;
Matches 1155; Conservative 0; Mismatches 924; Indels 12; Gaps 3;

Qy 275 CCGGGTCCGAGAGACCGCGCTTCCGGAAACCGACCTGGCGCACTGCTTCTACTCCGGCACCG 334
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Db 1784 ACAAAACCAAGAAATAATTAATTAACCGTCAAGCATGGCACTGGGATCTTGGGAT 1843
QY 1649 CTTGGGAGACTGTTTCGAGAACTGTGGGTGGAGGAGTCCAGTACAGATGAGGGAAATGTG 1708
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QY 1709 ACAACCCAGTCCCAAGAAATGAGGGAAGTACTGTGAAGCAAGAGTGGCTACAGAT 1768
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QY 1769 CTTGTAACCTTGAAGACTGTCCAGACAAATAATGGAACAACTTTTGAAGAGGAACAAATGTG 1828
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QY 1829 AAGCACAACAGATTTTCAAAAGCTTCTTGGGAGTGGGCTGGGTGGAAATGATTC 1888
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QY 1949 TTGGCTACTTCTTGTGTTTTGCAGCCCAAGGTTGTAGATGGTACTCCATGTAGCCAGATT 2008
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QY 2069 CCAAAAGAAAGTTTCATAAATGTGGTGTGGTGGGGGAAATGGATCTACTTGTAAAAAAA 2128
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RESULT 14

US-10-247-685-14
; Sequence 14, Application US/10247685
; Patent No. 6753176
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: AGGRECAN DEGRADING METALLO PROTEASES
; FILE REFERENCE: DM6909D
; CURRENT APPLICATION NUMBER: US/10/247,685
; CURRENT FILING DATE: 2002-09-19
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 14
; LENGTH: 3250
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (121)..(2910)
US-10-247-685-14

Query Match 17.1%; Score 558.6; DB 4; Length 3250;
Best Local Similarity 55.2%; Pred. No. 2.2e-120;
Matches 1155; Conservative 0; Mismatches 924; Indels 12; Gaps 3;

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Qy 1769 CTTGTAACCTTGAAGTCTGTCAGACAATAATGGAAGAAACCTTTAGAGGAGACATGTG 1828
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RESULT 15

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US-09-392-184-7/c
; Sequence 7, Application US/09392184
; Patent No. 6395889
; GENERAL INFORMATION:
; APPLICANT: Robison, Keith E.
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN
; TITLE OF INVENTION: PROTEASE HOMOLOGS
; FILE REFERENCE: 5800-55
; CURRENT APPLICATION NUMBER: US/09/392,184
; CURRENT FILING DATE: 1999-09-09
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 3126
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(3126)
; OTHER INFORMATION: repolysin (ADAM family of metalloprotease)
US-09-392-184-7
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Query Match 16.7%; Score 544.2; DB 3; Length 3126;
Best Local Similarity 55.0%; Pred. No. 5e-117;
Matches 1413; Conservative 0; Mismatches 1023; Indels 135; Gaps 12;
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QY 235 TTGGCGCCCGGCTTACGCTCCAGAACGTTGGGGCGCAATTCGGGTCCGAGACGCGGCTT 294
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QY 295 CCGGAAACCGACTGGCGCACTGCTTACTCCGGCACCGTGAATGGCGATCCAGCTCG 354
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QY 355 GCTGCGCCCTCAGCCTCTGCGAGGCGTGCAGCGGCGCTTCTACCTGCTGGGGAGGCG 414
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QY 415 TATTTATCAGCGGCTGCGCGCGCGCAGGAGCGCTCGCCACCGCGCCCGCAGGGGAG 474
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: May 23, 2005, 09:18:06 ; Search time 1733 Seconds
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Gapop 10.0 , Gapext 1.0

Searched: 5695437 seqs, 3066160638 residues

Total number of hits satisfying chosen parameters: 11390874

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

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SUMMARIES

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2	3257	99.9	3261	11	US-09-989-687-1
3	3192	97.9	4030	18	US-10-473-974-98
4	3161.6	97.0	4014	16	US-10-115-286-1
5	3161.6	97.0	4014	18	US-10-757-450-1
6	3160	96.9	4676	13	US-10-105-929-1
7	3158.4	96.9	4447	18	US-10-755-889-133
8	3157.4	96.8	4352	19	US-10-741-600-776
9	3157.4	96.8	4459	19	US-10-741-600-777
10	3157.4	96.8	4658	19	US-10-741-600-775
11	3156.8	96.8	3889	19	US-10-667-281-1
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					Sequence 98, Appl
					Sequence 1, Appli
					Sequence 1, Appli
					Sequence 133, App
					Sequence 776, App
					Sequence 777, App
					Sequence 775, App
					Sequence 1, Appli

12	3156.8	96.8	4459	17	US-10-159-563-192	Sequence 192, App
13	3156.8	96.8	4459	17	US-10-159-563-308	Sequence 308, App
14	3156.8	96.8	4760	10	US-09-971-4298-17	Sequence 17, Appl
15	3155.2	96.8	4309	16	US-10-210-120-57	Sequence 57, Appl
16	3139.2	96.3	4014	11	US-09-989-687-125	Sequence 125, Appl
17	2924	89.7	4848	17	US-10-425-114-28651	Sequence 26851, A
18	2131.6	65.4	2184	9	US-09-445-023A-2	Sequence 2, Appli
19	2131.6	65.4	2184	14	US-10-097-597-2	Sequence 2, Appli
20	2131.6	65.4	2184	14	US-10-097-597-2	Sequence 2, Appli
21	2052.6	62.9	4878	17	US-10-191-803-170	Sequence 170, App
22	2052.6	62.9	4878	17	US-10-152-319A-1840	Sequence 1840, App
23	2020.4	62.0	4180	10	US-09-373-658-20	Sequence 20, Appl
24	2020.4	62.0	4180	11	US-09-989-687-20	Sequence 20, Appl
25	2002.4	61.4	4858	19	US-10-764-420-37	Sequence 37, Appl
26	1954	59.9	3147	9	US-09-803-589-1	Sequence 1, Appli
27	1954	59.9	3147	18	US-10-718-332-1	Sequence 1, Appli
28	1934.4	59.3	2871	18	US-10-473-974-23	Sequence 23, Appl
29	1655	50.8	2184	9	US-09-445-023A-13	Sequence 13, Appl
30	1655	50.8	2184	14	US-10-097-597-13	Sequence 13, Appl
31	1655	50.8	2184	14	US-10-097-597-13	Sequence 13, Appl
32	1267.6	38.9	3145	9	US-09-803-589-9	Sequence 9, Appli
33	1267.6	38.9	3145	18	US-10-718-332-9	Sequence 9, Appli
34	1127.6	34.6	2134	10	US-09-887-527-23	Sequence 23, Appl
35	1124.6	34.5	2121	9	US-09-818-143-15	Sequence 15, Appl
36	1015.2	31.1	21130	19	US-10-741-600-17789	Sequence 17789, A
37	678.2	20.8	2804	17	US-10-093-463-27	Sequence 27, Appl
38	676.8	20.8	781	16	US-10-029-386-25317	Sequence 25317, A
39	666.2	20.4	3638	9	US-09-918-171A-8	Sequence 8, Appli
40	641.8	19.7	3715	17	US-10-425-114-26850	Sequence 26850, A
41	634.6	19.5	3008	10	US-09-373-658-3	Sequence 3, Appli
42	634.6	19.5	3008	11	US-09-989-687-3	Sequence 3, Appli
43	634.6	19.5	3711	18	US-10-283-975A-398	Sequence 398, App
44	629.8	19.3	2853	18	US-10-763-210-2	Sequence 2, Appli
45	628.2	19.3	2853	9	US-09-965-631-3	Sequence 3, Appli

ALIGNMENTS

RESULT 1

US-09-373-658-1
; Sequence 1, Application US/09373658
; Publication No. US20030092900A1
; GENERAL INFORMATION:
; APPLICANT: Iruela-Arispe, Luisa
; APPLICANT: Hastings, Gregg A.
; APPLICANT: Ruben, Steven M.
; APPLICANT: Jonak, Zdenka L.
; APPLICANT: Trulli, Stephen H.
; APPLICANT: Fronwald, James A.
; APPLICANT: Terrett, Jonathan A.
; TITLE OF INVENTION: Meth1 and Meth2 Polynucleotides and Polypeptides
; FILE REFERENCE: 1488.1070006
; CURRENT APPLICATION NUMBER: US/09/373,658
; CURRENT FILING DATE: 1999-08-13
; NUMBER OF SEQ ID NOS: 125
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 3261
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(2853)
; NAME/KEY: UNSURE
; LOCATION: (3095)
; OTHER INFORMATION: May be any nucleic acid
; NAME/KEY: UNSURE
; LOCATION: (3248)
; OTHER INFORMATION: May be any nucleic acid
; NAME/KEY: UNSURE
; LOCATION: (3255)
; OTHER INFORMATION: May be any nucleic acid

; NAME/KEY: UNSURE
 ; LOCATION: (3261)
 ; OTHER INFORMATION: May be any nucleic acid
 US-09-373-658-1

Query Match	99.9%;	Score 3257;	DB 10;	Length 3261;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 3260;	Conservative	0;	Mismatches 0;	Indels 0;
Gaps	0;			

Qy	1	ATGGGAAACGGAGACGGGGCTCCGGGGTCTCGAGACTTTGGGCCCGTACCAACGCTGCTG	60
Db	1	ATGGGAAACGGGAGCGGGCTCCGGGGTCTCGAGACTTTGGGCCCGTACCAACGCTGCTG	60
Qy	61	CTGCTCGCGCGGGCTACTGCGCGTGTGGAACGCACTCGGCGCCCTCCGAGGAGAC	120
Db	61	CTGCTCGCGCGGGCTACTGCGCGTGTGGAACGCACTCGGCGCCCTCCGAGGAGAC	120
Qy	121	GAGGAGCTAGTGGTGC CGGAGCTGGAGCGCGCCCGGGAACA CGGCGCTCCGC	180
Db	121	GAGGAGCTAGTGGTGC CGGAGCTGGAGCGCGCCCGGGAACA CGGCGCTCCGC	180
Qy	181	CTGACGCTTTTGAC CAGCAGCTGGATCTGAGCTGCGGCCGGA CAGCAGCTTTTGGCG	240
Db	181	CTGACGCTTTTGAC CAGCAGCTGGATCTGAGCTGCGGCCGGA CAGCAGCTTTTGGCG	240
Qy	241	CCCGCTTCAGCTCCAGAA CGTGGGGCGAAATCCGGGTCCGAGACGCCGCTTCCGAA	300
Db	241	CCCGCTTCAGCTCCAGAA CGTGGGGCGAAATCCGGGTCCGAGACGCCGCTTCCGAA	300
Qy	301	ACCGACTTGGGCGACTGCTTCTACTCCGGCACCGTGAATGGCGATCCAGCTCGGCTGCC	360
Db	301	ACCGACTTGGGCGACTGCTTCTACTCCGGCACCGTGAATGGCGATCCAGCTCGGCTGCC	360
Qy	361	GCCCTCAGCTTCGGAGGGCGTGGCGGGCGCTTCTACTGCTGGGGAGCGCTATTTC	420
Db	361	GCCCTCAGCTTCGGAGGGCGTGGCGGGCGCTTCTACTGCTGGGGAGCGCTATTTC	420
Qy	421	ATCCAGCGCTGCCCGCCGACGAGCGCTCGCCACCGCGCCCGCCAGGGGAGAGCGG	480
Db	421	ATCCAGCGCTGCCCGCCGACGAGCGCTCGCCACCGCGCCCGCCAGGGGAGAGCGG	480
Qy	481	CCGGCACCACTACAGTTCCACTCTCGCGGGGAATCGGCAGGGCGAGCTAGCGGCGACG	540
Db	481	CCGGCACCACTACAGTTCCACTCTCGCGGGGAATCGGCAGGGCGAGCTAGCGGCGACG	540
Qy	541	TGCGGGTCTGTGACGACGAGCCCGGCCGACTGGGAAAGGGAGACCGAGACGAGAC	600
Db	541	TGCGGGTCTGTGACGACGAGCCCGGCCGACTGGGAAAGGGAGACCGAGACGAGAC	600
Qy	601	GAAGGACTGAGGGCGAGAGCGAGGGCTCAGTGTGCGCGACGACCCGSCACTGCA	660
Db	601	GAAGGACTGAGGGCGAGAGCGAGGGCTCAGTGTGCGCGACGACCCGSCACTGCA	660
Qy	661	GGCGTAGGACGCCCA CAGGAACTGGAAGCAATAAGAAAGAGCGATTTGTCTCAGTCA	720
Db	661	GGCGTAGGACGCCCA CAGGAACTGGAAGCAATAAGAAAGAGCGATTTGTCTCAGTCA	720
Qy	721	CGCTATGTGGAACA CCAATGCTGTGCGACACGATGGGAGAAATTCACGGCAGTGGT	780
Db	721	CGCTATGTGGAACA CCAATGCTGTGCGACACGATGGGAGAAATTCACGGCAGTGGT	780
Qy	781	CTAAGCAATTACCTTCTCACGTTGTTTTTCGGTGGCAGCCAGATTCACAAACACCCACG	840
Db	781	CTAAGCAATTACCTTCTCACGTTGTTTTTCGGTGGCAGCCAGATTCACAAACACCCACG	840
Qy	841	ATTCGTAATTCAGTTAGCTGGTGGTGAAGATCTTGGTCAATCCAGTGAACAGAG	900
Db	841	ATTCGTAATTCAGTTAGCTGGTGGTGAAGATCTTGGTCAATCCAGTGAACAGAG	900
Qy	901	GGGCGGGAAGTGACCTCCAATGCTGCCCTCACTCTGCGGAACTTTTGGAACTGGCAGAG	960
Db	901	GGGCGGGAAGTGACCTCCAATGCTGCCCTCACTCTGCGGAACTTTTGGAACTGGCAGAG	960

Qy	361	GCCTCTCAGCCTCTCGAGAGGGCTGCGCGGCGCCTTCTACTCTGTGCGGGAGGCGGTATTTTC	420
Db	361	GCCTCTCAGCCTCTCGAGAGGGCTGCGCGGCGCCTTCTTACCTGTCTGGGGAGGCGGTATTTTC	420
Qy	421	ATCCAGCGGCTGCCGCGCGCAGCGAGGGCTCGCCACCGCCGCCCCAGGGGAGAGCCG	480
Db	421	ATCCAGCGGCTGCCGCGCGCAGCGAGGGCTCGCCACCGCCGCCCCAGGGGAGAGCCG	480
Qy	481	CCGGCACCACTACAGTTTCCACTCTCTCGGCGGAATCGGCAGGGCGCACTAGCGCGGCACG	540
Db	481	CCGGCACCACTACAGTTTCCACTCTCTCGGCGGGAATCGGCAGGGCGCACTAGCGCGGCACG	540
Qy	541	TGCGGGGTCTGGACGACGAGCCCGCCGACCTGGGAAACCGGAGACCGGAAGACGAGGAC	600
Db	541	TGCGGGGTCTGGACGACGAGCCCGCCGACCTGGGAAACCGGAGACCGGAAGACGAGGAC	600
Qy	601	GAAGGGACTGAGGGCGAGGACGAAGGGCCTCAGTGGTCGCGCAGGACCCGGCACTGCAAA	660
Db	601	GAAGGGACTGAGGGCGAGGACGAAGGGCCTCAGTGGTCGCGCAGGACCCGGCACTGCAAA	660
Qy	661	GGCGTAGGACAGCCCA CAGGAAC TGGGAAGCATAGAAAGAGCGATTGTGTCCAGTCAAC	720
Db	661	GGCGTAGGACAGCCCA CAGGAAC TGGGAAGCATAGAAAGAGCGATTGTGTCCAGTCAAC	720
Qy	721	CGCTATGTGGAACCATGCTTTGTGGCAGACCGAGTCGATGGCAGAAATTCACCGCAGTGGT	780
Db	721	CGCTATGTGGAACCATGCTTTGTGGCAGACCGAGTCGATGGCAGAAATTCACCGCAGTGGT	780
Qy	781	CTAAGGCAATTACCTTCTCA CGTTGTTTTCGGTGGCAGCCAGATTGTACAACACCCCGACG	840
Db	781	CTAAGGCAATTACCTTCTCA CGTTGTTTTCGGTGGCAGCCAGATTGTACAACACCCCGACG	840
Qy	841	ATTTCGTAATTACGTTAGCTGGTGGTGGTGAAGATCTTGGTCATCCACGATGAACAGAAAG	900
Db	841	ATTTCGTAATTACGTTAGCTGGTGGTGGTGAAGATCTTGGTCATCCACGATGAACAGAAAG	900
Qy	901	GGGCGGGAAGTGACCTCCAATGCTGCCCTCACCTCTCGGGAACCTTTTGCAACTGGCAGAAG	960
Db	901	GGGCGGGAAGTGACCTCCAATGCTGCCCTCACCTCTCGGGAACCTTTTGCAACTGGCAGAAG	960
Qy	961	CAGCACAAACCA CCGAGTGACCGGGATGACAGACATATGACACAGCAATTCCTTTTCACC	1020
Db	961	CAGCACAAACCA CCGAGTGACCGGGATGACAGACATATGACACAGCAATTCCTTTTCACC	1020
Qy	1021	AGACAGACTTGTCTGGGTCCACACATGTGATCTCTCGGATGGCTGATGTTGGAAC	1080
Db	1021	AGACAGACTTGTCTGGGTCCACACATGTGATCTCTCGGATGGCTGATGTTGGAAC	1080
Qy	1081	GTGTGTGATCCGAGCAGAAGCTGCTCCGTCATAGAAGATGATGGTTTACAAGCTGCCCTTC	1140
Db	1081	GTGTGTGATCCGAGCAGAAGCTGCTCCGTCATAGAAGATGATGGTTTACAAGCTGCCCTTC	1140
Qy	1141	ACCA CAGCCCATGAATTTAGGCCACGCTGTTTAA CATTGCCA CATTGATGATGAAGAGCAGTGT	1200
Db	1141	ACCA CAGCCCATGAATTTAGGCCACGCTGTTTAA CATTGCCA CATTGATGATGAAGAGCAGTGT	1200
Qy	1201	GCCAGCCTTAATGGTGTGAACCGAGGATCCCA CATTGATGGCTCAATGCTTCCCAACTG	1260
Db	1201	GCCAGCCTTAATGGTGTGAACCGAGGATCCCA CATTGATGGCTCAATGCTTCCCAACTG	1260
Qy	1261	GACCACAGCCAGCCTTGGTCTCTCTGCACTGCCCTTACATGATTACATCATTTCTGGATAAT	1320
Db	1261	GACCACAGCCAGCCTTGGTCTCTCTGCACTGCCCTTACATGATTACATCATTTCTGGATAAT	1320
Qy	1321	GGTCA TGGGGAATGTTGATGGACAAGCCTCAGAAATCCCATACAGTCCCAAGGGGATCTC	1380
Db	1321	GGTCA TGGGGAATGTTGATGGACAAGCCTCAGAAATCCCATACAGTCCCAAGGGGATCTC	1380
Qy	1381	CCTGGCACCTCGTACGATGCCAACCGGCAGTGCCAGTTTACATTTGGGGAGGACTCCAAA	1440
Db	1381	CCTGGCACCTCGTACGATGCCAACCGGCAGTGCCAGTTTACATTTGGGGAGGACTCCAAA	1440
Qy	1441	CACCTGCCTGATGCAGCCAGCACATGTAGCACCTTGTGGTGTACCGGCACCTCTGTGGGG	1500

[illegible]

Db 2521 TGGGTCAITGAAGAGTGGGCGGAATGTTCTAAGTCATGTGAATGGTTGGTGGCAGAGAAGA 2580
Qy 2581 CTGGTAGAATGCCGACACATTAATGACAGCCTGCTTCCGAGTGTCCAAAGGAAGTGAAG 2640
Db 2581 CTGGTAGAATGCCGACACATTAATGACAGCCTGCTTCCGAGTGTCCAAAGGAAGTGAAG 2640
Qy 2641 CCAGCCAGCACCAGACCTTTGTGCAGACCATCTCCCTGCCCCAGTGGCAGCTGGGGAGTGG 2700
Db 2641 CCAGCCAGCACCAGACCTTTGTGCAGACCATCTCCCTGCCCCAGTGGCAGCTGGGGAGTGG 2700
Qy 2701 TCATCATGTTCTAAGACCTGTGGGAAGGTTTACAAAAAAGAGCTTGAAGTGTCTGTCC 2760
Db 2701 TCATCATGTTCTAAGACCTGTGGGAAGGTTTACAAAAAAGAGCTTGAAGTGTCTGTCC 2760
Qy 2761 CATGATGGAGGGTGTATCTCATGAGAGCTGTGATCCTTTTAAAGAAACCTTAAACATTTTC 2820
Db 2761 CATGATGGAGGGTGTATCTCATGAGAGCTGTGATCCTTTTAAAGAAACCTTAAACATTTTC 2820
Qy 2821 ATAGACTTTTGCACAAATGGCAGAAATGAGTTAAGTGGTTTAAAGTGGTTTGTAGCTTTGAGG 2880
Db 2821 ATAGACTTTTGCACAAATGGCAGAAATGAGTTAAGTGGTTTAAAGTGGTTTGTAGCTTTGAGG 2880
Qy 2881 CAAAGCAAGTGAAGAGGCTGGTGCAGGGAAGCAAGAGCTGGAGGGATCCAGCGT 2940
Db 2881 CAAAGCAAGTGAAGAGGCTGGTGCAGGGAAGCAAGAGCTGGAGGGATCCAGCGT 2940
Qy 2941 ATCTTCCAGTAAACCACTGAGGTGTATCAGTAAGTGGGATTAATGGGGTAGATAGAAA 3000
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Qy 3001 GAGTTTGAATCATCAGAGTAAATCTGCCAGTTTGCATAATTTTATAGGATAGTTAGTGGAT 3060
Db 3001 GAGTTTGAATCATCAGAGTAAATCTGCCAGTTTGCATAATTTTATAGGATAGTTAGTGGAT 3060
Qy 3061 TATTAACTCTGAGAGTGAATAGCAATAAATAAANCCCGGGCATTTATTATTATTTC 3120
Db 3061 TATTAACTCTGAGAGTGAATAGCAATAAATAAANCCCGGGCATTTATTATTATTTC 3120
Qy 3121 TTTTGTACATCTATTACAGTTTATAGAAAAAACAAGCAATTTCTCAAAAAAATAAAAAA 3180
Db 3121 TTTTGTACATCTATTACAGTTTATAGAAAAAACAAGCAATTTCTCAAAAAAATAAAAAA 3180
Qy 3181 AAAAAAATAAAAAAAGGGCGCGCTCTAGAGGATCCCTCGAGGGGCCCAAGCTTACGC 3240
Db 3181 AAAAAAATAAAAAAAGGGCGCGCTCTAGAGGATCCCTCGAGGGGCCCAAGCTTACGC 3240
Qy 3241 GTGCATGNTGTCATNAGTCT 3260
Db 3241 GTGCATGNTGTCATNAGTCT 3260

RESULT 3

US-10-473-974-98
; Sequence 98, Application US/10473974
; Publication No. US20040265808A1
; GENERAL INFORMATION:
; APPLICANT: GARCIA, TERESA
; APPLICANT: ROMAN ROMAN, SERGIO
; APPLICANT: BARON, ROLAND
; APPLICANT: CALL, KATHERINE
; APPLICANT: THEILHABER, JOACHIM
; APPLICANT: CONNOLLY, TIMOTHY
; APPLICANT: JACKSON, AMANDA
; APPLICANT: BUSHNELL, STEVEN
; APPLICANT: RAWADI, GEORGES
; TITLE OF INVENTION: GENES INVOLVED IN OSTEOGENESIS, AND METHODS OF USE
; FILE REFERENCE: 37991-0023
; CURRENT APPLICATION NUMBER: US/10/473,974
; CURRENT FILING DATE: 2003-10-03
; PRIOR APPLICATION NUMBER: PCT/IB02/02211
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: 60/281,400
; PRIOR FILING DATE: 2001-04-05

; NUMBER OF SEQ ID NOS: 246
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 98
; LENGTH: 3430
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (3332)
; OTHER INFORMATION: a, c, g, t, other or unknown
US-10-473-974-98

Query Match 97.9%; Score 3192; DB 18; Length 3430;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3193; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ATGGGAAACGCGGAGCGGGCTCCGGGTCTCCGAGCTTTGGGCCCTTACCACGCTGCTG 60
Db 238 ATGGGAAACGCGGAGCGGGCTCCGGGTCTCCGAGCTTTGGGCCCTTACCACGCTGCTG 297
Qy 61 CTGCTCCGCGCGCGCTACTGCGCGTGTGCGAGCACTCGGGCGCCCTCCGAGGAGGAC 120
Db 298 CTGCTCCGCGCGCGCTACTGCGCGTGTGCGAGCACTCGGGCGCCCTCCGAGGAGGAC 357
Qy 121 GAGGAGCTAGTGTGCGGAGCTGAGCGCGCCCGGGAACAACGGACACGCGCTCCGC 180
Db 358 GAGGAGCTAGTGTGCGGAGCTGAGCGCGCCCGGGAACAACGGACACGCGCTCCGC 417
Qy 181 CTGCAAGCTTTTACACAGCAGCTGGATCTGGAGCTCGGCCCGCACAGCAGCTTTTGGCG 240
Db 418 CTGCAAGCTTTTACACAGCAGCTGGATCTGGAGCTCGGCCCGCACAGCAGCTTTTGGCG 477
Qy 241 CCGCGCTTCACTCCAGAAACGTGGGGCGCAATCCGGGTCCGAGACGCCCTTCCGGAA 300
Db 478 CCGCGCTTCACTCCAGAAACGTGGGGCGCAATCCGGGTCCGAGACGCCCTTCCGGAA 537
Qy 301 ACCGACTGGCGCACTGCTTCTACTCCGCAACCGTGAATGGCGATCCAGCTCGGCTGCC 360
Db 538 ACCGACTGGCGCACTGCTTCTACTCCGCAACCGTGAATGGCGATCCAGCTCGGCTGCC 597
Qy 361 GCCCTCAGCTCTGCGAGGGCGTGGCGCGCCCTTCTACCTGTGGGGAGGGCTATTTC 420
Db 598 GCCCTCAGCTCTGCGAGGGCGTGGCGCGCCCTTCTACCTGTGGGGAGGGCTATTTC 657
Qy 421 ATCCAGCGCTGCGCGCGCCAGCAGCGCTCGCCACCGCCCGCCAGGGGAGAGCCG 480
Db 658 ATCCAGCGCTGCGCGCGCCAGCAGCGCTCGCCACCGCCCGCCAGGGGAGAGCCG 717
Qy 481 CCGGCACTACTACAGTTTCACTCTCTGCGCGGGAATCGGAGGGCGAGCTAGGCGGACG 540
Db 718 CCGGCACTACTACAGTTTCACTCTCTGCGCGGGAATCGGAGGGCGAGCTAGGCGGACG 777
Qy 541 TCGGGGTGTGGAACGACGAGCCCGCGGACTGGGAAAGCGGAGCCGAGAGCAGAGAC 600
Db 778 TCGGGGTGTGGAACGACGAGCCCGCGGACTGGGAAAGCGGAGCCGAGAGCAGAGAC 837
Qy 601 GAAGGACTGAGGGCGAGGAGCGCTCAGTGTGTGCGCGAGGACCCGGCACTGCAA 660
Db 838 GAAGGACTGAGGGCGAGGAGCGCTCAGTGTGTGCGCGAGGACCCGGCACTGCAA 897
Qy 661 GCGGTAGGACAGCCACAGGAACTGGAAGCATTAAGAAAGAGGATTTGTTCAGTCA 720
Db 898 GCGGTAGGACAGCCACAGGAACTGGAAGCATTAAGAAAGAGGATTTGTTCAGTCA 957
Qy 721 CGCTATGTGAACCACTGCTTGTGGCAGCAGCTCGATGCGAGAAATTCACGGCAGTGGT 780
Db 958 CGCTATGTGAACCACTGCTTGTGGCAGCAGCTCGATGCGAGAAATTCACGGCAGTGGT 1017
Qy 781 CTAAGCATTAACCTTCTCAGCTTTGTTTTCGGTGGCAGCCAGATTGTATAAACCCCGC 840
Db 1018 CTAAGCATTAACCTTCTCAGCTTTGTTTTCGGTGGCAGCCAGATTGTATAAACCCCGC 1077
Qy 841 ATTCTGTAATTCAGTTAGCTTGGTGGTGAAGATCTTGGTTCATCCAGATGAACAGAG 900

|||||
1078 ATTCTTAATTCAGTTAGCTGTGTGTGTGTGAAGATCTTGGTCATCCAGTGAACAGAG 1137
QY GGGCCGGAAGTGAACCTCCAAATGCTGCCCTCACTTGGCGGAACCTTTGCAACTGGCAGAAG 960
Db GGGCCGGAAGTGAACCTCCAAATGCTGCCCTCACTTGGCGGAACCTTTGCAACTGGCAGAAG 1197
QY CAGCACACCCACCCAGTGAACCGGATGCGAGCACTATGACACAGCAATTCCTTTTCACC 1020
Db CAGCACACCCACCCAGTGAACCGGATGCGAGCACTATGACACAGCAATTCCTTTTCACC 1257
QY AGACAGGACTTGTGTGGGTGCCAGACATGTGATCTCTTGGGATGGCTGATGTGGAACT 1080
Db AGACAGGACTTGTGTGGGTGCCAGACATGTGATCTCTTGGGATGGCTGATGTGGAACT 1317
QY GTGTGTGATCCGAGCAGAAAGCTGCTCCGTATAGAAAGATGATGGTTTCAAGCTGCCCTTC 1140
Db GTGTGTGATCCGAGCAGAAAGCTGCTCCGTATAGAAAGATGATGGTTTCAAGCTGCCCTTC 1377
QY ACCACAGCCCATGAATTAGGCCACAGCTGTTTAAACATGCCACATGATGATGCAAGCAGTGT 1200
Db ACCACAGCCCATGAATTAGGCCACAGCTGTTTAAACATGCCACATGATGATGCAAGCAGTGT 1437
QY GCCAGCCTTAATGGTGTGAACCCAGGATCCCAATGATGGCGTCAATGCTTTCCAACTG 1260
Db GCCAGCCTTAATGGTGTGAACCCAGGATCCCAATGATGGCGTCAATGCTTTCCAACTG 1497
QY GACCAACAGCAGCCTTGTGCTCTCTTGGAGTGCTACATGATTAATCATATTTCTGGATTAAT 1320
Db GACCAACAGCAGCCTTGTGCTCTCTTGGAGTGCTACATGATTAATCATATTTCTGGATTAAT 1557
QY GGTCAATGGGGAATGTTTGAATGCAAGCCCTCAGAATCCCATACAGCTCCAGGCGCATCTC 1380
Db GGTCAATGGGGAATGTTTGAATGCAAGCCCTCAGAATCCCATACAGCTCCAGGCGCATCTC 1617
QY CCTGGCACCTGTGACGATGCCAACCGGAGTGCCAGTTTACATTTGGGAGGACTCCCAA 1440
Db CCTGGCACCTGTGACGATGCCAACCGGAGTGCCAGTTTACATTTGGGAGGACTCCCAA 1677
QY CACTGCCCTGTATCAACCGCAGCAATGTAGACCTTTGGTGTGACCGGACCTCTGGTGGG 1500
Db CACTGCCCTGTATCAACCGCAGCAATGTAGACCTTTGGTGTGACCGGACCTCTGGTGGG 1737
QY GTGCTGTGTGTCAAACCAACACTTCCGTGGGCGGATGGCAGCAGCTGTGGAGAGGG 1560
Db GTGCTGTGTGTCAAACCAACACTTCCGTGGGCGGATGGCAGCAGCTGTGGAGAGGG 1797
QY AAATGGTGTATCAACCGCAAGTGTGTGAACCAAAACCGACAGAAAGCATTTTGTATACGCT 1620
Db AAATGGTGTATCAACCGCAAGTGTGTGAACCAAAACCGACAGAAAGCATTTTGTATACGCT 1857
QY TTTTCATGGAAGCTGGGGAATGTGGGGGCTTTGGGAGAGCTGTTCAGAAACGTGCGGTGGA 1680
Db TTTTCATGGAAGCTGGGGAATGTGGGGGCTTTGGGAGAGCTGTTCAGAAACGTGCGGTGGA 1917
QY GGAGTCCAGTACACCATGAGGGAATGTGACAAACCCAGTCCCAAGAAATGGAGGAGTAC 1740
Db GGAGTCCAGTACACCATGAGGGAATGTGACAAACCCAGTCCCAAGAAATGGAGGAGTAC 1977
QY TGTGAAGGCAAAACGAGTGGCTTACAGATCTCTGTAACCTTTGAGGACTGTCCAGACAAATAT 1800
Db TGTGAAGGCAAAACGAGTGGCTTACAGATCTCTGTAACCTTTGAGGACTGTCCAGACAAATAT 2037
QY GGAAAAACCTTTAGAGAGGAACTGTGAGACACACAGAGTTTTCAAAAGCTTCCCTTT 1860
Db GGAAAAACCTTTAGAGAGGAACTGTGAGACACACAGAGTTTTCAAAAGCTTCCCTTT 2097
QY GGGAGTGGGCTGCGGTGGAATGGATTCCTCAAGTACGCTGGGCTCTCAACCAAGACAGG 1920
Db GGGAGTGGGCTGCGGTGGAATGGATTCCTCAAGTACGCTGGGCTCTCAACCAAGACAGG 2157
QY TGCAGAGCTCATCTGCCAACCCAAAGGCAATGGCTACTCTTCTCGTTTTCGAGCCCAAGGTT 1980
Db TGCAGAGCTCATCTGCCAACCCAAAGGCAATGGCTACTCTTCTCGTTTTCGAGCCCAAGGTT

Db TGCAAGCTCATCTGCCAAGCCAAAGGCATTTGGCTACTTCTTCTGTTTTCGAGCCCAAGGTT 2217
QY GTAGATGTGTACTCCATGTAGCCAGATTTCCAGCTCTGTCTGTGTCGAAGGACAGTGTGTA 2040
Db GTAGATGTGTACTCCATGTAGCCAGATTTCCAGCTCTGTCTGTGTCGAAGGACAGTGTGTA 2277
QY AAAGCTGTGTGTGATCGCATCATAGACTCCAAAAAAGAGTTTGATAAATGTGGTGTGTC 2100
Db AAAGCTGTGTGTGATCGCATCATAGACTCCAAAAAAGAGTTTGATAAATGTGGTGTGTC 2337
QY GGGGAAATGGATCTACTTTGAAAAAATATCAGGATCAGTTACTAGTGCAAAAACCTGGA 2160
Db GGGGAAATGGATCTACTTTGAAAAAATATCAGGATCAGTTACTAGTGCAAAAACCTGGA 2397
QY TATCATGATATCATCAAAATTTCCAACTGAGGCCAACCAATCGAAGTGAACAGCGGAAC 2220
Db TATCATGATATCATCAAAATTTCCAACTGAGGCCAACCAATCGAAGTGAACAGCGGAAC 2457
QY CAGAGGGGATCCAGGAACAAATGGCAGCTTTCTTGGCCATCAAAGCTGCTGATGGCACATAT 2280
Db CAGAGGGGATCCAGGAACAAATGGCAGCTTTCTTGGCCATCAAAGCTGCTGATGGCACATAT 2517
QY ATTCTTAATGGTGACTACACTTTTGTCCACTTTAGAGCAAGACATTTATGTACAAAAGTGT 2340
Db ATTCTTAATGGTGACTACACTTTTGTCCACTTTAGAGCAAGACATTTATGTACAAAAGTGT 2577
QY GTCTTGAGGTACAGGGCTCTCTGCGGCATTTGGAAGAAATTCGCGAGCTTTAGCCCTCTC 2400
Db GTCTTGAGGTACAGGGCTCTCTGCGGCATTTGGAAGAAATTCGCGAGCTTTAGCCCTCTC 2637
QY AAAGAGCCCTTGGACCATCCAGGTTCTTACTGTGGGCAATGCCCTTCGACCTCAAAAATTTAA 2460
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QY TACACCTACTTCTGTAAGAGAGTGGGCGAATGTTCTAAGTCATGTGAATTTGGTGTGGCAGAGA 2520
Db TACACCTACTTCTGTAAGAGAGTGGGCGAATGTTCTAAGTCATGTGAATTTGGTGTGGCAGAGA 2757
QY TGGGTCAATGTAGAGTGGGCGAATGTTCTAAGTCATGTGAATTTGGTGTGGCAGAGA 2580
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Db CTGCTAGAAATCCGAGACATTTAAATGGAACAGCTGCTCCGAGTGTGCAAGAAAGTGAAG 2877
QY CCAGCCAGCACAGACCTTTGTGCGAGACCATCTCCCTGCCCCAGTGGCAGCTGGGGAGTGG 2700
Db CCAGCCAGCACAGACCTTTGTGCGAGACCATCTCCCTGCCCCAGTGGCAGCTGGGGAGTGG 2937
QY TCATCATCTTCTTAAGACCTGTGGGAAGGTTACAAAAAAGAGCTTGAAGTGTCTGTCC 2760
Db TCATCATCTTCTTAAGACCTGTGGGAAGGTTACAAAAAAGAGCTTGAAGTGTCTGTCC 2997
QY CATGATGAGGGGTGTTATCTCATGAGAGCTGTGATCTCTTTAAAGAAACCTTAAACATTTTC 2820
Db CATGATGAGGGGTGTTATCTCATGAGAGCTGTGATCTCTTTAAAGAAACCTTAAACATTTTC 3057
QY ATAGACTTTTGGCAAAATGGCAGATTTAAGTGGTTTAAAGTGTGTAGCTTTGAGG 2880
Db ATAGACTTTTGGCAAAATGGCAGATTTAAGTGGTTTAAAGTGTGTAGCTTTGAGG 3117
QY CAAAGCAAGTGAAGAGGGCTGTGGCAGGAAACCAAGAGGCTTGGAGGATCCAGGCT 2940
Db CAAAGCAAGTGAAGAGGGCTGTGGCAGGAAACCAAGAGGCTTGGAGGATCCAGGCT 3177
QY ATCTTGGCCAGTAACCCAGTGAAGTGTATCAGTAAGTGGGATTTATGGGGGTAGATAGAAAA 3000
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QY GGAGTTGAATCATCAGAGTAACTGCCAGTTGCAAAATTTGATAGGATAGTGTAGTGGAT 3060
Db GGAGTTGAATCATCAGAGTAACTGCCAGTTGCAAAATTTGATAGGATAGTGTAGTGGAT 3297

QY 3061 TATTAACCTCTGAGCAGTGTATAGCATATAAANCCCGGGCAATTATTATTATTTC 3120
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QY 3121 TTTTGTACATCTATTACAAAGTTTGAAGAAAACAAAGCAATTGTCAAAAAA 3180
DB 3358 TTTTGTACATCTATTACAAAGTTTGAAGAAAACAAAGCAATTGTCAAAAAA 3417
QY 3181 AAAAAAAAAA 3193
DB 3418 AAAAAAAAAA 3430

RESULT 4

US-10-115-286-1
; Sequence 1, Application US/10115286
; Publication No. US20030166065A1
; GENERAL INFORMATION:
; APPLICANT: Jonak, Zdenka
; Trulli, Stephen
; Fornwald, James
; Terrett, Jonathan
; Hasting, Gregg
; TITLE OF INVENTION: No. US20030166065A1el Integrin Ligand ITGL-TSP
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ratner & Prestia
; STREET: Box 980
; CITY: Valley Forge
; STATE: PA
; COUNTRY: USA
; ZIP: 19482
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/115,286
; FILING DATE: 04-Apr-2002
; CLASSIFICATION: <Unknown>
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: 08/845,496
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Prestia, Paul F
; REGISTRATION NUMBER: 23,031
; REFERENCE/DOCKET NUMBER: GH-70000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-407-0700
; TELEFAX: 610-407-0701
; TELEX: 846169
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4014 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-115-286-1

Query Match 97.0%; Score 3161.6; DB 16; Length 4014;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 3178; Conservative 0; Mismatches 10; Indels 1; Gaps 1;
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QY 61 CTGCTCCGCGGGCGGTACTTGGCGGTGTGCGACCACTCTGGGCGCCCTCCGAGGAGGAC 120

DB 577 CTGCTCCGCGGGCGCTACTGCGCCGTGTGGAACGCACTCTGGGGCGCCCTCCGAGGAGGAC 636
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DB 877 GCCTCAGCTCTGCGAGGCGGTGCGGCGGCTTCTACTCTGCTGGGGGAGGCGTATTTC 936
QY 421 ATCCAGCGCTGCGCGCCGCGCAGGAGCGCTCTGCCACCGCGCCCGGAGGAGGAGCGG 480
DB 937 ATCCAGCGCTGCGCGCCGCGCAGGAGCGCTCTGCCACCGCGCCCGGAGGAGGAGCGG 996
QY 481 CCGGCACCACTACAGTTTCCACTCTCTGCGCGGAAATCGGCAGGCGGAGCTAGGCGGACG 540
DB 997 CCGGCACCACTACAGTTTCCACTCTCTGCGCGGAAATCGGCAGGCGGAGCTAGGCGGACG 1056
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QY 841 ATTCGTAATTCAGTTAGCTGTGGTGGTGAAGATCTTGGTTCATCCAGATGAACAGAG 900
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DB 1477 CAGCAACACCCAGCTGACCGGGATGACAGACCTATGACACAGCAATTTCTTTTACC 1536
QY 1021 AGACAGGACTTTGTGGGTCCAGACATGTGATACTCTTGGGATGGGTGTGTTGGAACT 1080
DB 1537 AGACAGGACTTTGTGGGTCCAGACATGTGATACTCTTGGGATGGGTGTGTTGGAACT 1596
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1897 CTGGCACCCTCTGACGATCCCAACCGGAGTGCAGTTTACATTTGGGAGGACTCCCAA 1956
1441 CACTGCCCTGATGACGACGACATGTAGCACCCTTGTGTGTACCGGCACTCTGTGGG 1500
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2017 GTGCTGGTGTGTAACCAACCAACCTTCCGCTGGGCGGATGGCACACAGCTGTGGAGAGGG 2076
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2317 GGAAAACTTTAGAGAGGAAACAATGTGAAGCACACAACAGTGTTCAAAAGCTTCTTTT 2376
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2497 GTAGATGGTACTCCATGTAGCCAGATTCACCTCTGTCTGTGTGCAAGGACAGTGTGTA 2556
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2281 ATTCTTAATGGTGACTACACTTTGTCCACTTTAGAGCAAGACATTTATGTACAAAGTGTT 2340
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2917 AAAGAGCCCTTGACCATCCAGGTTCTTACTGTGGGCAATGCGCTTCGACCTAAATTTAA 2976
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RESULT 5
US-10-757-450-1
; Sequence 1, Application US/10757450
; Publication No. US20040175794A1
; GENERAL INFORMATION:
; APPLICANT: Jonak, Zdenka
; Trulli, Stephen
; Fornwald, James

```
Terrett, Jonathan
Hasting, Gregg
TITLE OF INVENTION: Novel Integrin Ligand ITGL-TSP
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSER: Ratner & Prestia
STREET: Box 980
CITY: Valley Forge
STATE: PA
COUNTRY: USA
ZIP: 19482
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/757,450
FILING DATE: 04-Apr-2002
APPLICATION NUMBER: 08/845,496
FILING DATE: 15-Jan-2004
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/10/115,286
FILING DATE: 04-Apr-2002
APPLICATION NUMBER: 08/845,496
FILING DATE: 15-Jan-2004
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Prestia, Paul P
REGISTRATION NUMBER: 23,031
REFERENCE/DOCKET NUMBER: GH-70000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-407-0700
TELEFAX: 610-407-0701
TELEX: 846169
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4014 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-757-450-1
Query Match 97.08; Score 3161.6; DB 18; Length 4014;
Best Local Similarity 99.78; Pred. No. 0;
Matches 3178; Conservative 0; Mismatches 10; Indels 1; Gaps 1;
QY 1 ATGGGGAAACGGAGCGGGCTCCGGGCTCTCGGAGCTTTGGGCCCGTACCCACGCTGCTG 60
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DB 637 GAGAGCTAGTGTGTCGGAGCTGAGCGCGCCCGGGACACGGGACACGCGCTCCGC 696
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QY 361 GCGCTCAGCTCTCGAGGGGTGCGCGCGCTTCTACCTGCTGGGGAGGCGGTATTTC 420
DB 877 GCGCTCAGCTCTCGAGGGGTGCGCGCGCTTCTACCTGCTGGGGAGGCGGTATTTC 936
QY 421 ATCCAGCCGCTGCCCGCCGCGCAGCAGCGCTCTGCCACCGCCGCCCCAGGGAGAGCCG 480
DB 937 ATCCAGCCGCTGCCCGCCGCGCAGCAGCGCTCTGCCACCGCCGCCCCAGGGAGAGCCG 996
QY 481 CCGGACCACTACAGTTCCACCTCTCGCGCGGAATCGCAGCGCGCGCTAGGCGGCACG 540
DB 997 CCGGACCACTACAGTTCCACCTCTCGCGCGGAATCGCAGCGCGCGCTAGGCGGCACG 1056
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DB 1597 GTGTGTATCCGAGCAGAGCACTGCTCGCTCATAGAGATGATGTTTACAGCTGCGCTTC 1656
QY 1141 ACCACAGCCCATGAATTTAGGCCACGCTGTTTAAACATGCAATGATGATGCAAAAGCAGTGT 1200
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QY 1201 GCCAGCCTTAATGGTGTGAACCCAGGATTCACAGATGCGGCTCAATGCTTTTCAACCTG 1260
DB 1717 GCCAGCCTTAATGGTGTGAACCCAGGATTCACAGATGCGGCTCAATGCTTTTCAACCTG 1776
QY 1261 GACACAGCAGCGCTTGGTCTCTTTCAGTGGCTTACATGATTAATCATTTCTGGAATAAT 1320
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QY 1321 GGTTCATGGGAATGTTTGTGGAACAAGCTCCAGATCCCATACAGCTCCCAAGGCGATCTC 1380
DB 1837 GGTTCATGGGAATGTTTGTGGAACAAGCTCCAGATCCCATACAGCTCCCAAGGCGATCTC 1896
QY 1381 CCTGGCACTCTGTAAGTGAACCCAGGATTCAGAGTTCAGATTTTACATTTGGGGAGGATCTCAA 1440
DB 1897 CCTGGCACTCTGTAAGTGAACCCAGGATTCAGAGTTCAGATTTTACATTTGGGGAGGATCTCAA 1956
QY 1441 CACTGCGCTGATGAGCGCAGCAATGTAGCACTTTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1500
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QY 2161 TATCATGATATCATACAAATTCGAATCGAGCCCAACCAATCGAAGTGAACAGCGGAC 2220
Db 2677 TATCATGATATCATACAAATTCGAATCGAGCCCAACCAATCGAAGTGAACAGCGGAC 2736
QY 2221 CAGAGGGGATCAGGAACAAATGGCAGCTTCTTGCCATCAAAAGCTGCTGATGGCACATAT 2280
Db 2737 CAGAGGGGATCAGGAACAAATGGCAGCTTCTTGCCATCAAAAGCTGCTGATGGCACATAT 2796
QY 2281 ATTCTTAATGGTACTACACTTTGTCCACTTTAGAGCAAGACATATGTACAAAGGTGT 2340
Db 2797 ATTCTTAATGGTACTACACTTTGTCCACTTTAGAGCAAGACATATGTACAAAGGTGT 2856
QY 2341 GTCTTAGGTACAGGGCTTCTCTGGGCAATTTGGAAGAAATTCGACGCTTTAGCCCTCTC 2400
Db 2857 GTCTTAGGTACAGGGCTTCTCTGGGCAATTTGGAAGAAATTCGACGCTTTAGCCCTCTC 2916
QY 2401 AAAGAGCCCTTCACCATCCAGGTCTTACTGTGGGCAATGCCCTTCGACCTAAATTTAA 2460
Db 2917 AAAGAGCCCTTCACCATCCAGGTCTTACTGTGGGCAATGCCCTTCGACCTAAATTTAA 2976
QY 2461 TACACTACTTCTGAAGAAGAGGAATCTTTCAATGCTATCCCCACTTTTTCAGCA 2520
Db 2977 TACACTACTTCTGAAGAAGAGGAATCTTTCAATGCTATCCCCACTTTTTCAGCA 3036
QY 2521 TGGGTCAATGAAGTGGGCGAATGTTCTAAGTCATGTGAATGGTTGGGAGAGAGA 2580
Db 3037 TGGGTCAATGAAGTGGGCGAATGTTCTAAGTCATGTGAATGGTTGGGAGAGAGA 3096
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QY 2581 CTGGTAGAATCCGAGACATTAATGACAGCCTGCTCCGAGTGTGCAAGGAAGTGAAG 2640
Db 3097 CTGGTAGAATCCGAGACATTAATGACAGCCTGCTCCGAGTGTGCAAGGAAGTGAAG 3156
QY 2641 CCAGCCAGACACAGACCTTTGTGACACCATCTCCCTGCCCCAGTGGCAGCTGGGGAGTGG 2700
Db 3157 CCAGCCAGACACAGACCTTTGTGACACCATCTCCCTGCCCCAGTGGCAGCTGGGGAGTGG 3216
QY 2701 TCATCATGTTCTTAAGACCTGTGGGAGGTTTCAAAAAAAGAGCTTGAAGTGTCTGTCC 2760
Db 3217 TCATCATGTTCTTAAGACCTGTGGGAGGTTTCAAAAAAAGAGCTTGAAGTGTCTGTCC 3276
QY 2761 CATGATGGAGGGTGTATCTCATGAGAGCTGTGATCCTTTAAAGAAACCTTAAACATTTTC 2820
Db 3277 CATGATGGAGGGTGTATCTCATGAGAGCTGTGATCCTTTAAAGAAACCTTAAACATTTTC 3336
QY 2821 ATAGACTTTTGCACAAATGGCAGAAATGCAGTTAAAGTGGTTTAAAGTGGTGTAGCTTTGA-G 2879
Db 3337 ATAGACTTTTGCACAAATGGCAGAAATGCAGTTAAAGTGGTTTAAAGTGGTGTAGCTTTGAGG 3396
QY 2880 GCAAGCGCAAGTGAAGGAGGCTGTCAGGGAAGAGCAAGAGCTGGAGGATCCAGCG 2939
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Db 3457 TATCTTGGCAGTAACCAAGTGGTGTATCAGTAAGTGGGATTTATGGGGTAGATAGAAA 3516
QY 3000 AGGAGTTGAATCATCAGAGTAAACTGCGCAGTTGCAAAATTTGATAGATAGTTAGTGAGGA 3059
Db 3517 AGGAGTTGAATCATCAGAGTAAACTGCGCAGTTGCAAAATTTGATAGATAGTTAGTGAGGA 3576
QY 3060 TTATTAACCTCTGAGCAGTGATATAGCAATATAAANCCCCGGGCATTTATTATTATTT 3119
Db 3577 TTATTAACCTCTGAGCAGTGATATAGCAATATAAAGCCCCGGGCATTTATTATTATTT 3636
QY 3120 CTTTGTGTACATCTATTACAAAGTTTAGAAAAACAAAGCAATTTGCAAAAAAAGAAAAA 3179
Db 3637 CTTTGTGTACATCTATTACAGTTTAGAAAAACAAAGCAATTTGCAAAAAAAGTTAGAA 3696
QY 3180 AAAAAAAA 3188
Db 3697 CTATTACAA 3705

RESULT 6
US-10-105-929-1
; Sequence 1, Application US/10105929
; Publication No. US20020137142A1
; GENERAL INFORMATION:
; APPLICANT: Holtzman, Douglas A.
; APPLICANT: Goodearl, Andrew D.J.
; TITLE OF INVENTION: TANGO-71, TANGO-73, TANGO-74, TANGO-76, AND TANGO-83
; FILE REFERENCE: 09404/041001
; CURRENT APPLICATION NUMBER: US/10/105,929
; CURRENT FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/130,491
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-08-07
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/058,108
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-09-05
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/054,961
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-08-06
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 4676
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (460)...(3360)
US-10-105-929-1
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Db 2611 GGGGGAATGGATCTACTTTGTAATAAAAAATATCAGGATCAGTTACTAGTGCAAAACCTTGA 2670
QY 2161 TATCATGATATCATCACAAATTCCTACTGAGCCACCAACATCAAGTGAACAGCGGAC 2220
Db 2671 TATCATGATATCATCACAAATTCCTACTGAGCCACCAACATCAAGTGAACAGCGGAC 2730
QY 2221 CAGAGGGATCAGGAACAATGCGAGCTTCTTGCCATCAAAAGCTGCTGATGGCACATAT 2280
Db 2731 CAGAGGGATCAGGAACAATGCGAGCTTCTTGCCATCAAAAGCTGCTGATGGCACATAT 2790
QY 2281 ATTCTTAATGGTGAATACACTTTGTCCACTTTAGAGCAAGACATATGATACAAAGTGT 2340
Db 2791 ATTCTTAATGGTGAATACACTTTGTCCACTTTAGAGCAAGACATATGATACAAAGTGT 2850
QY 2341 GTCTTGAGTACAGCGGCTCTCTGGGCAATTTGGAAGAAATTCGAGCTTTAGCCCTCTC 2400
Db 2851 GTCTTGAGTACAGCGGCTCTCTGGGCAATTTGGAAGAAATTCGAGCTTTAGCCCTCTC 2910
QY 2401 AAAGAGCCCTTGACCATCCAGGTTCTTACTGTGGGCAATGCCCTTCGACCTAAATTTAA 2460
Db 2911 AAAGAGCCCTTGACCATCCAGGTTCTTACTGTGGGCAATGCCCTTCGACCTAAATTTAA 2970
QY 2461 TACACTACTCTCGTAAAGAAAGAAAGAAATCTTCAATGCTATCCCACTTTTTCAGCA 2520
Db 2971 TACACTACTCTCGTAAAGAAAGAAAGAAATCTTCAATGCTATCCCACTTTTTCAGCA 3030
QY 2521 TGGGTCAATGAGAGTGGGGCAATGTTCTTAAGTCAATGATGTAATGGTGGCAGAGAGA 2580
Db 3031 TGGGTCAATGAGAGTGGGGCAATGTTCTTAAGTCAATGATGTAATGGTGGCAGAGAGA 3090
QY 2581 CTGGTAGAATCCGAGACATTAATGACAGCTGCTTCCAGTGTGCAAGGAAGTGAAG 2640
Db 3091 CTGGTAGAATCCGAGACATTAATGACAGCTGCTTCCAGTGTGCAAGGAAGTGAAG 3150
QY 2641 CCAGCAGACACAGACCTTTGTGACAGACCAATCCCTGCCCCAGTGGAGTGG 2700
Db 3151 CCAGCAGACACAGACCTTTGTGACAGACCAATCCCTGCCCCAGTGGAGTGG 3210
QY 2701 TCATCATGTTCTAAGACCTGTGGAGGTTTACAAAGAAAGCTTGAAGTGTCTGTC 2760
Db 3211 TCATCATGTTCTAAGACCTGTGGAGGTTTACAAAGAAAGCTTGAAGTGTCTGTC 3270
QY 2761 CATGATGAGGGGTGTATCTCATGAGAGCTGTGATCTTTAAAGAAACCTTAAACATTTT 2820
Db 3271 CATGATGAGGGGTGTATCTCATGAGAGCTGTGATCTTTAAAGAAACCTTAAACATTTT 3330
QY 2821 ATAGACTTTTGCACAAATGCGAGATGCGATTAAGTGGTTTAAAGTGGTGTAGCTTTGA-G 2879
Db 3331 ATAGACTTTTGCACAAATGCGAGATGCGATTAAGTGGTTTAAAGTGGTGTAGCTTTGAGG 3390
QY 2880 GCAAGGCAAGTGAGAGGGCTGTGTCAGGGAAGCAAGAGGCTGGAGGGATCCAGCG 2939
Db 3391 GCAAGGCAAGTGAGAGGGCTGTGTCAGGGAAGCAAGAGGCTGGAGGGATCCAGCG 3450
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Db 3451 TATCTTGCAGGTAAACAGTGAAGTGTATCAGTAAAGTGGGATTTATGGGGTAGATAGAAA 3510
QY 3000 AGGAGTTGAATCATCAGAGTAAACTGCCAGTTGCAAAATTTGATAGATAGTTAGTAGAGA 3059
Db 3511 AGGAGTTGAATCATCAGAGTAAACTGCCAGTTGCAAAATTTGATAGATAGTTAGTAGAGA 3570
QY 3060 TTATTAACCTCTGAGCAGTGATATAGCAATAAANCCCCGGGCATTATTTATTTT 3119
Db 3571 TTATTAACCTCTGAGCAGTGATATAGCAATAAANCCCCGGGCATTATTTATTTT 3630
QY 3120 CTTTGTGTACATCTATTACAGTTTGTAGAAAAACCAAGCAATTTGTCAAAAAAATAAAAA 3179
Db 3631 CTTTGTGTACATCTATTACAGTTTGTAGAAAAACCAAGCAATTTGTCAAAAAAATAAAAA 3690
QY 3180 AAAAAAAA 3188
Db 3691 CTTATTACAA 3699

RESULT 7
US-10-755-889-133
; Sequence 133, Application US/10755889
; Publication No. US20040171823A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES ASSOCIATED WITH THE NF-KB
; TITLE OF INVENTION: PATHWAY
; FILE REFERENCE: D0284 NP
; CURRENT APPLICATION NUMBER: US/10/755,889
; CURRENT FILING DATE: 2004-01-13
; PRIOR APPLICATION NUMBER: U.S. 60/440,068
; PRIOR FILING DATE: 2003-01-14
; PRIOR APPLICATION NUMBER: U.S. 60/469,757
; PRIOR FILING DATE: 2003-05-12
; NUMBER OF SEQ ID NOS: 823
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 133
; LENGTH: 4447
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-755-889-133

Query Match 96.9%; Score 3158.4; DB 18; Length 4447;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 3176; Conservative 0; Mismatches 12; Indels 1; Gaps 1;

QY 1 ATGGGGAACGCGAGCGGGCTCCGGGGTCTCGAGCTTTGGCCCCGTACCCACGCTGCTG 60
Db 294 ATGGGGAACGCGAGCGGGCTCCGGGGTCTCGAGCTTTGGCCCCGTACCCACGCTGCTG 353
QY 61 CTGCTCGCGCGGGCCTACTGSCCCTGTGAGCAGCTCGGGCGCCCTCCCGAGGAGAC 120
Db 354 CTGCTCGCGCGGGCCTACTGSCCCTGTGAGCAGCTCGGGCGCCCTCCCGAGGAGAC 413
QY 121 GAGGAGCTAGTGTGCTCCGAGCTGAGCGCGCCCGGACACGGACACACGCGCTCCGC 180
Db 414 GAGGAGCTAGTGTGCTCCGAGCTGAGCGCGCCCGGACACGGACACACGCGCTCCGC 473
QY 181 CTGACAGCCTTTGACCAAGCAGCTGATCTGAGCTGCGGCGCCGACAGAGCTTTTGGCG 240
Db 474 CTGACAGCCTTTGACCAAGCAGCTGATCTGAGCTGCGGCGCCGACAGAGCTTTTGGCG 533
QY 241 CCGCGCTTCAAGCTCCAGAACTGGGGCGCAATCCGGGTCCGAGACGCGCTTCGGAA 300
Db 534 CCGCGCTTCAAGCTCCAGAACTGGGGCGCAATCCGGGTCCGAGACGCGCTTCGGAA 593
QY 301 ACCGACCTGGCGCACTGCTTCTACTCCGCGCACCGTGAATGGCGATCCAGCTTCGGCTGCC 360
Db 594 ACCGACCTGGCGCACTGCTTCTACTCCGCGCACCGTGAATGGCGATCCAGCTTCGGCTGCC 653
QY 361 GCGCTCAGCCTCTGAGGGGTGCGCGCGCTTCTACTCTGCTGGGGAGGCGTATTTTC 420
Db 654 GCGCTCAGCCTCTGAGGGGTGCGCGCGCTTCTACTCTGCTGGGGAGGCGTATTTTC 713
QY 421 ATCCAGCGCTGCGCGCGCCAGCGAGCGCTTCGCCACCGCGCCCGCCAGGGGAGAGCGCG 480
Db 714 ATCCAGCGCTGCGCGCGCCAGCGAGCGCTTCGCCACCGCGCCCGCCAGGGGAGAGCGCG 773
QY 481 CCGGCAACCACTACAGTTCCACCTCTGCGGGCGGAATCCGAGGGCGACCTAGCGCGCACG 540
Db 774 CCGGCAACCACTACAGTTCCACCTCTGCGGGCGGAATCCGAGGGCGACCTAGCGCGCACG 833
QY 541 TCGCGGGTCTGTGAGACGAGCGCGCGCGCTGCGGAAGCGGAGACCGAAGACGAGGAC 600
Db 834 TCGCGGGTCTGTGAGACGAGCGCGCGCGCTGCGGAAGCGGAGACCGAAGACGAGGAC 893
QY 601 GAAGGAGCTGAGGGGAGGACGAGAGGCTCTAGTGTGCTGCGCAGGACCCCGACCTGCAA 660
Db 894 GAAGGAGCTGAGGGGAGGACGAGAGGCTCTAGTGTGCTGCGCAGGACCCCGACCTGCAA 953

QY	661	GGCGTAGGACAGCCACAGGAACTGGAAGCATAGAAAGAGCGATTTGTGTCCAGTCAC	720
DB	954	GGGGTAGGACAGCCACAGGAACTGGAGCATAGAAAGAGCGATTTGTGTCCAGTCAC	1013
QY	721	CGCTATGTGGAAACCATGCTTGTGGCAGACCACTGATGCGAGATTTCCACGGCAGTGGT	780
DB	1014	CGCTATGTGGAAACCATGCTTGTGGCAGACCACTGATGCGAGATTTCCACGGCAGTGGT	1073
QY	781	CTAAGCATTTACCTTCTCAGTTGTTTTCGGTGGCAGCCAGATTTGTACAAACACCCAGC	840
DB	1074	CTAAGCATTTACCTTCTCAGTTGTTTTCGGTGGCAGCCAGATTTGTACAAACACCCAGC	1133
QY	841	ATTTCGTAATTCAGTTAGCCCTGGTGGTGAAGATCTTGGTCACTCCACGATGAACAGAAG	900
DB	1134	ATTTCGTAATTCAGTTAGCCCTGGTGGTGAAGATCTTGGTCACTCCACGATGAACAGAAG	1193
QY	901	GGCCCGGAAGTAGCTTCCAAATGCTGCCCTCACCTCTGGGGAACCTTTTGGCAACTGGCAGAAG	960
DB	1194	GGCCCGGAAGTAGCTTCCAAATGCTGCCCTCACCTCTGGGGAACCTTTTGGCAACTGGCAGAAG	1253
QY	961	CAGCAAAACCCACCGATGACCGGATGACAGACCATATGACACAGCAATTTCTTTTTCACC	1020
DB	1254	CAGCAAAACCCACCGATGACCGGATGACAGACCATATGACACAGCAATTTCTTTTTCACC	1313
QY	1021	AGACAGGACTTGTGTGGTCCCAGACATGTGATCTCTTGGGATGGCTGATGTGGAACT	1080
DB	1314	AGACAGGACTTGTGTGGTCCCAGACATGTGATCTCTTGGGATGGCTGATGTGGAACT	1373
QY	1081	GTGTGTATCCGAGCAGAAAGCTGCTCCGTATAGAAAGATGATGGTTTAAAGCTGCTTTC	1140
DB	1374	GTGTGTATCCGAGCAGAAAGCTGCTCCGTATAGAAAGATGATGGTTTAAAGCTGCTTTC	1433
QY	1141	ACCACAGCCCATGAATTTAGGCGCAGCTGTTTAAATGCGCATGATGATGCAAGACAGTGT	1200
DB	1434	ACCACAGCCCATGAATTTAGGCGCAGCTGTTTAAATGCGCATGATGATGCAAGACAGTGT	1493
QY	1201	GCCAGCCTTAATGTGTGAACAGGATTTCCACATGATGCGCTCAATGCTTTCACACCTG	1260
DB	1494	GCCAGCCTTAATGTGTGAACAGGATTTCCACATGATGCGCTCAATGCTTTCACACCTG	1553
QY	1261	GACCACAGCCAGCCTTGGTCTCCTTGCAGTGCCCTPACATGATTAATCATATTTCTGGATAAT	1320
DB	1554	GACCACAGCCAGCCTTGGTCTCCTTGCAGTGCCCTPACATGATTAATCATATTTCTGGATAAT	1613
QY	1321	GGTATGCGGAATGTTTGTATGAGCAAGCCTCAGATCCCATACAGCTCCCGAGGCGATCTC	1380
DB	1614	GGTATGCGGAATGTTTGTATGAGCAAGCCTCAGATCCCATACAGCTCCCGAGGCGATCTC	1673
QY	1381	CCTGGCACCTCGTACGATGCCAACCGCAGTGCCAGTTTACATTTGGGGAGGAGCTCCAAA	1440
DB	1674	CCTGGCACCTCGTACGATGCCAACCGCAGTGCCAGTTTACATTTGGGGAGGAGCTCCAAA	1733
QY	1441	CACCTGCCCTGATGAGCCAGCAGATGATGACCTTGTGGTGTACCCGACCTCTGTGGGG	1500
DB	1734	CACCTGCCCTGATGAGCCAGCAGATGATGACCTTGTGGTGTACCCGACCTCTGTGGGG	1793
QY	1501	GTGCTGTGTGTCAAACCAAACCTTCCGTGGCGGATGGCACCAGCTGTGGAGAGGG	1560
DB	1794	GTGCTGTGTGTCAAACCAAACCTTCCGTGGCGGATGGCACCAGCTGTGGAGAGGG	1853
QY	1561	AAATGTGTATCAACGGCAAGTGTGAACAAACCCAGACAGAAAGCATTTGTATCGCCT	1620
DB	1854	AAATGTGTATCAACGGCAAGTGTGAACAAACCCAGACAGAAAGCATTTGTATCGCCT	1913
QY	1621	TTTTCATGGAAGCTGGGGAATGTGGGGCTTTGGGGAGATGTTTCCAGAACGTGCGGTGGA	1680
DB	1914	TTTTCATGGAAGCTGGGGAATGTGGGGCTTTGGGGAGATGTTTCCAGAACGTGCGGTGGA	1973
QY	1681	GGAGTCCAGTACAGATGAGGAATGTGAACACCGATGCCAAGAAATGAGGGAAGTAC	1740
DB	1974	GGAGTCCAGTACAGATGAGGAATGTGAACACCGATGCCAAGAAATGAGGGAAGTAC	2033
QY	1741	TGTGAAGGCAACAGGTGCGCTACAGATCCTGTGTAACCTTTGAGGACTGTCCAGACAAATAAT	1800

DB	2034	TGTGAAGGCAACAGGTGCGCTACAGATCCTGTAACTTTGAGGACTGTCCAGACAAATAAT	2093
QY	1801	GGAAACACCTTTAGAGAGGAAACAAATGTGAAGCACACAAAGAGTTTCAAAGCTTCTCTTT	1860
DB	2094	GGAAACACCTTTAGAGAGGAAACAAATGTGAAGCACACAAAGAGTTTCAAAGCTTCTCTTT	2153
QY	1861	GGAGTGGGCTGCGGTGGGAATTCACAGTACGCTGGGCTCTCAACAAAGGACAGG	1920
DB	2154	GGAGTGGGCTGCGGTGGGAATTCACAGTACGCTGGGCTCTCAACAAAGGACAGG	2213
QY	1921	TGCAAGCTCATCTGCCAAGCACAAGCANTGGCTACTTCTTCTGTTTTGAGCCCAAGGTT	1980
DB	2214	TGCAAGCTCATCTGCCAAGCACAAGCANTGGCTACTTCTTCTGTTTTGAGCCCAAGGTT	2273
QY	1981	GTAGATGGTACTCCATGTAGCCAGATTCACCTCTGTCTGTGCAAGGACAGTGTGTA	2040
DB	2274	GTAGATGGTACTCCATGTAGCCAGATTCACCTCTGTCTGTGCAAGGACAGTGTGTA	2333
QY	2041	AAAGCTGGTGTGATCGCATCATAGACTCCAAAGAAAGTTTGATAAATGTGTGTTTGC	2100
DB	2334	AAAGCTGGTGTGATCGCATCATAGACTCCAAAGAAAGTTTGATAAATGTGTGTTTGC	2393
QY	2101	GGGGAAATGGATCTACTTTGTAAGAAATATCAGGATCAGTTACTAGTGAACACCTGGA	2160
DB	2394	GGGGAAATGGATCTACTTTGTAAGAAATATCAGGATCAGTTACTAGTGAACACCTGGA	2453
QY	2161	TATCATGATATCATCAAAATTCACCTGGAGCCACCAACATCGAAGTGAACACGCGAAC	2220
DB	2454	TATCATGATATCATCAAAATTCACCTGGAGCCACCAACATCGAAGTGAACACGCGAAC	2513
QY	2221	CAGAGGGGATCCAGGAACCAATGGCAGCTTTCTTGCCATCAAAGCTGCTGATGGCACATAT	2280
DB	2514	CAGAGGGGATCCAGGAACCAATGGCAGCTTTCTTGCCATCAAAGCTGCTGATGGCACATAT	2573
QY	2281	ATTCTTAATGGTGACTACCTTTGTCCAATTTAGCAAGACACATTTATGTAACAAAGTGT	2340
DB	2574	ATTCTTAATGGTGACTACCTTTGTCCAATTTAGCAAGACACATTTATGTAACAAAGTGT	2633
QY	2341	GTCTTGAGGTACAGCGGCTCTCTCGGGCATTCGMAAGAAATTCGACGCTTTAGGCCCTCTC	2400
DB	2634	GTCTTGAGGTACAGCGGCTCTCTCGGGCATTCGMAAGAAATTCGACGCTTTAGGCCCTCTC	2693
QY	2401	AAAGAGCCCTTGACCATCCAGGTTCTTACTGTGGGCAATGCCCTTCGACCTAAATTAATA	2460
DB	2694	AAAGAGCCCTTGACCATCCAGGTTCTTACTGTGGGCAATGCCCTTCGACCTAAATTAATA	2753
QY	2461	TACACCTATCTTCTGTAAGAAAGAAAGGAATCTTTCAATGCTATCCCCACCTTTTTCAGCA	2520
DB	2754	TACACCTATCTTCTGTAAGAAAGAAAGGAATCTTTCAATGCTATCCCCACCTTTTTCAGCA	2813
QY	2521	TGGGTCAATTCAGAGGTGGGCGGAATGTTCTAAGTCAATGCAATTTGGGTGGCAGAGAAGA	2580
DB	2814	TGGGTCAATTCAGAGGTGGGCGGAATGTTCTAAGTCAATGCAATTTGGGTGGCAGAGAAGA	2873
QY	2581	CTGCTAGAATGCCAGACATTAATGACAGCTGCTTCCGAGTGTGCAAAAGGAGTGAAG	2640
DB	2874	CTGCTAGAATGCCAGACATTAATGACAGCTGCTTCCGAGTGTGCAAAAGGAGTGAAG	2933
QY	2641	CCAGCCAGCACAGACCTTGTGAGACCATCCCTGCCCCCAAGTGGCAGCTGGGGAGTGG	2700
DB	2934	CCAGCCAGCACAGACCTTGTGAGACCATCCCTGCCCCCAAGTGGCAGCTGGGGAGTGG	2993
QY	2701	TCATCATGTTCTAAGACCTGTGGAGGGTTTACAAAAGAAAGACCTTTGAAGTGTCTGTCC	2760
DB	2994	TCATCATGTTCTAAGACCTGTGGAGGGTTTACAAAAGAAAGACCTTTGAAGTGTCTGTCC	3053
QY	2761	CATGATCGAGGGTGTATCTCATGAGAGCTGTGATCCTTTTAAAGAAACCTTAAACATTTTC	2820
DB	3054	CATGATCGAGGGTGTATCTCATGAGAGCTGTGATCCTTTTAAAGAAACCTTAAACATTTTC	3113
QY	2821	ATAGACTTTTGCACAAATGGCAGAAATGCAAGTGTAAAGTGTGTTAAGTGTGTTAGCTTTGA-G	2879

Db 3114 ATAGACTTTTGCACAATGCGAGATGCACTTAAGTGGTTTAAAGTGGTGTAGCTTTGAGG 3173
QY 2880 GCAAGCGAAAGTGAAGGGCTGGTGCAGGGAAGCAAGAGAGCTGGAGGATCCAGCG 2939
Db 3174 GCAAGCGAAAGTGAAGGGCTGGTGCAGGGAAGCAAGAGAGCTGGAGGATCCAGCG 3233
QY 2940 TATCTTGCAGTAACCAAGTGAAGTGTATCAGTAAGTGGGATTAAGTGGGATAGATAGAAA 2999
Db 3234 TATCTTGCAGTAACCAAGTGAAGTGTATCAGTAAGTGGGATTAAGTGGGATAGATAGAAA 3293
QY 3000 AGAGTTGAATCATCAGAGTAACCTGCCAGTTGCAAAATTTGATAGATAGTTAGTGAGGA 3059
Db 3294 AGAGTTGAATCATCAGAGTAACCTGCCAGTTGCAAAATTTGATAGATAGTTAGTGAGGA 3353
QY 3060 TTATTAACTCTGAGCAGTGATATAGCATTAATAAANCCCGGCATTATTATTATTATTT 3119
Db 3354 TTATTAACTCTGAGCAGTGATATAGCATTAATAAAGCCCCGGGCATTATTATTATTATTT 3413
QY 3120 CTTTGTGTACATCTATTACAAAGTTTAGAAAAAACAAGCAATTTGCAAAAAAATAAAAA 3179
Db 3414 CTTTGTGTACATCTATTACAAAGTTTAGAAAAAACAAGCAATTTGCAAAAAAATAAAAA 3473
QY 3180 AAAAAAAA 3188
Db 3474 CTATTACAA 3482

RESULT 8

US-10-741-600-776
; Sequence 776, Application US/10741600
; Publication No. US20050026169A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; FILE REFERENCE: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
; CURRENT APPLICATION NUMBER: US/10/741,600
; CURRENT FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 73997
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 776
; LENGTH: 4352
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(4352)
; OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables 1-
US-10-741-600-776

Query Match 96.8%; Score 3157.4; DB 19; Length 4352;
Best Local Similarity 99.4%; Pred. No. 0;
Matches 3169; Conservative 8; Mismatches 11; Indels 1; Gaps 1;
QY 1 ATGGGGAACCGCGAGCGGCTCCGGGCTCTCGAGCTTTGGGCCCGTACCACGCTGCTG 60
Db 513 ATGGGGAACCGCGAGCGGCTCCGGGCTCTCGAGCTTTGGGCCCGTACCACGCTGCTG 572
QY 61 CTGCTCGCGCGCGGCTACTGCGCGGTGTCGAGCGCACTCGGCGGCCCTCCGAGAGGAC 120
Db 573 CTGCTCGCGCGCGGCTACTGCGCGGTGTCGAGCGCACTCGGCGGCCCTCCGAGAGGAC 632
QY 121 GAGGAGCTAGTGGTCCGAGCTGAGCGCGGCCCGGACAGGACCGGCTCCGCG 180
Db 633 GAGGAGCTAGTGGTCCGAGCTGAGCGCGGCCCGGACAGGACCGGCTCCGCG 692
QY 181 CTGCAAGCTTTGACCAAGCTGATCTGAGCTGCGGCCCGGACAGCAGCTTTTGGCG 240
Db 693 CTGCAAGCTTTGACCAAGCTGATCTGAGCTGCGGCCCGGACAGCAGCTTTTGGCG 752
QY 241 CCCGGCTTCAAGCTCCAGAACTGGGGCGCAATTCGGGTCCGAGACGCGCTTCGGAA 300
Db 753 CCCGGCTTCAAGCTCCAGAACTGGGGCGCAATTCGGGTCCGAGACGCGCTTCGGAA 812

QY 301 ACCGACCTGGCGCACTGCTTCTTACTCCGCGCACCGTGAATGGCGATCCAGACTCGCTGCC 360
Db 813 ACCGACCTGGCGCACTGCTTCTTACTCCGCGCACCGTGAATGGCGATCCAGACTCGCTGCC 872
QY 361 GCCCTCAGCTCTCGAGGGGCTGCGCGCGCTTCTTACTCTGCTGGGGAGCGCTATTTTC 420
Db 873 GCCCTCAGCTCTCGAGGGGCTGCGCGCGCTTCTTACTCTGCTGGGGAGCGCTATTTTC 932
QY 421 ATCCAGCGCTGCCCGCGCGAGCGAGCGCTCGGCAACGCGCGCCCGCCAGGGGAGAGCCG 480
Db 933 ATCCAGCGCTGCCCGCGCGAGCGAGCGCTCGGCAACGCGCGCCCGCCAGGGGAGAGCCG 992
QY 481 CGGCGACCACTACAGTTCACCTCTGCGGGGGAATCGGCGAGGGGAGCTGTAGCGGCGAG 540
Db 993 CGGCGACCACTACAGTTCACCTCTGCGGGGGAATCGGCGAGGGGAGCTGTAGCGGCGAG 1052
QY 541 TCGCGGGTCTGGGACGAGCGAGCCCGCGCGACTGGGAAAGCGGAGACCGGAGACGAGAC 600
Db 1053 TCGCGGGTCTGGGACGAGCGAGCCCGCGCGACTGGGAAAGCGGAGACCGGAGACGAGAC 1112
QY 601 GAAGGACTGAGGGCGAGGACGAAGGGCTCTAGTGGTGGCGCAGGACCGGCGACTGCNA 660
Db 1113 GAAGGACTGAGGGCGAGGACGAAGGGCTCTAGTGGTGGCGCAGGACCGGCGACTGCNA 1172
QY 661 GCGGTAGGACAGCCCAAGGAACTGGAAGCATTAAGAAAGAGCGAGTGTGTCCAGTCA 720
Db 1173 GCGGTAGGACAGCCCAAGGAACTGGAAGCATTAAGAAAGAGCGAGTGTGTCCAGTCA 1232
QY 721 CGCTATGTGGAACCATCTGTGTGGCAGACCAAGTGCATGGCAGAAATCCAGCGAGTGT 780
Db 1233 CGCTATGTGGAACCATCTGTGTGGCAGACCAAGTGCATGGCAGAAATCCAGCGAGTGT 1292
QY 781 CTAAAGCATTTACTTCTCAGCTTGTTCGTGGCGAGCGAGTGTGTACAAACACCCAGC 840
Db 1293 CTAAAGCATTTACTTCTCAGCTTGTTCGTGGCGAGCGAGTGTGTACAAACACCCAGC 1352
QY 841 ATTCTTAATTCAGTTAGCTGTGTGTGAAGATCTTGTGTCTATCAGCATCAACAGAG 900
Db 1353 ATTCTTAATTCAGTTAGCTGTGTGTGAAGATCTTGTGTCTATCAGCATCAACAGAG 1412
QY 901 GGGCGGAAGTGACCTCCAATGCTGCCCTCACTCTCGGAACTTTTGAACCTGGCAGAG 960
Db 1413 GGGCGGAAGTGACCTCCAATGCTGCCCTCACTCTCGGAACTTTTGAACCTGGCAGAG 1472
QY 961 CAGCAACACCCAGTGAACCGGATGCGAGGACTATGACACAGCATTTCTTTTCAAC 1020
Db 1473 CAGCAACACCCAGTGAACCGGATGCGAGGACTATGACACAGCATTTCTTTTCAAC 1532
QY 1021 AGACAGGACTTGTGGGTCCAGACATGTGATCTCTTGGGATGGCTGATGTTGAACT 1080
Db 1533 AGACAGGACTTGTGGGTCCAGACATGTGATCTCTTGGGATGGCTGATGTTGAACT 1592
QY 1081 GTGTGTGATCCGAGCAGAGCTGCTCCGTCTATGAGAGATGATGTTTCAAGCTGCCCTTC 1140
Db 1593 GTGTGTGATCCGAGCAGAGCTGCTCCGTCTATGAGAGATGATGTTTCAAGCTGCCCTTC 1652
QY 1141 ACCACAGCCATGAATTAAGGCCACGTGTTTAACATGCCACATGATGATGATCAAGCATGT 1200
Db 1653 ACCACAGCCATGAATTAAGGCCACGTGTTTAACATGCCACATGATGATGATCAAGCATGT 1712
QY 1201 GCCAGCTTTAATGTGTGAACCCAGGATTTCCACATGATGGGCTCAATGCTTTCCAACTG 1260
Db 1713 GCCAGCTTTAATGTGTGAACCCAGGATTTCCACATGATGGGCTCAATGCTTTCCAACTG 1772
QY 1261 GACCAAGCCAGCTTGGTCTCTTTCAGTGCCTTACATGATTAATCAATTTCTGATAT 1320
Db 1773 GACCAAGCCAGCTTGGTCTCTTTCAGTGCCTTACATGATTAATCAATTTCTGATAT 1832
QY 1321 GGTCTAGGGGAATGTTTGAAGCAAGCTTCAGATTCAGATCCATACAGTCCCAGCGGATCTC 1380
Db 1833 GGTCTAGGGGAATGTTTGAAGCAAGCTTCAGATTCAGATCCATACAGTCCCAGCGGATCTC 1892

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QY 1381 CTTGGCACTCGTACGATGCCAACCGCGAGTGCAGTTTACATTTGGGGAGGACTCCAAA 1440
Db 1893 CTTGGCACTCGTACGATGCCAACCGCGAGTGCAGTTTACATTTGGGGAGGACTCCAAA 1952
QY 1441 CACTGCCCTGATGAGCGACGACAATGTAGCACTTGTGTGTGTACCGGACCTCTGTGTGG 1500
Db 1953 CACTGCCCTGATGAGCGACGACAATGTAGCACTTGTGTGTGTACCGGACCTCTGTGTGG 2012
QY 1501 GTCTCTGTGTGTCACCAACCAACTTCCCGTGGGCGGATGCGACAGCTGTGTGAGAGGG 1560
Db 2013 GTCTCTGTGTGTCACCAACCAACTTCCCGTGGGCGGATGCGACAGCTGTGTGAGAGGG 2072
QY 1561 AAATGTGTATCAACCGCAAGTGTGTGAAACAAACCGACAGAAAGCAATTTGTATCGCCT 1620
Db 2073 AAATGTGTATCAACCGCAAGTGTGTGAAACAAACCGACAGAAAGCAATTTGTATCGCCT 2132
QY 1621 TTTTCATGGAAGCTGGGGAATGTGGGGCCTTTGGGGAGACTGTTCGAGAAAGCTGGGTGGA 1680
Db 2133 TTTTCATGGAAGCTGGGGAATGTGGGGCCTTTGGGGAGACTGTTCGAGAAAGCTGGGTGGA 2192
QY 1681 GGAGTCCAGTACACGATGAGGGAATGTGACAAACCCAGTCCCAAGAAATGGAGGGAAGTAC 1740
Db 2193 GGAGTCCAGTACACGATGAGGGAATGTGACAAACCCAGTCCCAAGAAATGGAGGGAAGTAC 2252
QY 1741 TGTGAAGGCCAAAAGAGTGCCTACAGATCCTGTAAACCTTGAGGACTGTCCAGACAAATAAT 1800
Db 2253 TGTGAAGGCCAAAAGAGTGCCTACAGATCCTGTAAACCTTGAGGACTGTCCAGACAAATAAT 2312
QY 1801 GGAATAACCTTTAGAGAGGAAACAAATGTGAAGACACAAACGAGTTTTCAAAAGCTTCCTTT 1860
Db 2313 GGAATAACCTTTAGAGAGGAAACAAATGTGAAGACACAAACGAGTTTTCAAAAGCTTCCTTT 2372
QY 1861 GGGAGTGGGCTGGGTGGATGATTCACCAAGTACGCTGGCGCTCTCACCAAGAGGACAGG 1920
Db 2373 GGGAGTGGGCTGGGTGGATGATTCACCAAGTACGCTGGCGCTCTCACCAAGAGGACAGG 2432
QY 1921 TGCAGCTCATCTGCCAAGCAAGGCAATGGGCTACTCTTCCTGTTTTGCGAGCCCAAGGTT 1980
Db 2433 TGCAGCTCATCTGCCAAGCAAGGCAATGGGCTACTCTTCCTGTTTTGCGAGCCCAAGGTT 2492
QY 1981 GTAGATGGTACTCCATGTAGCCAGATTCCACCTCTCTGTGTGTGTGCAAGGACAGTGTGTA 2040
Db 2493 GTAGATGGTACTCCATGTAGCCAGATTCCACCTCTCTGTGTGTGCAAGGACAGTGTGTA 2552
QY 2041 AAAGCTGGTGTGATCCCATCATAGACTCCAAAAGAAAGTTGTGATAATGTGGTGTTCG 2100
Db 2553 AAAGCTGGTGTGATCCCATCATAGACTCCAAAAGAAAGTTGTGATAATGTGGTGTTCG 2612
QY 2101 GGGGGAATGGATCTACTTGTAAAAAATATCAGGATCAGTTACTAGTGCAAAACCTGGA 2160
Db 2613 GGGGGAATGGATCTACTTGTAAAAAATATCAGGATCAGTTACTAGTGCAAAACCTGGA 2672
QY 2161 TATCATGATATCATCAATTTCCAACCTGGAGCCACCAACATCGAAGTGAAACAGCGGAAC 2220
Db 2673 TATCATGATATCATCAATTTCCAACCTGGAGCCACCAACATCGAAGTGAAACAGCGGAAC 2732
QY 2221 CAGAGGGATCCAGGAACATGGGAGCTTTCTTCCCATCAAGCTGCTGATGGGCACATAT 2280
Db 2733 CAGAGGGATCCAGGAACATGGGAGCTTTCTTCCCATCAAGCTGCTGATGGGCACATAT 2792
QY 2281 ATTCTTAATGGTGACTACACTTTGTCCACCTTAGAGCAAGACATATGTATCAAAAGGTGTT 2340
Db 2793 ATTCTTAATGGTGACTACACTTTGTCCACCTTAGAGCAAGACATATGTATCAAAAGGTGTT 2852
QY 2341 GTCTTGGAGGTACAGCGCTCTCTGCGGCAATGGAAAGAAATTCGAGCTTTAGCCCTCTC 2400
Db 2853 GTCTTGGAGGTACAGCGCTCTCTGCGGCAATGGAAAGAAATTCGAGCTTTAGCCCTCTC 2912
QY 2401 AAAGAGCCCTTGACATCCAGGTTCTTACTGTGGGCAATGCCCTTCGACCTTAAATATAA 2460
Db 2913 AAAGAGCCCTTGACATCCAGGTTCTTACTGTGGGCAATGCCCTTCGACCTTAAATATAA 2972
QY 2461 TACACCTACTTCGTAAGAAGAAAGGAATCTTTCAATGTCTATCCCCACTTTTTCAGCA 2520
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RESULT 9

US-10-741-600-777

; Sequence 777, Application US/10741600

; Publication No. US20050026169A1

; GENERAL INFORMATION:

; APPLICANT: CARGILL, Michele et al.

; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH

; FILE REFERENCE: CL001499

; CURRENT APPLICATION NUMBER: US/10/741,600

; NUMBER OF SEQ ID NOS: 73997

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 777

; LENGTH: 4459

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: misc_feature

; LOCATION: (1)...(4459)

; OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables 1-

AND USES THEREOF

US-10-741-600-777

Query Match		96.8%;	Score 3157.4;	DB 19;	Length 4459;
Best Local Similarity		99.4%;	Pred. No. 0;		
Matches 3169;		Conservative 8;	Mismatches 11;	Indels 1;	Gaps 1;
QY	1	ATGGGGAACGCGGAGCGGCTCCGGGCTCTCGAGCTTTGGGCGCGTACCCAGCTGCTG 60			
DB	294	ATGGGGAACGCGGAGCGGCTCGGGCTCTCGAGCTTTGGGCGMTACCCAGCTGCTG 353			
QY	61	CTGCTCGCGCGCGCTACTGCGGTCTCGGACGCACTCGGCGCGCCCTCCGAGGAGGAC 120			
DB	354	CTGCTCGCGCGCGCTACTGCGGTCTCGGACGCACTCGGCGCGCCCTCCGAGGAGGAC 413			
QY	121	GAGGAGCTAGTGGTCCGAGCTGGAGCGCGCCCGGGACAGCGGACCAAGCGCTCCGC 180			
DB	414	GAGGAGCTAGTGGTCCGAGCTGGAGCGCGCCCGGGACAGCGGACCAAGCGCTCCGC 473			
QY	181	CTGCACGCTTTGACACGAGCTGGATCTGGAGCTGCGGCCCGACAGCAGCTTTTGGCG 240			
DB	474	CTGCACGCTTTGACACGAGCTGGATCTGGAGCTGCGGCCCGACAGCAGCTTTTGGCG 533			
QY	241	CCCGCTTCACTCCAGAACCTGGGGCGCAATCCGGTCCGAGACGCGCTTCCGGA 300			
DB	534	CCCGCTTCACTCCAGAACCTGGGGCGCAATCCGGTCCGAGACGCGCTTCCGGA 593			
QY	301	ACGACCTGGCGACTGCTTCTACTCCGACCGGTGAATGGGATCCAGCTCGGCTGCC 360			
DB	594	ACGACCTGGCGACTGCTTCTACTCCGACCGGTGAATGGGATCCAGCTCGGCTGCC 653			
QY	361	GCCTCAGCTCTGCGAGGCGTGGCGGCGCTTCTACTCTGGGGAGCGCTATTTC 420			
DB	654	GCCTCAGCTCTGCGAGGCGTGGCGGCGCTTCTACTCTGGGGAGCGCTATTTC 713			
QY	421	ATCCAGCTGCCCGCCCGCAGCGCTCGCCACCGCGCCCGCCAGGGGAGAGCGG 480			
DB	714	ATCCAGCTGCCCGCCCGCAGCGCTCGCCACCGCGCCCGCCAGGGGAGAGCGG 773			
QY	481	CGGCACCACTACAGTTCCACCTCTCGCGCGGATCCGACGGGCGAGTAGCGGCGAG 540			
DB	774	CGGCACCACTACAGTTCCACCTCTCGCGCGGATCCGACGGGCGAGTAGCGGCGAG 833			
QY	541	TGCGGGTCTGGACGACGAGCCCGCGCGACTGGGAAGCGGAGACGAGACGAGAC 600			
DB	834	TGCGGGTCTGGACGACGAGCCCGCGCGACTGGGAAGCGGAGACGAGACGAGAC 893			
QY	601	GAAGGACTGAGGGCGAGGACGAGGGCTCAGTGGTCCGCGCAGGACCCGCACTGCAA 660			
DB	894	GAAGGACTGAGGGCGAGGACGAGGGCTCAGTGGTCCGCGCAGGACCCGCACTGCAA 953			
QY	661	GGGCTAGGACGCCACAGGAACTGGAAGCATAGGAAGAGCGATTTGTCTCAGTCC 720			
DB	954	GGGCTAGGACGCCACAGGAACTGGAAGCATAGGAAGAGCGATTTGTCTCAGTCC 1013			
QY	721	CGCTATGTGGAACCATGCTGTGGCAGACCACTCGATGGCAGAAATTCACGCGCAGTGGT 780			
DB	1014	CGCTATGTGGAACCATGCTGTGGCAGACCACTCGATGGCAGAAATTCACGCGCAGTGGT 1073			
QY	781	CTAAAGCACTTACCTTCTCAGTTGTTTTCGGTGGCAGCCAGATTGTACAAACACCCCGACG 840			
DB	1074	CTAAAGCACTTACCTTCTCAGTTGTTTTCGGTGGCAGCCAGATTGTACAAACACCCCGACG 1133			
QY	841	ATTCTGAATTCAGTTAGCTGTGTGTGAGATCTTGGTCAATCCAGATGAACAGAG 900			
DB	1134	ATTCTGAATTCAGTTAGCTGTGTGTGAGATCTTGGTCAATCCAGATGAACAGAG 1193			
QY	901	GGGCGGAGTAGTACCTTCCAAATGCTGCTTCTGCGGAATTTTGAACCTGGCAGAG 960			
DB	1194	GGGCGGAGTAGTACCTTCCAAATGCTGCTTCTGCGGAATTTTGAACCTGGCAGAG 1253			
QY	961	CAGCAACACCCACCGAGTACCGGGATGAGAGCACTATGACACAGCAATCTTTTCC 1020			
DB	1254	CAGCAACACCCACCGAGTACCGGGATGAGAGCACTATGACACAGCAATCTTTTCC 1313			

QY	1021	AGACAGGACTTGTGTGGTCCAGACATGTGATCTCTTGGGATGGCTGATCTGGAAC 1080			
DB	1314	AGACAGGACTTGTGTGGTCCAGACATGTGATCTCTTGGGATGGCTGATCTGGAAC 1373			
QY	1081	GTGTGTGATCCGAGCAGAGCTGCTCCGTCATAGAGAGATGATGGTTTACAAGCTGCTTC 1140			
DB	1374	GTGTGTGATCCGAGCAGAGCTGCTCCGTCATAGAGAGATGATGGTTTACAAGCTGCTTC 1433			
QY	1141	ACCAAGCCATGAATTAGGCCACCTGTTTAAATGATGATGATGATGATGATGATGATGAT 1200			
DB	1434	ACCAAGCCATGAATTAGGCCACCTGTTTAAATGATGATGATGATGATGATGATGATGAT 1493			
QY	1201	GCAGGCTTAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1260			
DB	1494	GCAGGCTTAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1553			
QY	1261	GACACAGCCAGCTTGTCTCTTTCAGTGCATCATCATCATCATCATCATCATCATCATCAT 1320			
DB	1554	GACACAGCCAGCTTGTCTCTTTCAGTGCATCATCATCATCATCATCATCATCATCATCAT 1613			
QY	1321	GGTCAATGGGGAATTTTGTATGGAACAAGCTCAGAAATCCAAATCCAAATCCAAATCCAA 1380			
DB	1614	GGTCAATGGGGAATTTTGTATGGAACAAGCTCAGAAATCCAAATCCAAATCCAAATCCAA 1673			
QY	1381	CCTGGCAGCTCGTACGATGCCAAGCCGAGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAG 1440			
DB	1674	CCTGGCAGCTCGTACGATGCCAAGCCGAGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAG 1733			
QY	1441	CACTCCCTGTATGACGACGACATGTAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1500			
DB	1734	CACTCCCTGTATGACGACGACATGTAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1793			
QY	1501	GTGCTGT 1560			
DB	1794	GTGCTGT 1853			
QY	1561	AAATGGTGTATCAACGCGCAAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1620			
DB	1854	AAATGGTGTATCAACGCGCAAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1913			
QY	1621	TTTTCATGGAAGCTGGGGGCTGTGGGGGCTGTGGGGGCTGTGGGGGCTGTGGGGGCTGT 1680			
DB	1914	TTTTCATGGAAGCTGGGGGCTGTGGGGGCTGTGGGGGCTGTGGGGGCTGTGGGGGCTGT 1973			
QY	1681	GGAGTCCAGTACACATGAGGGAATGTGACAAACCAAGTCCCAAGTCCCAAGTCCCAAG 1740			
DB	1974	GGAGTCCAGTACACATGAGGGAATGTGACAAACCAAGTCCCAAGTCCCAAGTCCCAAG 2033			
QY	1741	TGTGAAGGCAACGAGTGGCTTACAGATCCCTGTAACTTGTAGGACTGTCCAGACAAAT 1800			
DB	2034	TGTGAAGGCAACGAGTGGCTTACAGATCCCTGTAACTTGTAGGACTGTCCAGACAAAT 2093			
QY	1801	GGAAAACTTTTAGAGAGGAACTGTGAAGCACAACAGAGTTTTCAAAACTTCTCTTT 1860			
DB	2094	GGAAAACTTTTAGAGAGGAACTGTGAAGCACAACAGAGTTTTCAAAACTTCTCTTT 2153			
QY	1861	GGGAGTGGGCTTGGGTTGGAATCCAGTACGCTGGGCTCTCACCAGGACAGG 1920			
DB	2154	GGGAGTGGGCTTGGGTTGGAATCCAGTACGCTGGGCTCTCACCAGGACAGG 2213			
QY	1921	TGCAGCTCATCTGCAAGCCAAAGGCAATGGCTACTTCTTCTTCTTCTTCTTCTTCTTCT 1980			
DB	2214	TGCAGCTCATCTGCAAGCCAAAGGCAATGGCTACTTCTTCTTCTTCTTCTTCTTCTTCT 2273			
QY	1981	GTAGTGGTACTTCCATGTAGCCCAATTCACCTCTGTGTGTGTGTGTGTGTGTGTGTGT 2040			
DB	2274	GTAGTGGTACTTCCATGTAGCCCAATTCACCTCTGTGTGTGTGTGTGTGTGTGTGTGT 2333			
QY	2041	AAAGCTGGTGTGATCGCATCATAGATCCAAAAAGAAAGTTTGAATAATGTGGTGTTC 2100			
DB	2334	AAAGCTGGTGTGATCGCATCATAGATCCAAAAAGAAAGTTTGAATAATGTGGTGTTC 2393			

2101 GGGGAAATGGATCTACTTTGTAATAAATAATACAGATCAGTTACTAGTGCAAAACCTGGA 2160
2394 GGGGAAATGGATCTACTTTGTAATAAATAATACAGATCAGTTACTAGTGCAAAACCTGGA 2453
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2454 TATCATGATATCATCAATTCGAGCCACCAATCGAAGTGAACAGCGGAC 2513
2221 CAGAGGGGATCCAGGAACCAATGCGAGCTTCTTCCATCAAGCTGCTGATGCAATAT 2280
2514 CAGAGGGGATCCAGGAACCAATGCGAGCTTCTTCCATCAAGCTGCTGATGCAATAT 2573
2281 ATTCTTAATGCTGACTACACTTTGTCCACTTAGAGCAAGACATATATGACAAAGTGT 2340
2574 ATTCTTAATGCTGACTACACTTTGTCCACTTAGAGCAAGACATATATGACAAAGTGT 2633
2341 GTCTTAGGATCAGCGGCTCTCTGCGGCATTCGGAAGATTCGAGCTTTAGCCCTCTC 2400
2634 GTCTTAGGATCAGCGGCTCTCTGCGGCATTCGGAAGATTCGAGCTTTAGCCCTCTC 2693
2401 AAAGAGCCCTTGACCATCCAGGTTCTTACTGTGGCAATGCCCTTCGACCTAAATATAA 2460
2694 AAAGAGCCCTTGACCATCCAGGTTCTTACTGTGGCAATGCCCTTCGACCTAAATATAA 2753
2461 TACACCTACTTCTGTAAGAGAGAGAGAAATCTTTCAATGCTATCCCACTTTTCAGCA 2520
2754 TACACCTACTTCTGTAAGAGAGAGAGAAATCTTTCAATGCTATCCCACTTTTCAGCA 2813
2521 TGGGTCAATGAAGTGGGCGGAATGTTCTTAAGTCATGTAATGGTTCGAGAGAGA 2580
2814 TGGGTCAATGAAGTGGGCGGAATGTTCTTAAGTCATGTAATGGTTCGAGAGAGA 2873
2581 CTGTTAGATGCCGAGACATTAATGACAGCTGCTTCCAGAGTGCAGAGAGAGTGAAG 2640
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2641 CCAGCAGACACAGACCTTGTGAGACATCCCTGCCCCCAGTGGCAGCTGGGGAGTGG 2700
2934 CCAGCAGACACAGACCTTGTGAGACATCCCTGCCCCCAGTGGCAGCTGGGGAGTGG 2993
2701 TCATCATGTTCTAAGACCTGTGGAGGGTTACAAAAGAGAGCTTGAAGTGTCTGTCC 2760
2994 TCATCATGTTCTAAGACCTGTGGAGGGTTACAAAAGAGAGCTTGAAGTGTCTGTCC 3053
2761 CATGATGGAGGGTGTATCTCATGAGCTGTGATCCTTTAAAGAAACCTTAAACATTTT 2820
3054 CATGATGGAGGGTGTATCTCATGAGCTGTGATCCTTTAAAGAAACCTTAAACATTTT 3113
2821 ATAGACTTTTGCAATGCGAGATGAGTTAAGTGTGTTAAGTGTGTTAGCTTTGA - G 2879
3114 ATAGACTTTTGCAATGCGAGATGAGTTAAGTGTGTTAAGTGTGTTAGCTTTGAAG 3173
2880 GCAAGGCAAGTGAAGAGGCTGGTGCAGGGAAAGCAAGAGCTGGAGGATCCAGCG 2939
3174 GCAAGGCAAGTGAAGAGGCTGGTGCAGGGAAAGCAAGAGCTGGAGGATCCAGCG 3233
2940 TATCTCCAGTAAACAGTGAAGTGTATCAGTAGGTGGATTTATGGGGCTAGTAGAAA 2999
3234 TATCTCCAGTAAACAGTGAAGTGTATCAGTAGGTGGATTTATGGGGCTAGTAGAAA 3293
3000 AGGAGTTGAATCATCAGAGTAAATGCGCAGTTGCAAAATTTGATAGGATAGTTAGTGA 3059
3294 AGGAGTTGAATCATCAGAGTAAATGCGCAGTTGCAAAATTTGATAGGATAGTTAGTGA 3353
3060 TTATTAACTCTGAGCAGTGTATAGCATATAAANCCCCGGGCATTTATTATTATTT 3119
3354 TTATTAACTCTGAGCAGTGTATAGCATATAAANCCCCGGGCATTTATTATTATTT 3413
3120 CTTTGTGATCATCTATTATGAGTTAGAAAAAACAAGCAATTTCTCAAAAAAATAAAA 3179
3414 CTTTGTGATCATCTATTATGAGTTAGAAAAAACAAGCAATTTCTCAAAAAAATAAAA 3473
3180 AAAAAAAA 3188

Db 3474 CTATTACAA 3482
RESULT 10
US-10-741-600-775
; Sequence 775, Application US/10741600
; Publication No. US20050026169A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001499
; CURRENT APPLICATION NUMBER: US/10/741,600
; CURRENT FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 73997
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 775
; LENGTH: 4658
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc. feature
; LOCATION: (1)...(4658)
; OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables 1-5)
US-10-741-600-775
Query Match 96.8%; Score 3157.4; DB 19; Length 4658;
Best Local Similarity 99.4%; Pred. No. 0;
Matches 3169; Conservative 8; Mismatches 11; Indels 1; Gaps 1;
QY 1 ATGGGGAACGCGGAGCGGCTCCGGGTCTCGAGCTTTGGGCCGCTACCCAGCTGCTG 60
DB 513 ATGGGGAACGCGGAGCGGCTCCGGGTCTCGAGCTTTGGGCCGCTACCCAGCTGCTG 572
QY 61 CTGCTGCGCGCGGCTACTGCGGCTGTGCGAGCTCGGCGGCCCTCCGAGGAGGAC 120
DB 573 CTGCTGCGCGCGGCTACTGCGGCTGTGCGAGCTCGGCGGCCCTCCGAGGAGGAC 632
QY 121 GAGGAGCTAGTGTGCGGAGCTGAGCGCGGCCCGGGAACACGCGGCTCCGCTCCGC 180
DB 633 GAGGAGCTAGTGTGCGGAGCTGAGCGCGGCCCGGGAACACGCGGCTCCGCTCCGC 692
QY 181 CTGACGCGCTTTCACAGCAGCTGAGATCTGAGAGCTGCGGCCGACAGCAGCTTTTGGCG 240
DB 693 CTGACGCGCTTTCACAGCAGCTGAGATCTGAGAGCTGCGGCCGACAGCAGCTTTTGGCG 752
QY 241 CCGGCTTTCAGCTTCCAGAACGTTGGGCGCAATCCGGGTCCGAGAGCGGCTTCCGGA 300
DB 753 CCGGCTTTCAGCTTCCAGAACGTTGGGCGCAATCCGGGTCCGAGAGCGGCTTCCGGA 812
QY 301 ACCGACTGGCGCACTGCTTCTACTCCGCGCACCGTGAATGGCGATCCAGCTCGGCTGCC 360
DB 813 ACCGACTGGCGCACTGCTTCTACTCCGCGCACCGTGAATGGCGATCCAGCTCGGCTGCC 872
QY 361 GCCTCTCAGCTCTGCGAGGCGCTGCGCGGCCCTTCTACCTGTGGGGAGGCGTATTTC 420
DB 873 GCCTCTCAGCTCTGCGAGGCGCTGCGCGGCCCTTCTACCTGTGGGGAGGCGTATTTC 932
QY 421 ATCAGCGCTGCGCGCGCGCAGGAGCGCTGCGCACCGCGGCCCGCAGGGGAGAGCCG 480
DB 933 ATCAGCGCTGCGCGCGCGCAGGAGCGCTGCGCACCGCGGCCCGCAGGGGAGAGCCG 992
QY 481 CCGGCACTTACAGTTTCCACCTCTCGCGCGGAATCCGAGGGCGGACGTAGGCGGCGACG 540
DB 993 CCGGCACTTACAGTTTCCACCTCTCGCGCGGAATCCGAGGGCGGACGTAGGCGGCGACG 1052
QY 541 TCGGGGTCTGTGACGACGAGCGGCCCGGCTGCGGAAAGCGGAGACCGAAGACGAGGAC 600
DB 1053 TCGGGGTCTGTGACGACGAGCGGCCCGGCTGCGGAAAGCGGAGACCGAAGACGAGGAC 1112
QY 601 GAAGGAGCTGAGGCGGAGGACGAAAGGCGCTCAGTGTGCGCGGAGGACCCCGGCTGCAA 660

Db 1113 GAAGGCACTGAGGCGAGGACGAAGGGCTCAGTGGTCGCGCAGGACCGGCACTGCAA 1172
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Db 1173 GCGGTAGGACACGCCACACAGGAACCTGGAAGCATAGAAAGACGATTTGTGTCCAGTCAC 1232
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Qy 841 ATTTCGTAATTCAGTTAGCTGGTGGTGGTGAAGATCTTGGTCATCCAGATGAACAGAG 900
Db 1353 ATTTCGTAATTCAGTTAGCTGGTGGTGGTGAAGATCTTGGTCATCCAGATGAACAGAG 1412
Qy 901 GGGCCGGAAGTGACCTCCAAATGCTGCCCTCACTCTGCGGAACCTTTTGCAACTGGCGAGAAG 960
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Qy 961 CAGCAACCCACCCAGTGACCGGATGCGAGCACTATGACACAGCAATTTCTTTCCACC 1020
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Db 1593 GTGTGTGATCCGAGCAGAAAGCTGCTCCGTCTATAGAAAGATGATGGTTTACAAGCTGCCCTTC 1652
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Db 1833 GGTATGGGGAATGTTGATGGAACAAGCCTCAGAAATCCATACAGCTCCAGGGGATCTC 1892
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Db 1893 CCTGGCACCCTGTACGATGCCAACCGGAGTGCCAGTTTACATTTGGGGAGGATCCCAA 1952
Qy 1441 CACTGCCCTGTATGACGACGACATGTAGCACCCTTGGTGTATCCGGCACCTCTGGTGGG 1500
Db 1953 CACTGCCCTGTATGACGACGACATGTAGCACCCTTGGTGTATCCGGCACCTCTGGTGGG 2012
Qy 1501 GTGTGTGTGTCAAACCAACACTTCCGTGGGCGGATGGCACAGCTGTGGAGAGGG 1560
Db 2013 GTGTGTGTGTCAAACCAACACTTCCGTGGGCGGATGGCACAGCTGTGGAGAGGG 2072
Qy 1561 AAATGGTGTATCAACGGCAAGTGTGTGAACAAACCGACAGAAAGCATTTTGTATCGGCT 1620
Db 2073 AAATGGTGTATCAACGGCAAGTGTGTGAACAAACCGACAGAAAGCATTTTGTATCGGCT 2132
Qy 1621 TTTTATGGAAGCTGGGGAATGTGGGGCTTGGGGAGACTGTTCAGAGAACCTGGCGTGA 1680
Db 2133 TTTTATGGAAGCTGGGGAATGTGGGGCTTGGGGAGACTGTTCAGAGAACCTGGCGTGA 2192
Qy 1681 GGAGTCCAGTACCATGAGGGAATGTGCAACCCAGTCCCAAGAAATGGAGGGAATGAC 1740
Db 2193 GGAGTCCAGTACCATGAGGGAATGTGCAACCCAGTCCCAAGAAATGGAGGGAATGAC 2252

Qy 1741 TGTGAAGGCAACGAGTGGCGCTACAGATCTCTGTAACTTGGAGTGTCCAGACAATAAT 1800
Db 2253 TGTGAAGGCAACGAGTGGCGCTACAGATCTCTGTAACTTGGAGTGTCCAGACAATAAT 2312
Qy 1801 GGAAGAACTTTAGAGAGGAACAATGTGAAGCACACAACAGATTTTCAAAAGCTTCTCTTT 1860
Db 2313 GGAAGAACTTTAGAGAGGAACAATGTGAAGCACACAACAGATTTTCAAAAGCTTCTCTTT 2372
Qy 1861 GGGAGTGGGCTTGGGTGGGAATGGATTTCCAAAGTACGCTGGCGTCTCAACAAAGACAGG 1920
Db 2373 GGGAGTGGGCTTGGGTGGGAATGGATTTCCAAAGTACGCTGGCGTCTCAACAAAGACAGG 2432
Qy 1921 TGCAGCTCATCTGCCAAGCCAAAGGCAATGGCTACTTCTTCGTTTTCAGCCCCAAGGT 1980
Db 2433 TGCAGCTCATCTGCCAAGCCAAAGGCAATGGCTACTTCTTCGTTTTCAGCCCCAAGGT 2492
Qy 1981 GTAGATGGTACTCCATGTAGCCCAAGATTTCCACCTCTGTCTGTGTCAGAGCAGTGTGTA 2040
Db 2493 GTAGATGGTACTCCATGTAGCCCAAGATTTCCACCTCTGTCTGTGTCAGAGCAGTGTGTA 2552
Qy 2041 AAAGCTGGTGTGTGATCGCATCATAGA CTCCAAAAAGAAAGTTTGATAATGTGTGTGGC 2100
Db 2553 AAAGCTGGTGTGTGATCGCATCATAGA CTCCAAAAAGAAAGTTTGATAATGTGTGTGGC 2612
Qy 2101 GGGGGAATGGATCTACTTGTAAAAAATATCAGGATCAGTTACTAGTGCAAAACCTCGA 2160
Db 2613 GGGGGAATGGATCTACTTGTAAAAAATATCAGGATCAGTTACTAGTGCAAAACCTCGA 2672
Qy 2161 TATCATGATATCATCAAAATTTCCAACTGGAGCCCAACATCGAAGTGAACAGCGGAAC 2220
Db 2673 TATCATGATATCATCAAAATTTCCAACTGGAGCCCAACATCGAAGTGAACAGCGGAAC 2732
Qy 2221 CAGAGGGATCCAGGAACAATGGCAGCTTTCTGCGCATCAAAAGCTGTGATGGCACATAT 2280
Db 2733 CAGAGGGATCCAGGAACAATGGCAGCTTTCTGCCATCAAAAGCTGTGATGGCACATAT 2792
Qy 2281 ATTCTTAATGTGTGACTACCTTTGTCACCTTAGCGCAAGACATTTAGTACAAAGTGTCT 2340
Db 2793 ATTCTTAATGTGTGACTACCTTTGTCACCTTAGCGCAAGACATTTAGTACAAAGTGTCT 2852
Qy 2341 GTCTTGAGGTACAGCGGCTCTCTCGGCAATTTGGAAGAAATTCGAGCTTTAGCCCTCTC 2400
Db 2853 GTCTTGAGGTACAGCGGCTCTCTCGGCAATTTGGAAGAAATTCGAGCTTTAGCCCTCTC 2912
Qy 2401 AAAGAGCCTTGAAGATCCAGGTTCTTACTGTGGGCAATGCCCTTCGACCTTAAATTTAA 2460
Db 2913 AAAGAGCCTTGAAGATCCAGGTTCTTACTGTGGGCAATGCCCTTCGACCTTAAATTTAA 2972
Qy 2461 TACACCTACTTTCTGTAAGAAAGAAAGAAATCTTTCAATGCTATCCCCACCTTTTTCAGCA 2520
Db 2973 TACACCTACTTTCTGTAAGAAAGAAAGAAATCTTTCAATGCTATCCCCACCTTTTTCAGCA 3032
Qy 2521 TGGGTCTATTGAAGAGTGGGCGAAATGTTCTAAGTCATGTGAATTTGGGTGGCAGAGAAGA 2580
Db 3033 TGGGTCTATTGAAGAGTGGGCGAAATGTTCTAAGTCATGTGAATTTGGGTGGCAGAGAAGA 3092
Qy 2581 CTGGTAGAATGCCAGACATTTAATGGACAGCTGCTCCGAGTGTGCAAGGAAGTGAAG 2640
Db 3093 CTGGTAGAATGCCAGACATTTAATGGACAGCTGCTCCGAGTGTGCAAGGAAGTGAAG 3152
Qy 2641 CCAGCAGCACGACCTTTGTGACAGCCATCCCTGCCCGCAGTGGCAGCTGGGGAGTGG 2700
Db 3153 CCAGCAGCACGACCTTTGTGACAGCCATCCCTGCCCGCAGTGGCAGCTGGGGAGTGG 3212
Qy 2701 TCATCATGTTCTTAAGACTGTGGGAAGGGTTTCAAAAAAGAAAGCTTGAAGTGTCTGTCC 2760
Db 3213 TCATCATGTTCTTAAGACTGTGGGAAGGGTTTCAAAAAAGAAAGCTTGAAGTGTCTGTCC 3272
Qy 2761 CATGATGGAGGGGTGTTATCTCATGAGAGCTGTGATCCTTTTAAAGAAACCTTAAACATTTTC 2820
Db 3273 CATGATGGAGGGGTGTTATCTCATGAGAGCTGTGATCCTTTTAAAGAAACCTTAAACATTTTC 3332

2821 ATAGACTTTTGCACAAATGCGAGATGAGTAAAGTGGTTAAAGTGGTGTAGCTTTGA-G 2879
3333 ATAGACTTTTGCACAAATGCGAGATGAGTAAAGTGGTTAAAGTGGTGTAGCTTTGAGG 3392
2880 GCAAGGCAAGTGAAGAGGCTGGTGGAGGAAAGCAAGAGAGGCTGGAGGATCCAGCG 2939
3393 GCAAGGCAAGTGAAGAGGCTGGTGGAGGAAAGCAAGAGAGGCTGGAGGATCCAGCG 3452
2940 TATCTTGGCCAGTAACCAAGTGAAGTGTATCAGTAAAGTGGGATTAATGGGGTAGATAGAAA 2999
3453 TATCTTGGCCAGTAACCAAGTGAAGTGTATCAGTAAAGTGGGATTAATGGGGTAGATAGAAA 3512
3000 AGGAGTTGAATCAATCAGAGTAAACTGCCAGTTCCAAATTTGATAGATAGTTAGTGAGGA 3059
3513 AGGAGTTGAATCAATCAGAGTAAACTGCCAGTTCCAAATTTGATAGATAGTTAGTGAGGA 3572
3060 TTATTAACCTCTGAGCAGTGATATAGCATATTAATTAATTAATTAATTAATTAATTAATTT 3119
3573 TTATTAACCTCTGAGCAGTGATATAGCATATTAATTAATTAATTAATTAATTAATTAATTT 3632
3120 CTTTCTGTACATCTATTACAAAGTTTGAAGAAACCAAGCAATTTGTCAAAAAAAGAAAAA 3179
3633 CTTTCTGTACATCTATTACAAAGTTTGAAGAAACCAAGCAATTTGTCAAAAAAAGTTAGAA 3692
3180 AAAAAAAA 3188
3693 CTATTACAA 3701

RESULT 11
US-10-667-281-1
; Sequence 1, Application US/10667281
; Publication No. US20050100916A1
; GENERAL INFORMATION:
; APPLICANT: Klonowski, Paul
; APPLICANT: Allard, John
; APPLICANT: Heller, Renu
; APPLICANT: Van Wart, Harold
; TITLE OF INVENTION: Human Aggrecanase and Nucleic Acid
; FILE OF INVENTION: Compositions Encoding the Same
; FILE REFERENCE: ROCH-002
; CURRENT APPLICATION NUMBER: US/10/667,281
; PRIOR FILING DATE: 2003-09-17
; PRIOR FILING DATE: 2003-09-17
; PRIOR FILING DATE: 2000-05-09
; PRIOR FILING DATE: 2000-05-09
; PRIOR FILING DATE: 2000-05-09
; PRIOR FILING DATE: 1999-05-10
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: Fast-Seq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 3889
; TYPE: DNA
; ORGANISM: human
US-10-667-281-1

Query Match 96.8%; Score 3156.8; DB 19; Length 3889;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 3175; Conservative 0; Mismatches 13; Indels 1; Gaps 1;

1 ATGGGGAACCGGAGCGGGCTCGGGGTCTCGGAGCTTTGGGCCCGTACCCAGCTGCTG 60
59 ATGGGGAACCGGAGCGGGCTCGGGGTCTCGGAGCTTTGGGCCCGTACCCAGCTGCTG 118
61 CTGCTCCCGCGGGCGCTACTGCGCGTGTGCGACCGACTCGGGCGCCCTCGGAGGAGAC 120
119 CTGCTCCCGCGGGCGCTACTGCGCGTGTGCGACCGACTCGGGCGCCCTCGGAGGAGAC 178
121 GAGGAGCTAGTGGTGGCGGAGCTGAGCGCGCCCGCGGACACGCGGACCGCGCTCCGC 180
179 GAGGAGCTAGTGGTGGCGGAGCTGAGCGCGCCCGCGGACACGCGGACCGCGCTCCGC 238
181 CTGACCGCTTTGACCAAGCAGCTGGATCTGGAGCTGGCGGCCCGGACGAGCAGCTTTTGGCG 240

239 CTGCAAGCCTTTGACACAGCAGCTGGATCTGAGCTCGGGCCGACAGCAGCTTTTGGCG 2398
241 CCGGCTTTCACGCTCCAGAAACGTGGGGCGCAATCCGGGTCCGAGACGCCGCTTCCGAA 300
299 CCGGCTTTCACGCTCCAGAAACGTGGGGCGCAATCCGGGTCCGAGACGCCGCTTCCGAA 358
301 ACCGACTCGGCGACTGCTTCTACTCCGGACCGTGAAATGGCGATCCAGCTCGGCTGCC 360
359 ACCGACTCGGCGACTGCTTCTACTCCGGACCGTGAAATGGCGATCCAGCTCGGCTGCC 418
361 GCCTCAGCCTCTGCGAGGCGGTGCGCGCGCTTCTACTCTGCTGGGGAGGCGTATTTTC 420
419 GCCTCAGCCTCTGCGAGGCGGTGCGCGCGCTTCTACTCTGCTGGGGAGGCGTATTTTC 478
421 ATCCAGCCTGCTGCGCGCGCGCGAGCGCTCTCGCCACCGCGCCGCCCGGAGGAGACCG 480
479 ATCCAGCCTGCTGCGCGCGCGCGAGCGCTCTCGCCACCGCGCCGCCCGGAGGAGACCG 538
481 CCGGACCACTACAGTTTCCACTCTCTGCGCGGAAATCGGCGAGGCGGCGATGAGCGGACG 540
539 CCGGACCACTACAGTTTCCACTCTCTGCGCGGAAATCGGCGAGGCGGCGATGAGCGGACG 598
541 TCGGGGCTGCTGGAACGACGAGCGCCCGCGACTGGGAAAGCGGAGACCGGAGACGAGGAC 600
599 TCGGGGCTGCTGGAACGACGAGCGCCCGCGACTGGGAAAGCGGAGACCGGAGACGAGGAC 658
601 GAAGGACTGAGGCGGAGGACGAAAGGCGCTCAGTGGTTCGCGGAGGACCGCGGACCTGCAA 660
659 GAAGGACTGAGGCGGAGGACGAAAGGCGCTCAGTGGTTCGCGGAGGACCGCGGACCTGCAA 718
661 GCGTAGGACAGCCCAAGAACTGGAAGCAATGAAGAAAGCGATTTGTTCAGTTCAC 720
719 GCGTAGGACAGCCCAAGAACTGGAAGCAATGAAGAAAGCGATTTGTGTCCAGTTCAC 778
721 CCGTATGGAAGCAATGCTTGTGGGAGACCACTCGATGCGGAGCAATTTCCAGCGAGTGT 780
779 CCGTATGGAAGCAATGCTTGTGGGAGACCACTCGATGCGGAGCAATTTCCAGCGAGTGT 838
781 CTAAAGCATTACCTTCTCAGTTTGTTCGCTGGGAGGACGAGATTTGTACAAACACCCGAGC 840
839 CTAAAGCATTACCTTCTCAGTTTGTTCGCTGGGAGGACGAGATTTGTACAAACACCCGAGC 898
841 ATTCTGTAATTCAGTTAGCTTGGTGGTGAAGATCTTGTGTCATCTCAGATGAACAGAG 900
899 ATTCTGTAATTCAGTTAGCTTGGTGGTGAAGATCTTGTGTCATCTCAGATGAACAGAG 958
901 GGGCCGGAAGTGAACCTTCAATGCTGCCCTCAGCTCGGGAACCTTTGCAACTGCGAGAG 960
959 GGGCCGGAAGTGAACCTTCAATGCTGCCCTCAGCTCGGGAACCTTTGCAACTGCGAGAG 1018
961 CAGCAACACCCAGCTGAGTGGGATGAGAGCACTATGACACAGCAATTTCTTTTCAACC 1020
1019 CAGCAACACCCAGCTGAGTGGGATGAGAGCACTATGACACAGCAATTTCTTTTCAACC 1078
1021 AGACAGACTTGTGGGTCCAGACATGTGATCTCTTGGGATGGCTGATGTTGGAACT 1080
1079 AGACAGACTTGTGGGTCCAGACATGTGATCTCTTGGGATGGCTGATGTTGGAACT 1138
1081 GTGTGTATCCGAGCAGCAAGCTGCTCGTCAATAGAGATGATGTTTACAGCTGCGCTTC 1140
1139 GTGTGTATCCGAGCAGCAAGCTGCTCGTCAATAGAGATGATGTTTACAGCTGCGCTTC 1198
1141 ACCACAGCCCATGAATTAGGCCAGCTGTTTAAATGCAATGATGATGCAAGAGCAGTGT 1200
1199 ACCACAGCCCATGAATTAGGCCAGCTGTTTAAATGCAATGATGATGCAAGAGCAGTGT 1258
1201 GCCAGCTTAAATGGTGTGAACCAAGGATTCACATGATGCGCTCAATGCTTTCCAACTGT 1260
1259 GCCAGCTTAAATGGTGTGAACCAAGGATTCACATGATGCGCTCAATGCTTTCCAACTGT 1318
1261 GACCACAGCAGCTTGGTCTCCTTGCAGTGGCTTACATGATGATGATGATGATGATGATGAT 1320
1319 GACCACAGCAGCTTGGTCTCCTTGCAGTGGCTTACATGATGATGATGATGATGATGATGAT 1378

1321 GGTCAATGGGGAATGTTTATGATGACAAGCCTCAGAAATCCCATACAGCTCCAGCGCATCTC 1380
Db
1379 GGTCAATGGGGAATGTTTATGATGACAAGCCTCAGAAATCCCATACAGCTCCAGCGCATCTC 1438
Qy
1381 CTTGGCACCTCGTAGCATCCAAACCGGAGTGCAGTGTTCATATTTGGGAGGACTCCAAA 1440
Db
1439 CTTGGCACCTCGTAGCATCCAAACCGGAGTGCAGTGTTCATATTTGGGAGGACTCCAAA 1498
Qy
1441 CACTGGCCCTGATGACGACGACATGTAGACCTTTGTGTGTATACCGGACCTCTGTGTGG 1500
Db
1499 CACTGGCCCTGATGACGACGACATGTAGACCTTTGTGTGTATACCGGACCTCTGTGTGG 1558
Qy
1501 GTGCTGTGTGTCAACCAACCAACACTTCCGCTGGGGGAGTGGCACCAGCTGTGGGAAGGG 1560
Db
1559 GTGCTGTGTGTCAACCAACCAACACTTCCGCTGGGGGAGTGGCACCAGCTGTGGGAAGGG 1618
Qy
1561 AAATGGTGTATCAACGGCAAGTGTGTGAACAAAACCGACAGAAAGCATTTTGTATACGCT 1620
Db
1619 AAATGGTGTATCAACGGCAAGTGTGTGAACAAAACCGACAGAAAGCATTTTGTATACGCT 1678
Qy
1621 TTTTCATGGAAGCTGGGGAATGTGGGGGCTTGGGGAGACTGTTCGAGAACTGTGGGTGGA 1680
Db
1679 TTTTCATGGAAGCTGGGGAATGTGGGGGCTTGGGGAGACTGTTCGAGAACTGTGGGTGGA 1738
Qy
1681 GGAGTCCAGTACACGATGAGGGAATGTGAACACCAGTCCCAAGAAATGGAGGGAAGTAC 1740
Db
1739 GGAGTCCAGTACACGATGAGGGAATGTGAACACCAGTCCCAAGAAATGGAGGGAAGTAC 1798
Qy
1741 TGTGAAGGCAACGAGTGGCTACAGATCTCTGTAACTTTGAGGACTGTCCAGACAAATAT 1800
Db
1799 TGTGAAGGCAACGAGTGGCTACAGATCTCTGTAACTTTGAGGACTGTCCAGACAAATAT 1858
Qy
1801 GGAATAACCTTTAGAGAGAAACAATGTGAAGCACACAGAGTTTTCAAAAGCTTCCCTTT 1860
Db
1859 GGAATAACCTTTAGAGAGAAACAATGTGAAGCACACAGAGTTTTCAAAAGCTTCCCTTT 1918
Qy
1861 GGGAGTGGGCTGGCGTGAAGTGAATCCCAAGTAGCTGGGCTCTCCAAAGGACACAGG 1920
Db
1919 GGGAGTGGGCTGGCGTGAAGTGAATCCCAAGTAGCTGGGCTCTCCAAAGGACACAGG 1978
Qy
1921 TGCAAGCTCATCTGCCAACCAAGGCAATGGCTACTTCTCGTTTTCAGGCCCAAGGTT 1980
Db
1979 TGCAAGCTCATCTGCCAACCAAGGCAATGGCTACTTCTCGTTTTCAGGCCCAAGGTT 2038
Qy
1981 GTAGATGGTACTCCATGTAGCCAGATTCCCACTCTGTCTGTGTGCAAGGACAGTGTGTA 2040
Db
2039 GTAGATGGTACTCCATGTAGCCAGATTCCCACTCTGTCTGTGTGCAAGGACAGTGTGTA 2098
Qy
2041 AAAGCTGGTGTGTGATCGCATCATAGACTCCAAAAGAGTTTGTATAAATGTGGTGTTCG 2100
Db
2099 AAAGCTGGTGTGTGATCGCATCATAGACTCCAAAAGAGTTTGTATAAATGTGGTGTTCG 2158
Qy
2101 GGGGGAATGGATCTACTTTGTAATAAATATCAGGATCAGTTACTAGTGCAAAAACCTGGA 2160
Db
2159 GGGGGAATGGATCTACTTTGTAATAAATATCAGGATCAGTTACTAGTGCAAAAACCTGGA 2218
Qy
2161 TATCATGATATCATCAAAATTCGAATCTGAGGCCACCAACATCGAAGTGAACAGCGGAAC 2220
Db
2219 TATCATGATATCATCAAAATTCGAATCTGAGGCCACCAACATCGAAGTGAACAGCGGAAC 2278
Qy
2221 CAGAGGGGATCAGGAAACAATGGAGCTTTCTTGCCATCAAGCTGCTGATGGCACATAT 2280
Db
2279 CAGAGGGGATCAGGAAACAATGGAGCTTTCTTGCCATCAAGCTGCTGATGGCACATAT 2338
Qy
2281 ATTCTTAATGGTCACTACACTTTGTCCACTTTAGAGCAAGACATTTATGACAAAGTGTT 2340
Db
2339 ATTCTTAATGGTCACTACACTTTGTCCACTTTAGAGCAAGACATTTATGACAAAGTGTT 2398
Qy
2341 GTCTTGAGGTACAGGGGCTCTCTGGGCAATTTGGAAGAAATTCGACGCTTTAGCGCTCTC 2400
Db
2399 GTCTTGAGGTACAGGGGCTCTCTGGGCAATTTGGAAGAAATTCGACGCTTTAGCGCTCTC 2458

2401 AAAAGAGCCCTTGACCATCCAGGTTCTTACTGTGGGCAATGCCCTTCGACCTAAAAATAAA 2460
Db
2459 AAAAGAGCCCTTGACCATCCAGGTTCTTACTGTGGGCAATGCCCTTCGACCTAAAAATAAA 2518
Qy
2461 TACACCTACTTCGTAAAAAGAAAGGAATCTTTCAATGCTATCCCACTTTTTCAGCA 2520
Db
2519 TACACCTACTTCGTAAAAAGAAAGGAATCTTTCAATGCTATCCCACTTTTTCAGCA 2578
Qy
2521 TGGGTCAATGAAGAGTGGGGCGAATGTTCTAAGTCAATGTAAGTGGTGGGAGAGAA 2580
Db
2579 TGGGTCAATGAAGAGTGGGGCGAATGTTCTAAGTCAATGTAAGTGGTGGGAGAGAA 2638
Qy
2581 CTGGTAGAATGCCGAGACATTAATGCACAGCCTGCTCCAGTGTGCAAGCAAGTGAAG 2640
Db
2639 CTGGTAGAATGCCGAGACATTAATGCACAGCCTGCTCCAGTGTGCAAGCAAGTGAAG 2698
Qy
2641 CCAGCAGCACAGACCTTGTGTGCAGACCATCCCTCCCCAGTGGCAGCTGGGGAGTGG 2700
Db
2699 CCAGCAGCACAGACCTTGTGTGCAGACCATCCCTCCCCAGTGGCAGCTGGGGAGTGG 2758
Qy
2701 TCATCATGTTTAAACACCTGTGGGAAGGTTACAAAAAAGAGCTTGAAGTGTCTGTCC 2760
Db
2759 TCATCATGTTTAAACACCTGTGGGAAGGTTACAAAAAAGAGCTTGAAGTGTCTGTCC 2818
Qy
2761 CATGATGAGGGGTGTATCTCATGAGAGCTGTGATCCCTTTAAAGAAACCTAAACATTT 2820
Db
2819 CATGATGAGGGGTGTATCTCATGAGAGCTGTGATCCCTTTAAAGAAACCTAAACATTT 2878
Qy
2821 ATAGACTTTTGCACAAATGGCAGAAATGCAGTTAAGTGGTTTAAAGTGGTGTAGCTTTGA-G 2879
Db
2879 ATAGACTTTTGCACAAATGGCAGAAATGCAGTTAAGTGGTTTAAAGTGGTGTAGCTTTGAGG 2938
Qy
2880 GCAAGGCAAGTGAAGAGGGCTGTGCAGGAAAGCAAGAGCTGGAGGATCCAGCG 2939
Db
2939 GCAAGGCAAGTGAAGAGGGCTGTGCAGGAAAGCAAGAGAGCTGGAGGATCCAGCG 2998
Qy
2940 TATCTTGCAGTAAACAGTGGTGTATCAGTAAAGTGGGATTTATGGGGGTAGATAGAAA 2999
Db
2999 TATCTTGCAGTAAACAGTGGTGTATCAGTAAAGTGGGATTTATGGGGGTAGATAGAAA 3058
Qy
3000 AGGAGTTGAATCATCAGAGTAAACTGCCAGTTTGCAGTTTGAATGATAGATAGTTAGTGAGA 3059
Db
3059 AGGAGTTGAATCATCAGAGTAAACTGCCAGTTTGCAGTTTGAATGATAGATAGTTAGTGAGA 3118
Qy
3060 TTATTTAACTCTGACAGAGTATAGCATATAAANCCCCGGGCATTATATTTATTTT 3119
Db
3119 TTATTTAACTCTGACAGAGTATAGCATATAAANCCCCGGGCATTATATTTATTTT 3178
Qy
3120 CTTTTTGTACATCTATTACAGTTTAGAAAAACAAAGCAATTTGTCAAAAAAAGAAAAA 3179
Db
3179 CTTTTTGTACATCTATTACAGTTTAGAAAAACAAAGCAATTTGTCAAAAAAAGTTAGAA 3238
Qy
3180 AAAAAA 3188
Db
3239 CTATTACAA 3247

RESULT 12

US-10-159-563-192
; Sequence 192, Application US/10159563
; Publication No. US20040009154A1
; GENERAL INFORMATION:
; APPLICANT: Khan, Javed
; APPLICANT: Ringner, Markus
; APPLICANT: Peterson, Carsten
; APPLICANT: Meltzer, Paul
; TITLE OF INVENTION: SELECTIONS OF GENES AND METHODS OF USING THE SAME FOR
; CURRENT APPLICATION NUMBER: US/10/159,563
; FILE REFERENCE: 11613.56US11
; CURRENT FILING DATE: 2002-12-09
; PRIOR APPLICATION NUMBER: US 10/133,937
; PRIOR FILING DATE: 2002-04-25

Db	2274	GTAGATGGTACTCCATGTAGCCAGATTCCACCTCTGTGTGTGCAAGGACAGGTGTGTA	2333
QY	2041	AAAGCTGGTGTGATCGCATCATAGACTCCAAAAGAGTTTGATTAATATGCTGTTTGC	2100
Db	2334	AAAGCTGGTGTGATCGCATCATAGACTCCAAAAGAGTTTGATTAATATGCTGTTTGC	2393
QY	2101	GGGGGAATGGATCTACTTTGTAATAAATAATCAGGATCAGTTACTAGTGCAAAACCTGGA	2160
Db	2394	GGGGGAATGGATCTACTTTGTAATAAATAATCAGGATCAGTTACTAGTGCAAAACCTGGA	2453
QY	2161	TATCATGATATCATCAAAATCCAACTGGAGCCACCAACATCAAGAGTGAACACAGCGGAAC	2220
Db	2454	TATCATGATATCATCAAAATCCAACTGGAGCCACCAACATCAAGAGTGAACACAGCGGAAC	2513
QY	2221	CAGAGGGATCAGGAACAATGGCAGCTTCTTGCCATCAAGAGCTGCTGATGGCACATAT	2280
Db	2514	CAGAGGGATCAGGAACAATGGCAGCTTCTTGCCATCAAGAGCTGCTGATGGCACATAT	2573
QY	2281	ATTCTTAATGGTGACTTACACTTTTGCCACTTTAGAGCAAGACATATATGTACAAAGTGTT	2340
Db	2574	ATTCTTAATGGTGACTTACACTTTTGCCACTTTAGAGCAAGACATATATGTACAAAGTGTT	2633
QY	2341	GTCTTGAGGTACAGCGGCTCCTCTGGGCATTTGGAAGAAATTCGAGCTTTAGCCCTCTC	2400
Db	2634	GTCTTGAGGTACAGCGGCTCCTCTGGGCATTTGGAAGAAATTCGAGCTTTAGCCCTCTC	2693
QY	2401	AAAGAGCCCTTGACCATCCAGCTTCTTACTGTGGGCAATGCCCTTCGACCTTAAATATAA	2460
Db	2694	AAAGAGCCCTTGACCATCCAGCTTCTTACTGTGGGCAATGCCCTTCGACCTTAAATATAA	2753
QY	2461	TACACTTACTTCGTAAGAAGAAAGGAATCTTTCAATGCTATCCCACTTTTTCAGCA	2520
Db	2754	TACACTTACTTCGTAAGAAGAAAGGAATCTTTCAATGCTATCCCACTTTTTCAGCA	2813
QY	2521	TGGGTCAATGAAGAGTGGGCGAATGTTCTTAAGTCATGTGAATGGTGTGGCAGAGAAGA	2580
Db	2814	TGGGTCAATGAAGAGTGGGCGAATGTTCTTAAGTCATGTGAATGGTGTGGCAGAGAAGA	2873
QY	2581	CTGGTAGAATCCGAGACATTAATGGACAGCTGCTTCGAGTGTGCAAGGAAGTGAAG	2640
Db	2874	CTGGTAGAATCCGAGACATTAATGGACAGCTGCTTCGAGTGTGCAAGGAAGTGAAG	2933
QY	2641	CCAGCCAGCACAGACCTTTGTGCAGACCATCCCTGCCCTCAGTGGCAGCTGGGGGAGTGG	2700
Db	2934	CCAGCCAGCACAGACCTTTGTGCAGACCATCCCTGCCCTCAGTGGCAGCTGGGGGAGTGG	2993
QY	2701	TCATCATGTTCTAAGACCTGTGGGAAGGGTTACAAAAAAGAAAGCTTGAAGTGTCTGTCC	2760
Db	2994	TCATCATGTTCTAAGACCTGTGGGAAGGGTTACAAAAAAGAAAGCTTGAAGTGTCTGTCC	3053
QY	2761	CATGATGGAGGGTGTATCTCATGAGAGCTGTGATCCTTTAAAGAAACCTTAAACATTTTC	2820
Db	3054	CATGATGGAGGGTGTATCTCATGAGAGCTGTGATCCTTTAAAGAAACCTTAAACATTTTC	3113
QY	2821	ATAGACTTTTGCACAAATGGCAGAAATGCAAGTAAAGTGGTTTAAGTGGTGTAGCTTTGA-G	2879
Db	3114	ATAGACTTTTGCACAAATGGCAGAAATGCAAGTAAAGTGGTTTAAGTGGTGTAGCTTTGA	3173
QY	2880	GCAAGGCAAGTGAAGAAAGGGTGTGTCAGGGAAGAAAGAGGCTGAGGGAATCCAGCG	2939
Db	3174	GCAAGGCAAGTGAAGAAAGGGTGTGTCAGGGAAGAAAGAGGCTGAGGGAATCCAGCG	3233
QY	2940	TATCTTGCAGTAACAGTGAAGTGTATCAGTAAGGTGGGATTTATGGGGTATAGAGAA	2999
Db	3234	TATCTTGCAGTAACAGTGAAGTGTATCAGTAAGGTGGGATTTATGGGGTATAGAGAA	3293
QY	3000	AGGAGTTGAATCATCAGAGTAACCTGCCAGTTTGCAAAATTTGTATAGGATAGTTAGTGAGGA	3059
Db	3294	AGGAGTTGAATCATCAGAGTAACCTGCCAGTTTGCAAAATTTGTATAGGATAGTTAGTGAGGA	3353
QY	3060	TTATTAACTCTGAGCAGTGATATAGCATAATAAANCCCCGGGCATTAATTATTAATTT	3119
Db	3354	TTATTAACTCTGAGCAGTGATATAGCATAATAAAGCCCCGGGCATTAATTATTAATTT	3413
QY	3120	CTTTTGTACATCTATTACAGTTTAGAAAAAACAAGCAATTGTCAAAAAAATAAAAAA	3179
Db	3414	CTTTTGTACATCTATTACAGTTTAGAAAAAACAAGCAATTGTCAAAAAAATAAAAAA	3473
QY	3180	AAAAAATAA 3188	
Db	3474	CTATTACAA 3482	
RESULT 13			
US-10-159-563-308			
; Sequence 308, Application US/10159563			
; Publication No. US20040009154M			
; GENERAL INFORMATION:			
; APPLICANT: Khan, Javed			
; APPLICANT: Ringner, Markus			
; APPLICANT: Peterson, Carsten			
; APPLICANT: Meltzer, Paul			
; TITLE OF INVENTION: SELECTIONS OF GENES AND METHODS OF USING THE SAME FOR			
; TITLE OF INVENTION: DIAGNOSIS AND FOR TARGETING THE THERAPY OF SELECT CANCERS			
; FILE REFERENCE: 11613.56US11			
; CURRENT APPLICATION NUMBER: US/10/159,563			
; CURRENT FILING DATE: 2002-12-09			
; PRIOR APPLICATION NUMBER: US 10/133,937			
; PRIOR FILING DATE: 2002-04-25			
; NUMBER OF SEQ ID NOS: 444			
; SOFTWARE: Patentin version 3.1			
; SEQ ID NO 308			
; LENGTH: 4459			
; TYPE: DNA			
; ORGANISM: Homo sapiens			
US-10-159-563-308			
Query Match			
Best Local Similarity 96.8%; Score 3156.8; DB 17; Length 4459;			
Matches 3175; Conservative 0; Mismatches 13; Indels 1; Gaps 1;			
QY	1	ATGGGGAACGGGAGCGGGCTCCGGGCTCGGAGCTTTGGCCCGTACCCACGCTGCTG 60	
Db	294	ATGGGGAACGGGAGCGGGCTCCGGGCTCGGAGCTTTGGCCCGTACCCACGCTGCTG 353	
QY	61	CTGCTCGCGCGGGCGCTACTGCGCGCTGTGCGACGACCTCGGGCGCCCTCCGAGGAGGAC 120	
Db	354	CTGCTCGCGCGGGCGCTACTGCGCGCTGTGCGACGACCTCGGGCGCCCTCCGAGGAGGAC 413	
QY	121	GAGGAGCTAGTGTGTCCCGGAGCTGAGCGCGCCCGGACACAGGACCAACGCGCTCCGC 180	
Db	414	GAGGAGCTAGTGTGTCCCGGAGCTGAGCGCGCCCGGACACAGGACCAACGCGCTCCGC 473	
QY	181	CTGCACGCGCTTTGACACGAGCTGGATCTGGAGCTGCGGCCCGGACAGAGCTTTTGGCG 240	
Db	474	CTGCACGCGCTTTGACACGAGCTGGATCTGGAGCTGCGGCCCGGACAGAGCTTTTGGCG 533	
QY	241	CCCGCTTTCAGCTCCAGAAAGTGGGGCGCAAAATCCGGGTCCGAGACGCGCTTCCGGAA 300	
Db	534	CCCGCTTTCAGCTCCAGAAAGTGGGGCGCAAAATCCGGGTCCGAGACGCGCTTCCGGAA 593	
QY	301	ACCGACTTGGGCGACTGTTCTTATCCGGGACCGGTGAATGGGATCCAGCTCGGCTGCC 360	
Db	594	ACCGACTTGGGCGACTGTTCTTATCCGGGACCGGTGAATGGGATCCAGCTCGGCTGCC 653	
QY	361	GCCCTCAGCCTCTGGAGGGGTGCGCGCGCTTCTACCTGCTGGGGAGGCGGTATTTC 420	
Db	654	GCCCTCAGCCTCTGGAGGGGTGCGCGCGCTTCTACCTGCTGGGGAGGCGGTATTTC 713	
QY	421	ATCCAGCGCTGCCCGCCCGCAGCGAGCGCTTCGCAACCGCCCGCCCGAGGGGAGAGCG 480	
Db	714	ATCCAGCGCTGCCCGCCCGCAGCGAGCGCTTCGCAACCGCCCGCCCGAGGGGAGAGCG 773	
QY	481	CGGCAACCACTACAGTTTCCACTCTCTGGGGGGAATCCGGCAGGGGAGAGTAGGCGGCAG 540	
Db	774	CGGCAACCACTACAGTTTCCACTCTCTGGGGGGAATCCGGCAGGGGAGAGTAGGCGGCAG 833	

541 TGCGGGTCTGTGACGACGAGCCCGCGCAGCTGGGAAAGCGGAGACCGAAGACGAGGAC 600
Db
834 TGCGGGGTCTGTGACGACGAGCCCGCGCAGCTGGGAAAGCGGAGACCGAAGACGAGGAC 893
Qy
601 GAAGGACCTGAGGGCGAGGACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 660
Db
894 GAAGGACCTGAGGGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 953
Qy
661 GGGGTAGGACGAGGACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 720
Db
954 GGGGTAGGACGAGGACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1013
Qy
721 CGCTATGTGAACCACTGCTTGTGGGACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 780
Db
1014 CGCTATGTGAACCACTGCTTGTGGGACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1073
Qy
781 CTAAGCACTTACCTTCTCAAGTGTGTTTGGGACGAGGAGGAGGAGGAGGAGGAGGAGGAG 840
Db
1074 CTAAGCACTTACCTTCTCAAGTGTGTTTGGGACGAGGAGGAGGAGGAGGAGGAGGAGGAG 1133
Qy
841 ATTCTGTAATTCAGTTAGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 900
Db
1134 ATTCTGTAATTCAGTTAGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1193
Qy
901 GGGCCGGAGTGTACCTTCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 960
Db
1194 GGGCCGGAGTGTACCTTCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1253
Qy
961 CAGCAACAACCCAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1020
Db
1254 CAGCAACAACCCAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1313
Qy
1021 AGCAGGACTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1080
Db
1314 AGCAGGACTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1373
Qy
1081 GTCTGTGATCCGAGCAGGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1140
Db
1374 GTCTGTGATCCGAGCAGGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1433
Qy
1141 ACCACAGCCCATGAATTTAGGCGCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1200
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1434 ACCACAGCCCATGAATTTAGGCGCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1493
Qy
1201 GCAGGCTTAAATGCTGTGAACAGGATTTCCCAATGATGCTGCTGCTGCTGCTGCTGCTGCT 1260
Db
1494 GCAGGCTTAAATGCTGTGAACAGGATTTCCCAATGATGCTGCTGCTGCTGCTGCTGCTGCT 1553
Qy
1261 GACCACAGCCGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1320
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1321 GGTGATGGGAAATTTGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1380
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1614 GGTGATGGGAAATTTGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1673
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1381 CTTGGGACCTGCTGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1440
Db
1674 CTTGGGACCTGCTGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1733
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1441 CACTGCTGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1500
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1734 CACTGCTGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1793
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1501 GTGCTGTGTGTCAAAACCAACCACTTCCGCTGGGCGGATGCGACAGCTGTGGAGAGGG 1560
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2401 AAAGAGCCCTTGACCACTCCAGGTTCTTCTGTTGGCAATGCTTCCCTCGACCTTAAATTTAA 2460
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2694 AAAGAGCCCTTGACCACTCCAGGTTCTTCTGTTGGCAATGCTTCCCTCGACCTTAAATTTAA 2753
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2641 CCAGCCAGCAGCAGACCTTGTGAGACCACTTCCCTGCCCCCAGTGGGAGGAGTGG 2700
Db
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RESULT 14

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US-09-971-429B-17
; Sequence 17, Application US/09971429B
; Publication No. US20030175704A1
; GENERAL INFORMATION:
; APPLICANT: Lasek, Amy K. W.
; APPLICANT: Shvjan, Andrew W.
; APPLICANT: Turner, Christopher M.
; TITLE OF INVENTION: GENES EXPRESSED IN LUNG CANCER
; FILE REFERENCE: PA-0040 US
; CURRENT APPLICATION NUMBER: US/09/971,429B
; PRIOR FILING DATE: 2001-10-04
; PRIOR APPLICATION NUMBER: 60/239,024
; PRIOR FILING DATE: 2000-04-10
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: PERL Program
; SEQ ID NO 17
; LENGTH: 4760
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US20030175704A1 007074.13
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 118
; OTHER INFORMATION: a, t, c, g, or other
US-09-971-429B-17
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Query Match 96.8%; Score 3156.8; DB 10; Length 4760;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 3175; Conservative 0; Mismatches 13; Indels 1; Gaps 1;
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Db 612 ATGGGGAACCGGAGCGGGCTCCGGGGTCTCGAGCTTTGGGCCGTACCCACGCTGCTG 671
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Db 732 GAGGAGCTAGTGTGCGGAGCTGAGGCGCGCCCGGGAACAGCGGACCAACGCGCTTCGCG 791
Qy 181 CTGACGCGCTTTGACACGACGCTGATCTGAGCTGCGGCGCCGACAGCAGCAGCTTTTGGCG 240
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Qy 241 CCGCGCTTCAGCGCTCCAGAAAGTGGGGCGCAAAATCCGGGTCCGAGACGCGCTTCGCGAA 300
Db 852 CCGCGCTTCAGCGCTCCAGAAAGTGGGGCGCAAAATCCGGGTCCGAGACGCGCTTCGCGAA 911
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Db 912 ACCGACTTGGGCGCACTGCTTTACTTCCGGCAACCGTGAATGGCGATCCAGCTCGGCTGCG 971
Qy 361 GCGCTCAGCGCTGCGAGGGGCTGCGCGCGCGCTTCTACCTGCTGGGGAGCGGTATTTTC 420
Db 972 GCGCTCAGCGCTGCGAGGGGCTGCGCGCGCGCTTCTACCTGCTGGGGAGCGGTATTTTC 1031
Qy 421 ATCCAGCGCGCTGCCCGCGCGCAGCGAGCGCTCGCCACCGCGCGCCCGAGGGGAGAGCGG 480
Db 1032 ATCCAGCGCGCTGCCCGCGCGCAGCGAGCGCTCGCCACCGCGCGCCCGAGGGGAGAGCGG 1091
Qy 481 CCGGCACCACTACAGTTCCACTCTCTGCGGGGGAATCGGCAGGGCGAGCTAGCGGGCAGG 540
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Db 1392 CTAAAGCAATTACCTTCTCAGCTTGTGTTTTCGGTGGCAGCCAGATTTGTACAAAACACCCG 1451
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[illegible]

RESULT 15
US-10-210-120-57
; Sequence 57; Application US10210120
; Publication No. US20030175736A1
; GENERAL INFORMATION:
; APPLICANT: Chinnaiyan, Arul M.

APPLICANT: Rubin, Mark A.
APPLICANT: Sreekumar, Arun
FILE OF INVENTION: Expression Profile of Prostate Cancer
CURRENT APPLICATION NUMBER: US/10/210,120
CURRENT FILING DATE: 2002-08-01
PRIOR APPLICATION NUMBER: US 60/309,581
PRIOR FILING DATE: 2001-08-02
PRIOR APPLICATION NUMBER: US 60/334,468
PRIOR FILING DATE: 2001-11-15
NUMBER OF SEQ ID NOS: 123
SOFTWARE: PatentIn version 3.2
SEQ ID NO 57
LENGTH: 4309
TYPE: DNA
ORGANISM: Homo sapiens
US-210-120-57

Query Match 96.8%; Score 3155.2; DB 16; Length 4309;
Best Local Similarity 99.5%; Pred No. 0;
Matches 3174; Conservative 0; Mismatches 14; Indels 1; Gaps 1;

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DB 287 GAGGAGCTAGTGTGCGCGAGCTGCGAGCGCGCCCGGAGACGCGGACCAACGCGCTCCGC 346
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DB 767 GAAGGAGCTGAGGGCGAGGACGAGGGCTCAGTGTGCTCGCCAGGACCCGCGACTGCA 826
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

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(without alignments)
9996.978 Million cell updates/sec

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Sequence: 1 cccacgcgtccgccacgcg.....cttttggagccactccag 4014

Scoring table: OLIGO_NUC
Gapop_60.0 , Gapext 60.0

Searched: 1202784 seqs, 818138359 residues

Word size : 0

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
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Post-processing: Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2922	72.8	4676	3	US-09-130-491-1
2	2904	72.3	4858	3	US-09-392-184-1
3	2471	61.6	3889	4	US-09-568-559-1
4	2090	52.1	3706	3	US-09-484-970B-58
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6	67	1.7	260	4	US-09-513-999C-32662
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27	25	0.6	266	4	US-09-023-655-693

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	31	25	0.6	878	4	US-09-774-639-35	Sequence 35, Appl
	32	25	0.6	944	3	US-09-227-357-122	Sequence 122, Appl
	33	25	0.6	1041	4	US-09-690-454-23	Sequence 23, Appl
	34	25	0.6	1052	4	US-09-489-847-23	Sequence 23, Appl
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	37	25	0.6	1139	4	US-10-012-542-81	Sequence 81, Appl
c	38	25	0.6	1139	4	US-10-115-123-81	Sequence 1, Appl
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ALIGNMENTS

RESULT 1

US-09-130-491-1
; Sequence 1, Application US/09130491
; Patent No. 6416974
; GENERAL INFORMATION:
; APPLICANT: Holtzman, Douglas A.
; APPLICANT: Goodearl, Andrew D.J.
; TITLE OF INVENTION: TANGO-71, TANGO-73, TANGO-74, TANGO-76, AND TANGO-83
; FILE REFERENCE: 09404/041001
; CURRENT APPLICATION NUMBER: US/09/130,491
; CURRENT FILING DATE: 1998-08-07
; EARLIER APPLICATION NUMBER: US 60/058,108
; EARLIER FILING DATE: 1997-09-05
; EARLIER APPLICATION NUMBER: US 60/054,961
; EARLIER FILING DATE: 1997-08-06
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 4676
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (460)...(3360)
US-09-130-491-1

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Qy	85	GC	CTGAGCAGGTGAGCAATCGCAGCCAGGCGGCGGAGGGGCGCCAGGCA	144
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Qy	145	CC	ATATCTCCGGTTGGCTTCAGCCCGGAGGGCGCCCGAGCGCTTCTTGTCCAGCAG	204
Db	139	CC	ATATCTCCGGTTGGCTTCAGCCCGGAGGGCGCCCGAGCGCTTCTTGTCCAGCAG	198
Qy	205	CC	ATCTGCGCTGCGCTGCTCTCAGTGTCTTCCAACTTGGCTGGAAGAAAATTTCCC	264
Db	199	CC	ATCTGCGCTGCGCTGCTCTCAGTGTCTTCCAACTTGGCTGGAAGAAAATTTCCC	258
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Query Match 72.8%; Score 2922; DB 3; Length 4676;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 3772; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

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RESULT 2

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; Sequence 1, Application US/09392184
; Patent No. 6395889
; GENERAL INFORMATION:
; APPLICANT: Robison, Keith E.
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN
; FILE OF INVENTION: PROTEASE HOMOLOGS
; FILE REFERENCE: 5800-55
; CURRENT APPLICATION NUMBER: US/09/392,184
; CURRENT FILING DATE: 1999-09-09
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 4858
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(4858)
; OTHER INFORMATION: repolysin (ADAM family of metalloprotease)
; NAME/KEY: misc_feature
; LOCATION: (1)...(4858)
; OTHER INFORMATION: n = A,T,C or G
; US-09-392-184-1
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Query Match 72.3%; Score 2904; DB 3; Length 4858;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 3774; Conservative 0; Mismatches 15; Indels 1; Gaps 1;
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1513 AATTCCTTTTCAACGACAGGACTCTGTGGGTCCAGACATGTGATCTCTTTGGGATGC 1572
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1584 TGATGTGGAACTGTGTGTGATCCGAGCAGAAGCTGCTCCGTATAGAAAGATGATGGTTT 1643
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1573 TGATGTGGAACTGTGTGTGATCCGAGCAGAAGCTGCTCCGTATAGAAAGATGATGGTTT 1632
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1693 TGCAAGCAGTGTGCCAGCTTAAATGTTGTAACAGAGATCCCAATGATGGCGTCAAT 1752
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1813 ATTTCTGGATATGATGTCATGAGGAAATGTTGATGACAAAGCTCAGAAATCCCATACAGT 1872
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1873 CCCAGCGATCTCCCTGCGACCTCGTACGATGCCAACCGGACGTGCCAGTTTACATTTG 1932
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1944 GGAGGACTCCAAACACTGCTGATGACCCAGCACATGTAGCACCTTTGTGTTGATCCGG 2003
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1933 GGAGGACTCCAAACACTGCTGATGACCCAGCACATGTAGCACCTTTGTGTTGATCCGG 1992
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2004 CACCTCTGGTGGGTGCTGCTGTCACAAACCAACACTTTCCGTTGGGGATGCGACACAG 2063
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1993 CACCTCTGGTGGGTGCTGCTGTCACAAACCAACACTTTCCGTTGGGGATGCGACACAG 2052
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2473 GCAGCCCAAGTGTGTAGATGGTACTCCATGTAGCCCAATTCACCTCTGTCTGTGTGA 2532
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2533 AGGACAGTGTGTAAGAGTGGTGTGATCGCATCATAGATCTCAAAAAGAGTTTGTATAA 2592

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Db 3553 TAGTTAGTAGGATTTATTAACCTCTGAGCAGTGAATATAGCATATAAAGCCCGGGCATTT 3612
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Db 3733 GGGGGTTGGGAAATGAAAAAGTAGGAGAAAGTGAGATTTTACTAAGACCTGTTTACTTTT 3792
QY 3804 ACCTCACTAA 3813
Db 3793 ACCTCACTAA 3802

RESULT 3
US-09-568-559-1
; Sequence 1, Application US/09568559
; Patent No. 6649377
; GENERAL INFORMATION:
; APPLICANT: Klonowski, Paul
; APPLICANT: Allard, John
; APPLICANT: Heller, Renu
; APPLICANT: Van Wart, Harold
; TITLE OF INVENTION: Human Aggrecanase and Nucleic Acid
; TITLE OF INVENTION: Compositions Encoding the Same
; FILE REFERENCE: ROCH-002
; CURRENT APPLICATION NUMBER: US/09/568,559
; CURRENT FILING DATE: 2000-05-09
; PRIOR APPLICATION NUMBER: 60/133,343
; PRIOR FILING DATE: 1999-05-10
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 3889
; TYPE: DNA
; ORGANISM: human
US-09-568-559-1
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Query Match 61.6%; Score 2471; DB 4; Length 3889;
Best Local Similarity 99.5%; Pred. No. 0;
Matches 3221; Conservative 0; Mismatches 15; Indels 0; Gaps 0;
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QY 536 CTCGGGGTCTCGAGAGCTTTGGGCGCGTACCGACGCTGCTGCTCGCCGCGCGCTAC 595
Db 78 CTCGGGGTCTCGAGAGCTTTGGGCGCGTACCGACGCTGCTGCTCGCCGCGCGCTAC 137
QY 596 TGGCCGCTGTCCGACGCACTCGGGCGCCCTTCGAGGAGGACGAGGAGCTAGTGTGCGCG 655
Db 138 TGGCCGCTGTCCGACGCACTCGGGCGCCCTTCGAGGAGGACGAGGAGCTAGTGTGCGCG 197
QY 656 AGCTGAGAGCGCTGCCGGGACACGGAACACAGCGGCTTCCGCTGACGCTTTGACACAG 715
Db 198 AGCTGAGAGCGCTGCCGGGACACGGAACACAGCGGCTTCCGCTGACGCTTTGACACAG 257
QY 716 AGCTGAGCTGGAGCTGCCCGGACGACGAGCTTTTGGCGCCCGGCTTCAAGCTCCAGA 775
Db 258 AGCTGAGCTGGAGCTGCCCGGACGACGAGCTTTTGGCGCCCGGCTTCAAGCTCCAGA 317
QY 776 ACCTGGGGCCAAATCCGGGTTCGACACACCCCGCTTCGGAACACCGACTGGCGCACTGCT 835
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QY 836 TCTACTCCGGCACCGTGAATGGCGATCCAGCTCGGCTGCGGCTCAGCTCTTCGCGAGG 895
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QY 896 GCGTGGCGGCGCTTCTACTGCTGGGGAGGCGGTATTTTCATCCAGCGCTGCCCGCG 955
Db 438 GCGTGGCGGCGCTTCTACTGCTGGGGAGGCGGTATTTTCATCCAGCGCTGCCCGCG 497
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QY	956	CCAGGAGCGCTTCGCCACCGCGCCGCCAGGGGAGAGCGCGGCACCACTACAGTTCC	1015
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QY	1016	ACCTCTCGCGGGAATCCGCGAGGCGACGTTAGGCGGCGACGTCGCGGGTCGTGGACGACG	1075
Db	558	ACCTCTCGCGGGAATCCGCGAGGCGACGTTAGGCGGCGACGTCGCGGGTCGTGGACGACG	617
QY	1076	AGCCCGGCGGACTGGGAAGCGGAGACCGAGAGCGAGGACGAGGAGCTGAGGCGGAGG	1135
Db	618	AGCCCGGCGGACTGGGAAGCGGAGACCGAGAGCGAGGAGCTGAGGCGGAGG	677
QY	1136	ACGAAGGGGCTCAGTGGTCGCGCAGGACCCGCGCACTGCAAGCGGTAGGACAGCCACAG	1195
Db	678	ACGAAGGGGCTCAGTGGTCGCGCAGGACCCGCGCACTGCAAGCGGTAGGACAGCCACAG	737
QY	1196	GAACCTGGGAAGCATAAGAAAGAGCGGATTTGTCTCAGTCCACGCTATGTGGAAACCATGC	1255
Db	738	GAACCTGGGAAGCATAAGAAAGAGCGGATTTGTCTCAGTCCACGCTATGTGGAAACCATGC	797
QY	1256	TTGTGGCAGACCACTCGATGGCAGATTTCCAGGCGAGTGGTCTAAAGCAATTAACCTTCTCA	1315
Db	798	TTGTGGCAGACCACTCGATGGCAGATTTCCAGGCGAGTGGTCTAAAGCAATTAACCTTCTCA	857
QY	1316	CGTTGTTTTCGCTGGCAGCAGATTTGTACAAACACCCAGCAATTCGTAATTCAGTTAGCC	1375
Db	858	CGTTGTTTTCGCTGGCAGCAGATTTGTACAAACACCCAGCAATTCGTAATTCAGTTAGCC	917
QY	1376	TGGTGGTGGTGAAGATCTTTGGTCATCCAGATGAACAGAAAGGGGCGGAGTGAACCTCCA	1435
Db	918	TGGTGGTGGTGAAGATCTTTGGTCATCCAGATGAACAGAAAGGGGCGGAGTGAACCTCCA	977
QY	1436	ATGCTGCCCTCACTCGCGGAATTTTGCACTGGCAGAGCAGCACACCCAGTCG	1495
Db	978	ATGCTGCCCTCACTCGCGGAATTTTGCACTGGCAGAGCAGCACACCCAGTCG	1037
QY	1496	ACCGGATCGAGACACTATGACACAGCAATTTCTTTTCCACAGACAGGACTTGTGGGT	1555
Db	1038	ACCGGATCGAGACACTATGACACAGCAATTTCTTTTCCACAGACAGGACTTGTGGGT	1097
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Db	1098	CCGACATGTGATCTCTTGGGATGGCTGATTTGGAACTGTGTGTGATCCGAGCAGAA	1157
QY	1616	GCTGCTCCCTCATAGAGATGTTTACAGCTGCTTCCACAGAGCAGTCCATGATGAT	1675
Db	1158	GCTGCTCCCTCATAGAGATGTTTACAGCTGCTTCCACAGAGCAGTCCATGATGAT	1217
QY	1676	GCACGTGTTTAACTGCCACATGATGATGCAAGCAGTGTGCCAGCCTTAATGTTGA	1735
Db	1218	GCACGTGTTTAACTGCCACATGATGATGCAAGCAGTGTGCCAGCCTTAATGTTGA	1277
QY	1736	ACCAGGATTTCCACATGATGGCGTCAATGCTTTCCAACTTGACACCAAGCCCTTGGT	1795
Db	1278	ACCAGGATTTCCACATGATGGCGTCAATGCTTTCCAACTTGACACCAAGCCCTTGGT	1337
QY	1796	CTCCTTGAGTGGCTACATGATTTACATCATTTCTGGATTAATGGTCATGGGATGTTGA	1855
Db	1338	CTCCTTGAGTGGCTACATGATTTACATCATTTCTGGATTAATGGTCATGGGATGTTGA	1397
QY	1856	TGGACAAGGCTCAGAACTCCATACAGCTCCAGGCGATCTCCCTGGCAGCTCGTACGATG	1915
Db	1398	TGGACAAGGCTCAGAACTCCATACAGCTCCAGGCGATCTCCCTGGCAGCTCGTACGATG	1457
QY	1916	CCAAACCGGAGTCCAGTTTACATTTGGGAGGAGCTCCAAAACACTGCTGATGAGGCA	1975
Db	1458	CCAAACCGGAGTCCAGTTTACATTTGGGAGGAGCTCCAAAACACTGCTGATGAGGCA	1517
QY	1976	GCACATGATGACCTTGTGGTGTACCGGACCTCTGCTGGGCTGCTGGTGTCTCAAAACCA	2035
Db	1518	GCACATGATGACCTTGTGGTGTACCGGACCTCTGCTGGGCTGCTGGTGTCTCAAAACCA	1577
QY	2036	AACACTTCCGTTGGGCGGATGGCACCGAGTGTGGAGAGGAAATGGTGTATCAACGGCA	2095

Db	1578	AACACTTCCGTTGGGCGGATGGCACCGAGTGTGGAGAGGAAATGGTGTATCAACGGCA	1637
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Db	1638	AGTGTGTGAACAAAAACACAGAAAGCATTTTGTATACGCTTTTTCATGGAAGCTGGGAA	1697
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QY	2276	GCTACAGATCTCTGTAAACCTTGAAGACTGTCCAGACAAATAATGGAAGAAACCTTTAGAGAG	2335
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QY	2336	AACAATGTGAAGCACACAAACGAGTTTCAAAAAGCTTCTTTGGGAGTGGGCTGCGGTGG	2395
Db	1878	AACAATGTGAAGCACACAAACGAGTTTCAAAAAGCTTCTTTGGGAGTGGGCTGCGGTGG	1937
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Db	1938	AATGGATTTCCCAAGTACGCTGGCGTCTCACAAAGGACAGAGTGCAGAGCTCATCTGCCAAG	1997
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Db	1998	CCAAAGGCAATTTGGCTACTTTCTTGGTTTTCGAGCCCAAGTGTGTAGATGGTACTCATGTA	2057
QY	2516	GCCAGATTTCCACCTCTGCTGTGCAAGGACAGTGTGTAAGAGCTGTTGTGATCGCA	2575
Db	2058	GCCAGATTTCCACCTCTGCTGTGCAAGGACAGTGTGTAAGAGCTGTTGTGATCGCA	2117
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QY	2696	TTCCAACTGGAGCCACCAACATCGAAGTGAAACAGCGAAACAGAGGGGATCCAGGAACA	2755
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QY	2756	ATGGCAGCTTTCTTCCATCAAAGCTGCTGATGGCACATATATTCTTAATGGTGAATA	2815
Db	2298	ATGGCAGCTTTCTTCCATCAAAGCTGCTGATGGCACATATATTCTTAATGGTGAATA	2357
QY	2816	CTTTGTCCACCTTAGAGCAAGACATATGTAACAAAGTGTGCTCTTGGAGTACAGCGCT	2875
Db	2358	CTTTGTCCACCTTAGAGCAAGACATATGTAACAAAGTGTGCTCTTGGAGTACAGCGCT	2417
QY	2876	CCTCTGGGCAATTTGAAAGAAATTCGAGCTTTAGCCCTCTCAAAAGAGCCTTTGACCATCC	2935
Db	2418	CCTCTGGGCAATTTGAAAGAAATTCGAGCTTTAGCCCTCTCAAAAGAGCCTTTGACCATCC	2477
QY	2936	AGGTTCTTATCTGTGGGCAATGCCCTTCGACCTTAAATTAATAATACCTACTTTCGTAAGA	2995
Db	2478	AGGTTCTTATCTGTGGGCAATGCCCTTCGACCTTAAATTAATAATACCTACTTTCGTAAGA	2537
QY	2996	AGAAAGGAAATCTTTCAATGCTATCCCACTTTTTCAGCATGGGCTCATTTAGAGTGGG	3055
Db	2538	AGAAAGGAAATCTTTCAATGCTATCCCACTTTTTCAGCATGGGCTCATTTAGAGTGGG	2597
QY	3056	GGCAATGTTCTAAGTCATGTGAATTTGGGTTGGCAGAGAGACTGGTAGAATGCCAGACA	3115
Db	2598	GGCAATGTTCTAAGTCATGTGAATTTGGGTTGGCAGAGAGACTGGTAGAATGCCAGACA	2657
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Db 2718 GTGCAGACCATCCCTGCCCCCAGTGGCAGCTGGGGAGTGGTCAATCATCTTCTAAGACCT 2777
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Qy 3296 CTCATGACAGCTGTGATCTCTTTAAAGAACCTTAAACATTTTATAGACTTTTGCACAAATG 3355
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Qy 3656 AGTTTAGAAAAAACAAGCAATGTCAAAAAAGTTAGAACTATTACAAACCCCTG 3711
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RESULT 4

US-09-484-970B-58
; Sequence 58, Application US/09484970B
; Patent No. 6426186
; GENERAL INFORMATION:
; APPLICANT: Jones, Karen A.
; APPLICANT: Volkmut, Wayne
; APPLICANT: Walker, Michael G.
; TITLE OF INVENTION: BONE REMODELING GENES
; FILE REFERENCE: PB-0014 US
; CURRENT APPLICATION NUMBER: US/09/484,970B
; CURRENT FILING DATE: 2000-01-18
; NUMBER OF SEQ ID NOS: 172
; SOFTWARE: PERL Program
; SEQ ID NO 58
; LENGTH: 3706
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. 6426186 007074.1
; NAME/KEY: unsure
; LOCATION: 3634, 3638-3639, 3642-3643, 3647-3648, 3652, 3654-3658, 3664, 3674, 3681
; OTHER INFORMATION: a, t, c, g, or other
US-09-484-970B-58

Query Match 52.1%; Score 2090; DB 3; Length 3706;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 2610; Conservative 0; Mismatches 8; Indels 1; Gaps 1;
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Db 1 GGAGGGCGACGTAGGCGGACGTCGGGGTCTGTGACGACGAGCCCCCGCCACTGGGA 60

Qy 1094 AAGCGGAGACCGAAGACGAGGACGAGGACCTGAGGGCGAGGACGAGGGCCCTCACTGCT 1153
Db 61 AAGCGGAGACCGAAGACGAGGACGAGGACCTGAGGGCGAGGACGAGGGCCCTCACTGCT 120
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Db 181 AGAAGCGATTTGTGTCCAGTCAACCGCTATGTGGAAACCAATGTGTGGCAGACCACTGCA 240
Qy 1274 TGGCAGAAATTCACGGCAGTGTCTAAGCATTTCTCTCAGTGTGTTTTCGGTGGCAG 1333
Db 241 TGGCAGAAATTCACGGCAGTGTCTAAGCATTTCTCTCAGTGTGTTTTCGGTGGCAG 300
Qy 1334 CCAGATTTGACAAACACCCAGCATTTGCTAAATTCAGTTAGCCTGTGGTGGTGAAGATCT 1393
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Qy 1394 TGGTCATCCAGATGAACAGAGGGGCCGAAAGTGAACCTTCAATGTGTGCTTCACTCTGC 1453
Db 361 TGGTCATCCAGATGAACAGAGGGGCCGAAAGTGAACCTTCAATGTGTGCTTCACTCTGC 420
Qy 1454 GGAATTTTGGAACTGGGAGAGCAGCAACCCACCCAGTGAACCGGATGACAGCACT 1513
Db 421 GGAATTTTGGAACTGGGAGAGCAGCAACCCACCCAGTGAACCGGATGACAGCACT 480
Qy 1514 ATGACACACCAATTTCTTTTACAGACAGGACTTTGTGGTGGTCCAGACATGTGATACTC 1573
Db 481 ATGACACACCAATTTCTTTTACAGACAGGACTTTGTGGTGGTCCAGACATGTGATACTC 540
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Db 541 TTGGGATGGCTGATTTTGAACCTGTGTGATCCGAGCAGAACTGCTCCGTCAATGAAG 600
Qy 1634 ATGATGGTTTACAGCTGCTTTCACACAGCCCATGAATAGGCCAGCTGTTTAAATGC 1693
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Db 661 CACATGATGATGCAAAAGCAGTGTGCCAGCTTAAATGTGTGAACACAGGATTTCCACATGA 720
Qy 1754 TGGCGTCAATGCTTTCACACCTGGACCAACAGCCAGCTTGGTCTCTCTTGCAGTGGCTACA 1813
Db 721 TGGCGTCAATGCTTTCACACCTGGACCAACAGCCAGCTTGGTCTCTCTTGCAGTGGCTACA 780
Qy 1814 TGATTAATCATCTTCTGGATTAATGGTCAATGGGGAATTTGTGAGCAAGCCTCAGNATC 1873
Db 781 TGATTAATCATCTTCTGGATTAATGGTCAATGGGGAATTTGTGAGCAAGCCTCAGNATC 840
Qy 1874 CCATACAGCTCCAGGGGATCTCCCTGGGACCTCTGACGATGCAACCCGAGTGGCCAGT 1933
Db 841 CCATACAGCTCCAGGGGATCTCCCTGGGACCTCTGACGATGCAACCCGAGTGGCCAGT 900
Qy 1934 TTACATTTGGGAGGAGTCTCCAAACACTGCTGATGACGAGCAGCAGATGTAGCACCTTGT 1993
Db 901 TTACATTTGGGAGGAGTCTCCAAACACTGCTGATGACGAGCAGCAGATGTAGCACCTTGT 960
Qy 1994 GGTGTACCGGACCTCTGTGGGGTGTGTGTGTCMAACCAACCACTTCCGTGGGGCGG 2053
Db 961 GGTGTACCGGACCTCTGTGGGGTGTGTGTGTCMAACCAACCACTTCCGTGGGGCGG 1020
Qy 2054 ATGGCACAGCTGTGAGAGGGAATGGTATCAACGGCAAGTGTGCAACAAACACC 2113
Db 1021 ATGGCACAGCTGTGAGAGGGAATGGTATCAACGGCAAGTGTGTCMAACCAACACC 1080
Qy 2114 ACAGAAAGCATTTTGTATACGCTTTTTCATGGAAGCTGGGGAATGTGGGGCCTTGGGGAG 2173
Db 1081 ACAGAAAGCATTTTGTATACGCTTTTTCATGGAAGCTGGGGAATGTGGGGCCTTGGGGAG 1140
Qy 2174 ACTGTTGAGAACTGCGGTGGAGGAGTCCAGTACAGATGAGGGGAATGTGACAAACCCAG 2233

FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 119
; OTHER INFORMATION: r=a or g
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 259
; OTHER INFORMATION: k=g or t
US-09-513-999C-32662

Query Match 1.7%; Score 67; DB 4; Length 260;
Best Local Similarity 99.2%; Pred. No. 1.6e-22;
Matches 117; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3653 TACAAGTTTAGAAAAAACAAGCAATTTGCAAAAAAGTTAGAACTATTACAAACCCCTGC 3712
DB 1 TACAAGTTTAGAAAAAACAAGCAATTTGCAAAAAAGTTAGAACTATTACAAACCCCTGT 60
QY 3713 TTCTGGTACTTATCAATACTTAGTATCATCGGGGTTGGGAAATGAAAAAGTAGGAGA 3770
DB 61 TTCTGGTACTTATCAATACTTAGTATCATCGGGGTTGGGAAATGAAAAAGTAGGAGA 118

RESULT 7
US-09-445-023A-13
; Sequence 13, Application US/09445023A
; Patent No. 6565858

GENERAL INFORMATION:
; APPLICANT: Hirose, Kunitaka
; APPLICANT: Inoguchi, Biiji
; APPLICANT: Hakoziaki, Michinori
; APPLICANT: Ishioka, Keiko
; APPLICANT: Ishida, Yukako
; APPLICANT: Matsushima, Kouji
; APPLICANT: Kuno, Kouji

; TITLE OF INVENTION: Human ADAMTS-1 protein, gene encoding the same, pharmaceutical
; FILE REFERENCE: Q57092
; CURRENT APPLICATION NUMBER: US/09/445, 023A
; CURRENT FILING DATE: 1999-12-03
; PRIOR APPLICATION NUMBER: JP 9-160422
; PRIOR FILING DATE: 1997-06-03
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 13
; LENGTH: 2184
; TYPE: DNA
; ORGANISM: Mus sp.
; FEATURE:
; NAME/KEY: exon
; LOCATION: (1)..(2184)
US-09-445-023A-13

Query Match 0.9%; Score 38; DB 4; Length 2184;
Best Local Similarity 100.0%; Pred. No. 4.1e-08;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2566 TGTGATCGCATCATGACTCCAAAAAGAGTTTGATAA 2603
DB 1381 TGTGATCGCATCATGACTCCAAAAAGAGTTTGATAA 1418

RESULT 8
US-09-445-023A-14
; Sequence 14, Application US/09445023A
; Patent No. 6565858

GENERAL INFORMATION:
; APPLICANT: Hirose, Kunitaka
; APPLICANT: Inoguchi, Biiji
; APPLICANT: Hakoziaki, Michinori
; APPLICANT: Ishioka, Keiko
; APPLICANT: Ishida, Yukako
; APPLICANT: Matsushima, Kouji

; APPLICANT: Kuno, Kouji
; TITLE OF INVENTION: Human ADAMTS-1 protein, gene encoding the same, pharmaceutical
; FILE REFERENCE: Q57092
; CURRENT APPLICATION NUMBER: US/09/445, 023A
; CURRENT FILING DATE: 1999-12-03
; PRIOR APPLICATION NUMBER: JP 9-160422
; PRIOR FILING DATE: 1997-06-03
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 14
; LENGTH: 303
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-445-023A-14

Query Match 0.8%; Score 34; DB 4; Length 303;
Best Local Similarity 100.0%; Pred. No. 3.6e-06;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2415 TGGCGTCTCACAAGGACAGGTGCAAGCTCATC 2448
DB 240 TGGCGTCTCACAAGGACAGGTGCAAGCTCATC 273

RESULT 9
US-09-063-743-2
; Sequence 2, Application US/09063743
; Patent No. 6242214

GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Lal, Preeti
; APPLICANT: Guegler, Karl J.
; APPLICANT: Corley, Neil C.
; APPLICANT: Patterson, Chandra
; TITLE OF INVENTION: HUMAN GTPASE-ASSOCIATED PROTEINS
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304

COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/063,743
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Cerrone, Michael C
; REGISTRATION NUMBER: 39,132
; REFERENCE/DOCKET NUMBER: PF-0508 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; TELEX:

INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
; LENGTH: 1211 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: LUNGNOT01
; CLONE: 059953

US-09-063-743-2

Query Match 0.7%; Score 29; DB 3; Length 1211;
Best Local Similarity 100.0%; Pred. No. 0.0012;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCACGCGTCCGCCACGCGTCCGGCGGC 29
DB 1 CCCACGCGTCCGCCACGCGTCCGGCGGC 29

RESULT 10

US-09-590-540-2
Sequence 2, Application US/09590540

Patent No. 6410267

GENERAL INFORMATION:

APPLICANT: Bandman, Olga
Lal, Preeti
Guegler, Karl J.
Corley, Neil C.
Patterson, Chandra

TITLE OF INVENTION: HUMAN GTPASE-ASSOCIATED PROTEINS

NUMBER OF SEQUENCES: 6

CORRESPONDENCE ADDRESS:

ADDRESSEE: Incyte Genomics, Inc.
STREET: 3160 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS

SOFTWARE: FastSeq for Windows Version 3.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/590,540

FILING DATE: 08-Jun-2000

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/063,743

FILING DATE: April 21, 1998

ATTORNEY/AGENT INFORMATION:

NAME: David G. Streeter

REGISTRATION NUMBER: 43,168

REFERENCE/DOCKET NUMBER: PF-0508-1 DIV

TELECOMMUNICATION INFORMATION:

TELEPHONE: 650-855-0555

TELEFAX: 650-845-4166

TELEX: <Unknown>

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 1211 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

IMMEDIATE SOURCE:

LIBRARY: LUNGN0T01

CLONE: 059953

SEQUENCE DESCRIPTION: SEQ ID NO: 2:

Query Match 0.7%; Score 29; DB 3; Length 1211;
Best Local Similarity 100.0%; Pred. No. 0.0012;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCACGCGTCCGCCACGCGTCCGGCGGC 29
DB 1 CCCACGCGTCCGCCACGCGTCCGGCGGC 29

RESULT 11

US-09-205-258-239

Sequence 239, Application US/09205258
Patent No. 6525174
GENERAL INFORMATION:
APPLICANT: Young et al.
TITLE OF INVENTION: 207 Human Secreted Proteins
FILE REFERENCE: P2007P1
CURRENT APPLICATION NUMBER: US/09/205,258
CURRENT FILING DATE: 1998-12-04
EARLIER APPLICATION NUMBER: PCT/US98/11422
EARLIER FILING DATE: 1998-06-04
EARLIER APPLICATION NUMBER: 60/048,885
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/049,375
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,881
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,880
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,896
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/049,020
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,876
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,895
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,884
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,894
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,971
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,964
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,882
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,899
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,893
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,900
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,901
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,892
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,915
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/049,019
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,970
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,972
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,916
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/049,373
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,875
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/049,374
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,917
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,949
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,974
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,883
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,897
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,898

; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,962
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,963
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,877
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,878
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/070,923
; EARLIER FILING DATE: 1997-12-18
; EARLIER APPLICATION NUMBER: 60/092,921
; EARLIER FILING DATE: 1998-07-15
; EARLIER APPLICATION NUMBER: 60/094,657
; EARLIER FILING DATE: 1998-07-30
; NUMBER OF SEQ ID NOS: 1227
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 239
; LENGTH: 1250
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-205-258-239

Query Match 0.7%; Score 28; DB 4; Length 1250;
Best Local Similarity 100.0%; Pred.No. 0.0036;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CCCACGCTCCGCCACCGTCGCGCGG 28
Db 2 CCCACGCTCCGCCACCGTCGCGCGG 29

RESULT 12

US-09-205-258-166
; Sequence 166, Application US/09205258
; Patent No. 6525174
; GENERAL INFORMATION:
; APPLICANT: Young et al.
; TITLE OF INVENTION: 207 Human Secreted Proteins
; FILE REFERENCE: PZ007P1
; CURRENT APPLICATION NUMBER: US/09/205,258
; CURRENT FILING DATE: 1998-12-04
; EARLIER APPLICATION NUMBER: PCT/US98/11422
; EARLIER FILING DATE: 1998-06-04
; EARLIER APPLICATION NUMBER: 60/048,885
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,375
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,881
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,880
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,896
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,020
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,876
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,895
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,884
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,894
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,971
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,964
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,882
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,899
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,893

; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,900
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,901
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,892
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,915
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,019
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,970
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,972
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,916
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,373
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,875
; EARLIER FILING DATE: 1997-06-06
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; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,917
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,949
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,974
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,883
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,897
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,898
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,962
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,963
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,877
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,878
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/070,923
; EARLIER FILING DATE: 1997-12-18
; EARLIER APPLICATION NUMBER: 60/092,921
; EARLIER FILING DATE: 1998-07-15
; EARLIER APPLICATION NUMBER: 60/094,657
; EARLIER FILING DATE: 1998-07-30
; NUMBER OF SEQ ID NOS: 1227
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 166
; LENGTH: 1251
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-205-258-166

Query Match 0.7%; Score 28; DB 4; Length 1251;
Best Local Similarity 100.0%; Pred.No. 0.0036;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CCCACGCTCCGCCACCGTCGCGCGG 28
Db 2 CCCACGCTCCGCCACCGTCGCGCGG 29

RESULT 13

US-09-150-460B-9
; Sequence 9, Application US/09150460B
; Patent No. 6190882
; GENERAL INFORMATION:
; APPLICANT: Lee, Cheng-Chi
; APPLICANT: Albrecht, Urs

APPLICANT: Eichele, Gregor
APPLICANT: Sun, Zhong Sheng
TITLE OF INVENTION: Mammalian Circadian Rhythm-Like Gene
FILE REFERENCE: D6039
CURRENT APPLICATION NUMBER: US/09/150,460B
CURRENT FILING DATE: 1998-09-09
PRIOR APPLICATION NUMBER: US 60/058,256
PRIOR FILING DATE: 1997-09-09
NUMBER OF SEQ ID NOS: 21
SEQ ID NO 9
LENGTH: 4700
TYPE: DNA
ORGANISM: artificial sequence
FEATURE:
OTHER INFORMATION: Nucleotide sequence of m-rigui, a murine brain cDNA
OTHER INFORMATION: homologous to a human RIGUI 4.7 cDNA probe
US-09-150-460B-9

Query Match 0.7%; Score 28; DB 3; Length 4700;
Best Local Similarity 100.0%; Pred. No. 0.0038;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCACGCGTCCGCCACGCGTCCGGCGG 28
DB 9 CCCACGCGTCCGCCACGCGTCCGGCGG 36

RESULT 14
US-09-620-312D-68
Sequence 68, Application US/09620312D
Patent No. 6569662
GENERAL INFORMATION:
APPLICANT: Tang, Y. Tom
APPLICANT: Liu, Chenghua
APPLICANT: Asundi, Vinod
APPLICANT: Zhang, Jie
APPLICANT: Ren, Feiyan
APPLICANT: Chen, Rui-hong
APPLICANT: Zhao, Qing A.
APPLICANT: Wehrman, Tom
APPLICANT: Xue, Aidong J.
APPLICANT: Yang, Yonghong
APPLICANT: Wang, Jian-Rui
APPLICANT: Zhou, Ping
APPLICANT: Ma, Yunqing
APPLICANT: Wang, Dunrui
APPLICANT: Wang, Zhiwei
APPLICANT: John Tillinghast
APPLICANT: Drmanac, Radoje T.
TITLE OF INVENTION: Polypeptides
FILE REFERENCE: 784CIP2B
CURRENT APPLICATION NUMBER: US/09/620,312D
CURRENT FILING DATE: 2000-07-19
PRIOR APPLICATION NUMBER: 09/552,317
PRIOR FILING DATE: 2000-04-25
PRIOR APPLICATION NUMBER: 09/488,725
PRIOR FILING DATE: 2000-01-21
NUMBER OF SEQ ID NOS: 1105
SOFTWARE: pt_FL_genes Version 1.0
SEQ ID NO 68
LENGTH: 1956
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (76)..(1665)
FEATURE:
NAME/KEY: misc feature
LOCATION: (1)...(1956)
OTHER INFORMATION: n = a,t,c or g
US-09-620-312D-68

Query Match 0.7%; Score 27; DB 4; Length 1956;
Best Local Similarity 100.0%; Pred. No. 0.012;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCACGCGTCCGCCACGCGTCCGGCGG 27
DB 17 CCCACGCGTCCGCCACGCGTCCGGCGG 43

RESULT 15
US-09-311-689B-25
Sequence 25, Application US/09311689B
Patent No. 6800726
GENERAL INFORMATION:
APPLICANT: Rao, Gururaj A.
APPLICANT: Roesler, Keith
TITLE OF INVENTION: Proteins With Enhanced Levels of
TITLE OF INVENTION: Essential Amino Acids
FILE REFERENCE: 0571R2
CURRENT APPLICATION NUMBER: US/09/311,689B
CURRENT FILING DATE: 1999-05-13
PRIOR APPLICATION NUMBER: 08/740,682
PRIOR FILING DATE: 1996-11-01
PRIOR APPLICATION NUMBER: PCT/US97/20441
PRIOR FILING DATE: 1997-10-31
NUMBER OF SEQ ID NOS: 74
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 25
LENGTH: 428
TYPE: DNA
ORGANISM: Zea mays
FEATURE:
NAME/KEY: CDS
LOCATION: (1)...(303)
US-09-311-689B-25

Query Match 0.6%; Score 26; DB 4; Length 428;
Best Local Similarity 100.0%; Pred. No. 0.034;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCACGCGTCCGCCACGCGTCCGGCGG 26
DB 4 CCCACGCGTCCGCCACGCGTCCGGCGG 29

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Job time : 663 secs

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OM nucleic - nucleic search, using sw model

Run on: May 23, 2005, 13:41:07 ; Search time 2115 Seconds
(without alignments)
11638.363 Million cell updates/sec

Title: US-09-373-658C-125
Perfect score: 4014
Sequence: 1 ccacagctccgccacgcg.....cttttggaccactccag 4014

Scoring table: OLIGO NUC
Gapop_60.0 , Gapext 60.0

Searched: 5695437 seqs, 3066160638 residues

Word size : 0
Total number of hits satisfying chosen parameters: 11390874

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Published Applications NA:
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2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:
3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:
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9: /cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq:
10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq:
11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:
12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:
13: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:
14: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:
15: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq:
16: /cgn2_6/ptodata/2/pubpna/US10D_PUBCOMB.seq:
17: /cgn2_6/ptodata/2/pubpna/US10E_PUBCOMB.seq:
18: /cgn2_6/ptodata/2/pubpna/US10F_PUBCOMB.seq:
19: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	4014	100.0	4014	11	US-09-989-687-125
2	3147	78.4	4014	16	Sequence 125, App
3	3147	78.4	4014	18	Sequence 1, Appli
4	2922	72.8	4676	13	US-10-115-286-1
5	2871	71.5	4760	10	US-10-757-450-1
6	2672	66.6	4447	18	US-10-105-929-1
7	2570	64.0	4459	17	US-09-971-429B-17
8	2570	64.0	4459	17	US-10-755-889-133
9	2548	63.5	3430	18	US-10-159-563-192
10	2471	61.6	3889	19	US-10-159-563-308
11	2463	61.4	4352	19	US-10-473-974-98
					US-10-667-281-1
					US-10-741-600-776

12	2463	61.4	4658	19	US-10-741-600-775	Sequence 775, App
13	2443	60.9	4309	16	US-10-210-120-57	Sequence 57, Appl
14	2329	58.0	3261	10	US-09-373-658-1	Sequence 1, Appli
15	2329	58.0	3261	11	US-09-989-687-1	Sequence 1, Appli
16	2213	55.1	4459	19	US-10-741-600-777	Sequence 777, App
17	1506	37.5	4848	17	US-10-425-114-26851	Sequence 26851, A
18	1443	35.9	3147	9	US-09-803-589-1	Sequence 1, Appli
19	1443	35.9	3147	18	US-10-718-332-1	Sequence 1, Appli
20	1303	32.5	2184	9	US-09-445-023A-2	Sequence 2, Appli
21	1303	32.5	2184	14	US-10-097-597-2	Sequence 2, Appli
22	1303	32.5	2184	14	US-10-097-580-2	Sequence 2, Appli
23	1008	25.1	2124	10	US-09-887-527-23	Sequence 23, Appl
24	1005	25.0	2121	9	US-09-818-143-15	Sequence 15, Appl
25	787	19.6	21130	19	US-10-741-600-17789	Sequence 17789, A
26	506	12.6	506	16	US-10-029-386-22939	Sequence 22939, A
27	467	11.6	569	16	US-10-029-386-9236	Sequence 9236, Ap
28	466	11.6	475	10	US-09-373-658-105	Sequence 105, App
29	466	11.6	475	11	US-09-989-687-105	Sequence 105, App
30	396	9.9	527	19	US-10-696-639-2878	Sequence 2678, Ap
31	391	9.7	504	16	US-10-029-386-11612	Sequence 11612, A
32	389	9.7	632	10	US-09-373-658-103	Sequence 103, App
33	389	9.7	632	11	US-09-989-687-103	Sequence 103, App
34	358	8.9	481	15	US-10-106-698-3692	Sequence 3692, Ap
35	346	8.6	485	17	US-10-242-535A-33817	Sequence 33817, A
36	346	8.6	485	17	US-10-085-783A-33817	Sequence 33817, A
37	315	7.8	519	10	US-09-373-658-104	Sequence 104, App
38	315	7.8	519	11	US-09-989-687-104	Sequence 104, App
39	312	7.8	542	10	US-09-373-658-14	Sequence 14, Appl
40	312	7.8	542	11	US-09-989-687-14	Sequence 14, Appl
41	309	7.7	320	10	US-09-373-658-15	Sequence 15, Appl
42	309	7.7	320	10	US-09-373-658-109	Sequence 109, App
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44	309	7.7	320	11	US-09-989-687-109	Sequence 109, App
45	301	7.5	539	16	US-10-029-386-4132	Sequence 4132, Ap

ALIGNMENTS

RESULT 1
US-09-989-687-125
; Sequence 125, Application US/09989687
; Publication No. US20040002449A1
; GENERAL INFORMATION:
; APPLICANT: Ruben, Steven M.
; APPLICANT: Hastings, Gregg A.
; TITLE OF INVENTION: Meth1 and Meth2 Polynucleotides and Polypeptides
; FILE REFERENCE: 1488.107000D
; CURRENT APPLICATION NUMBER: US/09/989,687
; CURRENT FILING DATE: 2001-11-21
; NUMBER OF SEQ ID NOS: 126
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 125
; LENGTH: 4014
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (456)..(3366)
; OTHER INFORMATION:
US-09-989-687-125

Query Match	100.0%;	Score 4014;	DB 11;	Length 4014;
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; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Prestia, Paul F.
; REGISTRATION NUMBER: 23,031
; REFERENCE/DOCKET NUMBER: GH-70000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-407-0700
; TELEFAX: 610-407-0701
; TELEX: 846169
;
; INFORMATION FOR SEQ ID NO: 1:
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; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
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US-10-115-286-1

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3301 GACAGCTGTGATCCTTTTAAAGAAACCTAAACATTTTATAGACTTTTTCACAATGGCAGAA 3360
3361 TGCAGTTAAGTGGTTTAAAGTGGTGTAGCTTTTTCAGGCAAGCAAGTGAAGAGGGCTG 3420
3361 TGCAGTTAAGTGGTTTAAAGTGGTGTAGCTTTTTCAGGCAAGCAAGTGAAGAGGGCTG 3420
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3421 GTCAGGAAAGCAAGAGCTGGAAGGATCTTCCAGCTGATCTTCCAGTAAACAGTGAAGGT 3480
3481 GTATCAGTAAAGTGGGATTTATGGGCTAGATAGAAAAGGAGTTGAATCATCAGAGTAAAC 3540
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3541 TGCAGTTGCAATTTTATAGATGATGATGATGATGATGATGATGATGATGATGATGAT 3600
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3601 AGCATTAATAAGCCCGGCAATTTATTTATTTATTTATTTATTTATTTATTTATTTATTT 3660
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RESULT 3

US-10-757-450-1
; Sequence 1, Application US/10757450
; Publication No. US2004017594A1
; GENERAL INFORMATION:
; APPLICANT: Jonak, Zdenka
; Trulli, Stephen
; Forwald, James
; Terrett, Jonathan
; Hasting, Gregg
; TITLE OF INVENTION: Novel Integrin Ligand ITGL-TSP
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ratner & Prestia
; STREET: Box 980
; CITY: Valley Forge
; STATE: PA
; COUNTRY: USA
; ZIP: 19482
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/757,450
; FILING DATE: 15-Jan-2004
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/10/115,286
; FILING DATE: 04-Apr-2002
; APPLICATION NUMBER: 08/845,496
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Prestia, Paul F
; REGISTRATION NUMBER: 23,031
; REFERENCE/DOCKET NUMBER: GH-70000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-407-0700
; TELEFAX: 610-407-0701
; TELEX: 846169
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4014 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-757-450-1

Query Match 78.4%; Score 3147; DB 18; Length 4014;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 3997; Conservative 0; Mismatches 17; Indels 0; Gaps 0;
QY 1 CCCAGCGTCCGCCACCGCTCCGGCTCCGAGCCAGGGCTATTGCAAGCCAGGGT 60
DB 1 CCCAGCGTCCGCCACCGCTCCGGCTCCGAGCCAGGGCTATTGCAAGCCAGGGT 60
QY 61 GCGCTACCGGAGGAGGGAGAGCCCTGAGCAGAGTGAGCAACATCGCAGCAAGGGC 120
DB 61 GCGCTACCGGAGGAGGGAGAGCCCTGAGCAGAGTGAGCAACATCGCAGCAAGGGC 120
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DB 301 CTCCGGGAGCTTTGGCTGTAGCGGCTCTGCGCGCCCTTCCAAACGAATATAGAAATGT 360
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DB 421 CCCTCGCTCCGTGCGCTGTCTACGAGCGGTGTCTCTCTGGGGCTTCCAAATGAGCGAGCTGTG 480
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DB 601 GTGTCGAGCGCACTCGGGCGCCCTTCCGAGGAGGACGAGGAGCTAGTGTGCGCGAGCTG 660
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DB 721 GATCTGGAGCTGCGCGCCGACAGAGCTTTTGGGCGCGCGCTTCCAGCTTCCAGAACCTG 780
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DB 901 CCGCGCGCTTCTACTCTGCGGGAGGCGTATTTCATCCAGCGCTGCGCGCGCGCTG 960
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DB 961 GAGCGCTTCCGACCCCGCGCTCCGAGGAGAGCGCGCGGACCACTACAGTTCCACCTC 1020
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DB 1021 CTGCGCGGATCCGAGGCGGACGCTAGGCGGACGCTGGGGTCTGAGACGAGGCC 1080
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DB 1081 CCGCGCGCTGCGGAACCGGACCGAAGACGAGGAGGAGCTGAGGGCGAGGACGAA 1140
QY 1141 GGGCTCTAGTGTGCTCCCGACGACCCCGCTTCCAGGCGTAGGACAGCCACAGAACT 1200
DB 1141 GGGCTCTAGTGTGCTCCCGACGACCCCGCTTCCAGGCGTAGGACAGCCACAGAACT 1200
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DB 1201 GGAAGCATTAAGAAAGGATTTGTGTCAGTACCCTATGTGGAACCATGCTTGTG 1260
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Db	3541	TGCCAGTTCGAATTTGATAGATAGTATTAGTGGAGTATTAACTCTGAGCAGTAT	3600		Db	139	CCAACTCTCGCGTTGCTTCAGCCCGGAGGCGCCACAGACGCTTCTTGTCACGAG	198	
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Db	3601	AGCATAATAAAGCCCGGCATTAATTAATTAATTTCTTTGTTACATCTAATCAAGTT	3660		Db	199	CCACTCTGCTGCGCTCGCTCTCAGTGTCTCAAACTTTGCGCTCGAAGAAACTTCCC	258	
QY	3661	TAGAAAAACAAGCAATTTGTCAAAAAAGTTAGAACTTAACTTAACTTAACTTAACTT	3720		QY	265	GGCGCCGCGCAAACTGCGAGCGCTCTCTTGTAGTACCTCCGAGAGCTTTCGGCTGTAGCCG	324	
Db	3661	TAGAAAAACAAGCAATTTGTCAAAAAAGTTAGAACTTAACTTAACTTAACTTAACTT	3720		Db	259	GGCGCCGCGCAAACTGCGAGCGCTCTCTTGTAGTACCTCCGAGAGCTTTCGGCTGTAGCCG	318	
QY	3721	ACTTATCAATTAATCTAGTATCATGGGGTTGGGAAATGAAAGTAGAGAAAGTACAGAT	3780		QY	325	GCTCTGCGCGCCCTTCCAAACGAATTAAGAAATTTGTTAAATTTTAACTTAACTTAACTT	384	
Db	3721	ACTTATCAATTAATCTAGTATCATGGGGTTGGGAAATGAAAGTAGAGAAAGTACAGAT	3780		Db	319	GCTCTGCGCGCCCTTCCAAACGAATTAAGAAATTTGTTAAATTTTAACTTAACTTAACTT	378	
QY	3781	TTTACTAAGACCTGTTTACTTTTACTTCTAATTAATTAATTAATTAATTAATTAATTAAT	3840		QY	385	CAACGAGGTTTGTCTCTCCGACCCGAACTTAAGCTCCCTCGCTCGCTCGCTCGCTCGCA	444	
Db	3781	TTTACTAAGACCTGTTTACTTTTACTTCTAATTAATTAATTAATTAATTAATTAATTAAT	3840		Db	379	CAACGAGGTTTGTCTCTCCGACCCGAACTTAAGCTCCCTCGCTCGCTCGCTCGCTCGCA	438	
QY	3841	AGGATCTTTTGACCAAGCACTGTTTATGGGCTGCTATGGTTTTCAGAGAACTTATACATT	3900		QY	445	GGGTTGTCTCTTGGGGCTCCCAATGACGAGCTGTGCGGAGGGTTCGGAAGGCGCAAG	504	
Db	3841	AGGATCTTTTGACCAAGCACTGTTTATGGGCTGCTATGGTTTTCAGAGAACTTATACATT	3900		Db	439	ACGGTGTCTCTTGGGGCTCCCAATGACGAGCTGTGCGGAGGGTTCGGAAGGCGCAAG	498	
QY	3901	ATTCTTACCGAGGATTTAAATCTCCAGATTTTCCAACTGAGAGGAAAGGCTCAGGC	3960		QY	505	CTGGCAGCGACATCGGGGAAACGCGAGCGGGCTCCGGGGTCTTCGAGCTTTTGGGCCCGTA	564	
Db	3901	ATTCTTACCGAGGATTTAAATCTCCAGATTTTCCAACTGAGAGGAAAGGCTCAGGC	3960		Db	499	CTGGCAGCGACATCGGGGAAACGCGAGCGGGCTCCGGGGTCTTCGAGCTTTTGGGCCCGTA	558	
QY	3961	AACGTGGAATAACGCAATGGGCTTCCCTTCCCTTTTGGGACCCACTCCAG	4014		QY	565	CCACGCTGTGCTGCTCGCGCGGGCTACTTGGCCGCTGTGCGAGCGCACTCGGGCGCCCC	624	
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US-10-105-929-1									
; Sequence 1, Application US/10105929									
; Publication No. US20020137142A1									
; GENERAL INFORMATION:									
; APPLICANT: Holtzman, Douglas A.									
; TITLE OF INVENTION: TANGO-71, TANGO-73, TANGO-74, TANGO-76, AND TANGO-83									
; FILE REFERENCE: 09404/041001									
; CURRENT APPLICATION NUMBER: US/10/105,929									
; CURRENT FILING DATE: 2002-03-25									
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/130,491									
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-08-07									
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/058,108									
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-09-05									
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/054,961									
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-08-06									
; NUMBER OF SEQ ID NOS: 16									
; SOFTWARE: FastSeq for Windows Version 3.0									
; SEQ ID NO 1									
; LENGTH: 4676									
; TYPE: DNA									
; ORGANISM: Homo sapiens									
; FEATURE:									
; NAME/KEY: CDS									
; LOCATION: (460)...(3360)									
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Query Match									
Best Local Similarity 72.8%; Score 2922; DB 13; Length 4676;									
Matches 3772; Conservative 0; Mismatches 17; Indels 0; Gaps 0;									
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Db	19	GGCGTCCGAGCCAGGGGCTATTGCAAGCCAGGGTGCCTACCGGACGGAGGGGAGA	78		Db	1099	GAAGACGAGGACGAAAGGACCTGAGGCGGAGGACGAGGCGCTCAGTGGTTCGCGGAGGAC	1158	
QY	85	GCCTTGAGCAGAGTGAACAATCGCAGCAAGGCGAGGCGGCAAGAGGGCGCCAGGCA	144		QY	1165	CCGCGCTCAAGCGGTAGGACAGCCACAGGAACTGGAAGCATTAAGAAAGCGATTT	1224	
Db	79	GCCTTGAGCAGAGTGAACAATCGCAGCAAGGCGAGGCGGCAAGAGGGCGCCAGGCA	138		Db	1159	CCGCGCTCAAGCGGTAGGACAGCCACAGGAACTGGAAGCATTAAGAAAGCGATTT	1218	
QY	145	CCAACTCTCGCGTTGCTTCAGCCCGGAGGCGCCACGAGCGCTTCTTGTCACGAGAG	204		QY	1225	GTGTCTCAGTCCGCTATGTGGAAACCATGCTTGTGGCAGACCACTCGATCGATGCGAGATTC	1284	

1219	GTGTCAGTCACCGCTAATGTGGAAA	CCATGCTGTGTGGCAGACCAAGTCGATGGCAGAAATTC	1276
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1279	CACGGCAGTGGTCTAAAGCAATTAACCTTCTCACGTTGTGTTTCGGTGGCAGCCAGATTTGTAC	1338	
1345	AAACACCCCAAGCAATTCGTAAATTCAGTTAGCTGGTGGTGGTGAAGATCTTTGGTCATCCAC	1404	
1339	AAACACCCCAAGCAATTCGTAAATTCAGTTAGCTGGTGGTGGTGAAGATCTTTGGTCATCCAC	1398	
1405	GATGAAACAGAAAGGGCCCGAAGTGACCTCCAAATGCTGSCCCTCACTCTGCGGAACCTTTTGC	1464	
1399	GATGAAACAGAAAGGGCCCGAAGTGACCTCCAAATGCTGSCCCTCACTCTGCGGAACCTTTTGC	1458	
1465	AACTGGCAGAAGCAGACACAAACCCACCCAGTGACCCGGGATGACAGAGCACTATGACACAGCA	1524	
1459	AACTGGCAGAAGCAGACACAAACCCACCCAGTGACCCGGGATGACAGAGCACTATGACACAGCA	1518	
1525	ATTCTTTTCAACAGACATTTGTGTGGTCCAGACATGTGATACTCTTTGGGATGGCT	1584	
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1579	GATGTTGGAACTGTGTGTGATCCGAGCAGAAAGCTGCTCCGTCACTAGAAGATGATGTTTA	1638	
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2005	ACCTCTGTGGGTGCTGTGTGTCGTAACAAACAAACACTTCCCGTGGGCGGATGGCACCAGC	2064	
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2119	TTTGATACGCTTTTTCATGGAAGCTGGGGAATGTGGGGGCTTTGGGGAGACTGTTTCGAGA	2178	
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2305	CCAGCAATAATGAAAAACCTTTAGAGAGGAAACATGTGAGGACACAAACGAGTTTTC	2364	
2299	CCAGCAATAATGAAAAACCTTTAGAGAGGAAACATGTGAGGACACAAACGAGTTTTC	2358	

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Db	2359	AAAGCTTCCTTTGGGAGTGGGCGCTCGGGTGGAAATGAATTCGCCAAGTACGCTGGCGTCTCA	2418
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Db	2419	CCAAAGCAGAGTGCAGAGCTCATCTGCCAAGCCAAAGGCAATGGCTACTCTCTTCGTTTTTG	2478
Qy	2485	CAGCCCAAGGTTGTAGATGSGTACTCCATGTAGCCCAAGATTCACCTCTGTCGTGTGCAAA	2544
Db	2479	CAGCCCAAGGTTGTAGATGSGTACTCCATGTAGCCCAAGATTCACCTCTGTCGTGTGCAAA	2538
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Db	2599	TGTGTTGTTTTGGCGGGGAAATGATCTACTTGTAAAAAAAATATCAGGATCAGTTACTTAGT	2658
Qy	2665	GCAAAACCTCGEATATCATATGATATCATCAAAATCCAACTGGAGCCACCAATCGAAGTG	2724
Db	2659	GCAAAACCTCGEATATCATATGATATCATCAAAATCCAACTGGAGCCACCAATCGAAGTG	2718
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Db	2719	AAACAGCGGAACAGAGGGGATCCAGAAACAATGGCAGCTTTCTTGCCATCAAGAGCTGCT	2778
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Db	2779	GATGGCACATATATCTTAATGTGTGACTACACTTTGTCACCTTAGAGCAAGACATTATG	2838
Qy	2845	TACAAAGGCTGTGTCTTTGAGGTACAGCGGCTCTCTGCGGCATTTGGAAGAAATTCGACGC	2904
Db	2839	TACAAAGGCTGTGTCTTTGAGGTACAGCGGCTCTCTGCGGCATTTGGAAGAAATTCGACGC	2898
Qy	2905	TTTTAGCCCTCTCAAAGAGCCCTTGACCATCCAGGTTCTTACTGTGGCAATGCCCTTCGA	2964
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Db	3019	ACTTTTTTCAGATGGGTCATTGAAAGAGTGGGCGAATGTTCTAAGTCATGTGAATTGGGT	3078
Qy	3085	TGGCAGAGAAGACTGGTAGAATCCGACGACATTAATGGACAGCCTGCTCCGAGTGTGCA	3144
Db	3079	TGGCAGAGAAGACTGGTAGAATCCGACGACATTAATGGACAGCCTGCTCCGAGTGTGCA	3138
Qy	3145	AAGAAAGTGAAGCCAGCCAGCAACGACCTTGTGTGACAGACCATCCCTGCCCCAGTGGCAG	3204
Db	3139	AAGAAAGTGAAGCCAGCCAGCAACGACCTTGTGTGACAGACCATCCCTGCCCCAGTGGCAG	3198
Qy	3205	CTGGGGAGTGGTCATCATCTTCTTAAGACCTGTGGGAAGGTTTACAAAAAACAAGCTTG	3264
Db	3199	CTGGGGAGTGGTCATCATCTTCTTAAGACCTGTGGGAAGGTTTACAAAAAACAAGCTTG	3258
Qy	3265	AAGTGTCTGTCCCATGATGAGGGGTGTATCTCATGACAGCTGTGATCTCTTTAAAGAAA	3324
Db	3259	AAGTGTCTGTCCCATGATGAGGGGTGTATCTCATGAGAGCTGTGATCTTTAAAGAAA	3318
Qy	3325	CCTAAACATTTCTATAGACTTTTGCAAAATGGCAGAAATGCAATTAAAGTGGTTTAAAGTGGT	3384
Db	3319	CCTAAACATTTCTATAGACTTTTGCAAAATGGCAGAAATGCAATTAAAGTGGTTTAAAGTGGT	3378
Qy	3385	TTAGCTTTGAGGGCAAGCCAAAGTGCAGAGGGCTGTGTCAGGGAAGCAAGAGGCTGG	3444
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QY 3505 GGTAGATGAAAGAGTTGATCATCAGAGTAACCTGCCAGTTCGCAATTTGATAGGAT 3564
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QY 3739 GGGGTTGGGAATGAAAGTAGGAGAAAGTGAGATTTTACTAAGACCTGTTTACTTTTA 3798
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QY 3805 CCTCACTAA 3813
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QY 3799 CCTCACTAA 3807
Db |||||

RESULT 5
US-09-971-429B-17
; Sequence 17, Application US/09971429B
; Publication No. US20030175704A1
; GENERAL INFORMATION:
; APPLICANT: Lasek, Amy K. W.
; APPLICANT: Shyjan, Andrew W.
; APPLICANT: Turner, Christopher M.
; TITLE OF INVENTION: GENES EXPRESSED IN LUNG CANCER
; FILE REFERENCE: PA-0040 US
; CURRENT APPLICATION NUMBER: US/09/971,429B
; CURRENT FILING DATE: 2001-10-04
; PRIOR APPLICATION NUMBER: 60/239,024
; PRIOR FILING DATE: 2000-04-10
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: PERL Program
; SEQ ID NO 17
; LENGTH: 4760
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20030175704A1 007074.13
;
;
; NAME/KEY: unsure
; LOCATION: 118
; OTHER INFORMATION: a, t, c, g, or other
US-09-971-429B-17

Query Match 71.5%; Score 2871; DB 10; Length 4760;
Best Local Similarity 99.5%; Pred. No. 0;
Matches 3771; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

QY 25 GCGGCTCCGAGCCAGGGCTATTGCAAGCCAGGTCGCTACCGGAGGAGGGGAGA 84
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QY 85 GCGCTGAGCAGAGTTCAGCAACATCGCAGCCAGGCGGAGCCGAAAGAGGGGCGCCAGGCA 144
Db |||||
QY 180 GCGCTGAGCAGAGTTCAGCAACATCGCAGCCAGGCGGAGCCGAAAGAGGGGCGCCAGGCA 239
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QY 145 CCAATCTCGCGTTGCTTCAGCCCGGAGGCGCCGAGCGCTTCTGTGCCAGCAGAG 204
Db |||||
QY 240 CCAATCTCGCGTTGCTTCAGCCCGGAGGCGCCGAGCGCTTCTGTGCCAGCAGAG 299
Db |||||
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QY 205 CCACCTCTCCCTGCGCTTCCCTCTCAGTGTCTCCAACTTTGCGCTGGAAGAAAACCTTCCC 264
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QY 300 CCACCTCTCCCTGCGCTTCCCTCTCAGTGTCTCCAACTTTGCGCTGGAAGAAAACCTTCCC 359
Db |||||
QY 265 GCGGCGCGGAGAACTGCGAGCGCTTCTCTTAGTGACTCCGGGAGCTTCGGCTGAGCGG 324
Db |||||
QY 360 GCGGCGCGGAGAACTGCGAGCGCTTCTCTTAGTGACTCCGGGAGCTTCGGCTGAGCGG 419
Db |||||
QY 325 GCTCTGCGCGGCTTCCAACTTAATAGAAATTTGTTAAATTTTAACTTCCAGACGAGC 384
Db |||||
QY 420 GCTCTGCGCGGCTTCCAACTTAATAGAAATTTGTTAAATTTTAACTTCCAGACGAGC 479
Db |||||
QY 385 CAACGAGGCTTTGCTCTCCCGAACCCGAACTAAAGCTCCCTCGCTCGCTGCGCTGCTACGA 444
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QY 480 CAACGAGGCTTTGCTCTCCCGAACCCGAACTAAAGCTCCCTCGCTCGCTGCGCTGCTACGA 539
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QY 445 GCGGTGCTCTCTGCGGCTTCCAACTGACGAGCTGTGCGGAGGGTTCCGAAAGGCGCAAG 504
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QY 625 TCCGAGGAGGACGAGGAGCTAGTGTGCGGAGCTGCGAGCGGCTCCCGGACACCGGAGCC 684
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QY 840 AGCTTTTGGCGCGCGCTTCAAGCTCCAGAACGTTGGGGCGCAATCCGGGTCCGAGGAGC 899
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QY 805 CCGCTTCCGAGAAACGAGCTCGGCGCATGTTCTACTCCGCGACCGTGAATGCGGATGCC 864
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QY 960 AGCTCGGCTGCGCGCTTCAAGCTCCAGAACGTTGGGGCGCAATCCGGGTCCGAGCACC 1019
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QY 925 GAGGCGTATTTTCACTCAGCGCTGCGCGCGCGAGCGCTCCGCAACCGCGCGCGCGCA 984
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QY 985 GGGGAGAAAGCCCGGCAACCTACAGTTTCACTCTCTGCGCGGAAATCGGAGGCGGAGC 1044
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QY 1045 GTAGGCGGCACTGCGGCGCTGCGAGCGAGCGCGCGCGCGAGCTGGGAAAGCGGAGC 1104
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QY 1225 GTGTTCAGTCAAGCGTATGAGGAACTGTTGCGGAGCGCGCGAGCTCCAGTCCAGGAAATTC 1284
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QY	1285	CACGGCAGTGGTCTAAAGCATTAACCTTCTCACGTTGTTTTCGGTGGCAGCCAGATTGTAC	1344	Db	2460	AAAGCTTCCTTGGGAGTGGGCTCGGTTGGAAATGGAATCCCAAGTACGCTGGCGTCTCA	2519
Db	1380	CACGGCAGTGGTCTAAAGCATTAACCTTCTCACGTTGTTTTCGGTGGCAGCCAGATTGTAC	1439	QY	2425	CCAAAGGACAGGTGCAAGCTCATCTGCCAAGCCAAAGGCATTGGCTACTTCTTCGTTTTG	2484
QY	1345	AAACACCCAGAGATTGTTAAATCAGTTAGCTGGTGGTGAAGATCTTGGTCAATCAC	1404	Db	2520	CCAAAGGACAGGTGCAAGCTCATCTGCCAAGCCAAAGGCATTGGCTACTTCTTCGTTTTG	2579
Db	1440	AAACACCCAGAGATTGTTAAATCAGTTAGCTGGTGGTGAAGATCTTGGTCAATCAC	1499	QY	2485	CAGCCCAAGTTGTAGATGGTACTCCATGTAGCCCAAGATCCACCTCTGTCTGTGTGCAA	2544
QY	1405	GATGAACAGAGGGCCCGAAGTGACTCCAAATGCTGCCCTCACTCTGGGAACTTTTGG	1464	Db	2580	CAGCCCAAGTTGTAGATGGTACTCCATGTAGCCCAAGATCCACCTCTGTCTGTGTGCAA	2639
Db	1500	GATGAACAGAGGGCCCGAAGTGACTCCAAATGCTGCCCTCACTCTGGGAACTTTTGG	1559	QY	2545	GGACAGTGTGTTAAAGCTGGTGTGATCGCATATAGATCCCAAAAGAGATTGTGATAA	2604
QY	1465	AACTGGCAGAGCAGACACACCCACCCAGTACCGGGATGCAGACATATGACACAGCA	1524	Db	2640	GGACAGTGTGTTAAAGCTGGTGTGATCGCATATAGATCCCAAAAGAGATTGTGATAA	2699
Db	1560	AACTGGCAGAGCAGACACACCCACCCAGTACCGGGATGCAGACATATGACACAGCA	1619	QY	2605	TGTGGTGTGTTGGGGGAAATGATCTACTTGTAAAAAAATATCAGGATCAGTTACTAGT	2664
QY	1525	ATTCTTTTCAACAGACAGGACTTGTGGTGGTCCAGACATATGATCTTGGGATGGCT	1584	Db	2700	TGTGGTGTGTTGGGGGAAATGATCTACTTGTAAAAAAATATCAGGATCAGTTACTAGT	2759
Db	1620	ATTCTTTTCAACAGACAGGACTTGTGGTGGTCCAGACATATGATCTTGGGATGGCT	1679	QY	2665	GCAAAACCTGGATATCATGATATCATCAATTCAACTGGAGCCACCAACATCGAAGTG	2724
QY	1585	GATGTTGGAACCTGTGTGATCCGAGCAGAGCTGCTCCGTATAGAGATGATGTTTA	1644	Db	2760	GCAAAACCTGGATATCATGATATCATCAATTCAACTGGAGCCACCAACATCGAAGTG	2819
Db	1680	GATGTTGGAACCTGTGTGATCCGAGCAGAGCTGCTCCGTATAGAGATGATGTTTA	1739	QY	2725	AAACACGGGACAGAGGGGATCCAGGAACTATGCGAGCTTCTTGCATCAAGCTGCT	2784
QY	1645	CAAGCTGCCCTTCAACACAGCCCATGAATTAAGGCCACGTGTTAACATGCCACATGATGAT	1704	Db	2820	AAACACGGGACAGAGGGGATCCAGGAACTATGCGAGCTTCTTGCATCAAGCTGCT	2879
Db	1740	CAAGCTGCCCTTCAACACAGCCCATGAATTAAGGCCACGTGTTAACATGCCACATGATGAT	1799	QY	2785	GATGGCACATATATCTTAATGGTGACTACACCTTGTCCACCTTAGAGCAAGACATTATG	2844
QY	1705	GCAAGCAGTGGCCAGCCTTAATGTTGTGAACACAGGATTCACACATGATGGGCTCAATG	1764	Db	2880	GATGGCACATATATCTTAATGGTGACTACACCTTGTCCACCTTAGAGCAAGACATTATG	2939
Db	1800	GCAAGCAGTGGCCAGCCTTAATGTTGTGAACACAGGATTCACACATGATGGGCTCAATG	1859	QY	2845	TACAAAGGTGTTGTTCTTGAGGTACAGCGGCTCCTCTGCGGCAATGGAAGAAATTCGCGC	2904
QY	1765	CTTTCCAACTGTGACACACAGCCAGCTTGTCTCTTGCAGTGGCTACATGATTACATCA	1824	Db	2940	TACAAAGGTGTTGTTCTTGAGGTACAGCGGCTCCTCTGCGGCAATGGAAGAAATTCGCGC	2999
Db	1860	CTTTCCAACTGTGACACACAGCCAGCTTGTCTCTTGCAGTGGCTACATGATTACATCA	1919	QY	2905	TTTAGCCCTCTCAAGAGCCCTTGACCATCCAGGTTCTTACTGTGGCAATGCCCTCGA	2964
QY	1825	TTTCTGGATAATGGTATGATGGGGAATGTTGATGGAACAAGCCTCAGAAATCCCATACAGCTC	1884	Db	3000	TTTAGCCCTCTCAAGAGCCCTTGACCATCCAGGTTCTTACTGTGGCAATGCCCTCGA	3059
Db	1920	TTTCTGGATAATGGTATGATGGGGAATGTTGATGGAACAAGCCTCAGAAATCCCATACAGCTC	1979	QY	2965	CCTAAAAATAAATACACCTACTTCTGTAAGAAGAAAGAAATCTTCAATGCTATCCCC	3024
QY	1885	CCAGGCGATCTCCCTGGCAGCTCGTAGATGCCAACCGGCAAGTGCAGTTTACATTTGGG	1944	Db	3060	CCTAAAAATAAATACACCTACTTCTGTAAGAAGAAAGAAATCTTCAATGCTATCCCC	3119
Db	1980	CCAGGCGATCTCCCTGGCAGCTCGTAGATGCCAACCGGCAAGTGCAGTTTACATTTGGG	2039	QY	3025	ACTTTTTCAGCATGGGTCAATTGAAGAGTGGGGCGAATGTTCTAAGTCATGTGAATGGGT	3084
QY	1945	GAGGACTCCAAACACTGCTGATGAGCCAGCAGACATGTAGCACCTTGTGCTGACGGC	2004	Db	3120	ACTTTTTCAGCATGGGTCAATTGAAGAGTGGGGCGAATGTTCTAAGTCATGTGAATGGGT	3179
Db	2040	GAGGACTCCAAACACTGCTGATGAGCCAGCAGACATGTAGCACCTTGTGCTGACGGC	2099	QY	3085	TGGCAGAGAAGACTGGTAGAATGCCGAGACATTAATGGACAGCCTGCTTCGGAGTGTGCA	3144
QY	2005	ACCTCTGGTGGGTGCTGGTGTCTAAACCAACACACTTCCCGTGGGCGGATGGCACCAGC	2064	Db	3180	TGGCAGAGAAGACTGGTAGAATGCCGAGACATTAATGGACAGCCTGCTTCGGAGTGTGCA	3239
Db	2100	ACCTCTGGTGGGTGCTGGTGTCTAAACCAACACACTTCCCGTGGGCGGATGGCACCAGC	2159	QY	3145	AAGGAAGTGAAGCCAGCCAGCACAGACCTTGTGACAGCATCCCTGCCCCAGTGGCAG	3204
QY	2065	TGTGGAGAAGGGAATGGTGTATCAACGGCAAGTGTGTGAACAAAAACCAAGAAAGCAT	2124	Db	3240	AAGGAAGTGAAGCCAGCCAGCACAGACCTTGTGACAGCATCCCTGCCCCAGTGGCAG	3299
Db	2160	TGTGGAGAAGGGAATGGTGTATCAACGGCAAGTGTGTGAACAAAAACCAAGAAAGCAT	2219	QY	3205	CTGGGGAGTGGTGTATCATCTTCTAAGACCTGTGGGAAGGGTTACAAAAAACAAGCTTG	3264
QY	2125	TTTGTATACGCTTTTCAATGAGCTGGGGAATGTTGGGGCTTGGGGAGACTGTTCCAGA	2184	Db	3300	CTGGGGAGTGGTGTATCATCTTCTAAGACCTGTGGGAAGGGTTACAAAAAACAAGCTTG	3359
Db	2220	TTTGTATACGCTTTTCAATGAGCTGGGGAATGTTGGGGCTTGGGGAGACTGTTCCAGA	2279	QY	3265	AAGTGTCTGCCATGATGGAGGGGTGTATCTCATGACAGCTGTGATCTTTTAAAGAA	3324
QY	2185	ACGTGGGTGGAGGTCCAGTACACGATGAGGGAATGTGACAAACCCAGTCCCAAGAAAT	2244	Db	3360	AAGTGTCTGCCATGATGGAGGGGTGTATCTCATGACAGCTGTGATCTTTTAAAGAA	3419
Db	2280	ACGTGGGTGGAGGTCCAGTACACGATGAGGGAATGTGACAAACCCAGTCCCAAGAAAT	2339	QY	3325	CCTTAAACATTTTATAGACTTTTGCACAAATGGCAGAAATGCAAGTAAAGTGGTG	3384
QY	2245	GGAGGGAAGTACTGTGAAGGCAACAGTGGCTTACAGATCTCTGTAAACCTTGAAGACTGT	2304	Db	3420	CCTTAAACATTTTATAGACTTTTGCACAAATGGCAGAAATGCAAGTAAAGTGGTG	3479
Db	2340	GGAGGGAAGTACTGTGAAGGCAACAGTGGCTTACAGATCTCTGTAAACCTTGAAGACTGT	2399	QY	3385	TTAGCTTTGAGGGCAAGCCAAAGTGAAGAGGGCTGGTGCAGGGAAGCAAGAGGCTGG	3444
QY	2305	CCAGACATTAATGGAATAAATCTTTAGAGAGGAACAATGTGAGCACAACAACGAGTTTCA	2364	Db	3480	TTAGCTTTGAGGGCAAGCCAAAGTGAAGAGGGCTGGTGCAGGGAAGCAAGAGGCTGG	3539
Db	2400	CCAGACATTAATGGAATAAATCTTTAGAGAGGAACAATGTGAGCACAACAACGAGTTTCA	2459	QY	3445	AGGATCCAGCGTATCTTCCAGTAACCAAGTGGTGTATCAGTAAGGTGGATTTGGG	3504
QY	2365	AAAGCTTCTTTGGGAGTGGGCTCGCGTGGAAATGGATTCACAGTACGCTGGCGTCTCA	2424				

Db 3540 AGGGATCCAGCGTATCTTCCAGTAACCAAGTGAAGTGTATCAGTAAGGTGGATTAATGGG 3599
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Db 3600 GGTAGATAGAAAGAGTGTGAATCATCAGATAACTGCCAGTTGCCAAATTTGATAGGAT 3659
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Qy 3625 TTATTATTATTTCTTTTGTGTACATCTACTACAGTTTGTAGAAAAAACAAGCAATTTCTCAA 3684
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Qy 3685 AAAAGTTAGAACTATTACAAACCTCTGCTTCTGCTGTTTACTTAAAGCACTTTTACTTTA 3744
Db 3780 AAAAGTTAGAACTATTACAAACCTCTGCTTCTGCTGTTTACTTAAAGCACTTTTACTTTA 3839
Qy 3745 GGGGTTGGGAAATGAAAGTGTAGAGAAAGTGTAGATTTTACTAAGACCTGTGTACTTTA 3804
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Qy 3805 CCTCACTAA 3813
Db 3900 CCTCACTAA 3908

RESULT 6
US-10-755-889-133
; Sequence 133, Application US/10755889
; Publication No. US20040171823A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES ASSOCIATED WITH THE NF-KB
; FILE OF INVENTION: PATHWAY
; FILE REFERENCE: D0284 NP
; CURRENT APPLICATION NUMBER: US/10/755,889
; CURRENT FILING DATE: 2004-01-13
; PRIOR APPLICATION NUMBER: U.S. 60/440,068
; PRIOR FILING DATE: 2003-01-14
; PRIOR APPLICATION NUMBER: U.S. 60/469,757
; PRIOR FILING DATE: 2003-05-12
; NUMBER OF SEQ ID NOS: 823
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 133
; LENGTH: 4447
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-755-889-133

Query Match 66.6%; Score 2672; DB 18; Length 4447;
Best Local Similarity 99.5%; Pred. No. 0;
Matches 3572; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

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Qy 284 GGGCCTCTCTTAGTGACTCCGGAGCTTCGGCTGTAGCCGGCTCTGCGCGCCCTTCCAA 343
Db 61 GGGCCTCTCTTAGTGACTCCGGAGCTTCGGCTGTAGCCGGCTCTGCGCGCCCTTCCAA 120
Qy 344 CGAATAATAGAAATTTGTTAAATTTTAAATTCAGAGAGGCCAAAGAGCTTTGCTCTCC 403
Db 121 CGAATAATAGAAATTTGTTAAATTTTAAATTCAGAGAGGCCAAAGAGCTTTGCTCTCC 180
Qy 404 CGACCCGAACTAAAGTCTCCCTCGCTCGCTGCTGCTAGAGCGGTGTCTCTGGGGCTC 463
Db 181 CGACCCGAACTAAAGTCTCCCTCGCTCGCTGCTGCTAGAGCGGTGTCTCTGGGGCTC 240
Qy 464 CAATGAGCGAGTGTGCGCGGGGTTCGGAAGCGCAAGCTGGGACGACATGGGGA 523
Db 241 CAATGAGCGAGTGTGCGCGGGGTTCGGAAGCGCAAGCTGGGACGACATGGGGA 300

Qy 524 ACGCGAGCGGGCTCCGGGCTCTCGGAGCTTTGGGCGCGTACCCAGCTGCTGCTGCTCG 583
Db 301 ACGCGAGCGGGCTCCGGGCTCTCGGAGCTTTGGGCGCGTACCCAGCTGCTGCTGCTCG 360
Qy 584 CCGCGCGCTACTGCGCGTGTGCGAGCGACTCGGCGCGCCCTCCGAGAGGACGAGGAGC 643
Db 361 CCGCGCGCTACTGCGCGTGTGCGAGCGACTCGGCGCGCCCTCCGAGAGGACGAGGAGC 420
Qy 644 TAGTGGTCCGAGTGTGAGCGCTCCGGGACACGGGACACCGCGCTCCCGCTGACG 703
Db 421 TAGTGGTCCGAGCTGTGAGCGCGCCCGGGACACGGGACACCGCGCTCCCGCTGACG 480
Qy 704 CTTTTGACAGCAGCTGATCTGGAGCTGCCCGCGACAGCAGCTTTTGGGCGCGCGCT 763
Db 481 CTTTTGACAGCAGCTGATCTGGAGCTGCCCGCGACAGCAGCTTTTGGGCGCGCGCT 540
Qy 764 TCACGCTCCAGAACTGGGGCGCAATCCGGGTCCGACACCCCGCTTCCGGAAACCGGAC 823
Db 541 TCACGCTCCAGAACTGGGGCGCAATCCGGGTCCGAGACGCGCTTCCGGAAACCGGAC 600
Qy 824 TGGCGCACTGCTTCTACTCCGGCACCGTGAATGGCGATCCAGCTCGGCTGCGCGCTCA 883
Db 601 TGGCGCACTGCTTCTACTCCGGCACCGTGAATGGCGATCCAGCTCGGCTGCGCGCTCA 660
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Qy 944 CGCTGCCCGCGCCAGCGAGCGCTCGCCACCGCGCGCCCGAGGAGAACCGCGGAC 1003
Db 721 CGCTGCCCGCGCCAGCGAGCGCTCGCCACCGCGCGCCCGAGGAGAACCGCGGAC 780
Qy 1004 CACTACAGTTCCACTCTCTGCGCGGCAATCGGACGGGCGACGTAGCGGCG 1063
Db 781 CACTACAGTTCCACTCTCTGCGCGGCAATCGGACGGGCGACGTAGCGGCG 840
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Db 841 TCGTGGACGACGAGCCCGCGCGCTGGGNAAGCGGAGCCGAGACGAGGACGAGGGA 900
Qy 1124 CTGAGGGGAGGACGAAAGGGCTCTAGTGTGCTCCCGCAGGACCCCGCACTGCAAGGCGTAG 1183
Db 901 CTGAGGGGAGGACGAAAGGGCTCTAGTGTGCTCCCGCAGGACCCCGCACTGCAAGGCGTAG 960
Qy 1184 GACAGCCACAGGAACTGGAAGCATAAGAAAGCGGATTTGTGTCAGTCAACCGTATG 1243
Db 961 GACAGCCACAGGAACTGGAAGCATAAGAAAGCGGATTTGTGTCAGTCAACCGTATG 1020
Qy 1244 TGGAAACCATGCTTGTGGCAGACAGTCGATGGCAGAAATTCACGGCAGTGGTCTAAAGC 1303
Db 1021 TGGAAACCATGCTTGTGGCAGACAGTCGATGGCAGAAATTCACGGCAGTGGTCTAAAGC 1080
Qy 1304 ATTACTCTTCTACGTTGTTTTCGGTGGCAGCCAGATTTGACAAACACCCGCACTTCGTA 1363
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1604	QY	ATCCGACGAGAGCTGCTCCGTCAATAGAGATGATGGTTTTAAAGCTGCGCTTTCACACAG	1661
1381	DB	ATCCGACGAGAGCTGCTCCGTCAATAGAGATGATGGTTTTAAAGCTGCGCTTTCACACAG	
1664	QY	CCCATGAAATTAGGCCACGCTGTTTTAAACATGCCATCATGATGCAAAAGCAGTGTGCCAGCC	1723
1441	DB	CCCATGAAATTAGGCCACGCTGTTTTAAACATGCCATCATGATGCAAAAGCAGTGTGCCAGCC	1500
1724	QY	TTAATGGTGTGAACACGAGGATTCGCCATGATGGCGTCAATGTCTTCCAACTGSGACCA	1783
1501	DB	TTAATGGTGTGAACACGAGGATTCGCCATGATGGCGTCAATGTCTTCCAACTGSGACCA	1560
1784	QY	GCAGCGCTTGGTCTCTTTGAGTGGCTACATGATTTACATCTTCTGGATTAATGTGTCA	1843
1561	DB	GCAGCGCTTGGTCTCTTTGAGTGGCTACATGATTTACATCTTCTGGATTAATGTGTCA	1620
1844	QY	GGGAATGTTTGTATGGAACAGCCCTCAGAACTCCCATACAGCTCCCAAGCGATCTCCCTGGCA	1903
1621	DB	GGGAATGTTTGTATGGAACAGCCCTCAGAACTCCCATACAGCTCCCAAGCGATCTCCCTGGCA	1680
1904	QY	CCTCGTACGATGCCAACCGGCAGTGCAGCTTTACATTTGGGGAGGACTCCAAACACTGCC	1963
1681	DB	CCTCGTACGATGCCAACCGGCAGTGCAGCTTTACATTTGGGGAGGACTCCAAACACTGCC	1740
1964	QY	CTGATCAGCCAGACATGTAGACCTTGTGTGTACCGGCACTCTGTGTGGGTGCTGTG	2023
1741	DB	CTGATCAGCCAGACATGTAGACCTTGTGTGTACCGGCACTCTGTGTGGGTGCTGTG	1800
2024	QY	TGTGTCAAAACCAACACTTCCGTGGCGGATGGCACCGACTCTGTGAGAGGAGGAATGTT	2083
1801	DB	TGTGTCAAAACCAACACTTCCGTGGCGGATGGCACCGACTCTGTGAGAGGAGGAATGTT	1860
2084	QY	GTATCAACGGCAAGTGTGTGAAACAAAAACACAGAAAGCAATTTTGATACGCCCTTTTCATG	2143
1861	DB	GTATCAACGGCAAGTGTGTGAAACAAAAACACAGAAAGCAATTTTGATACGCCCTTTTCATG	1920
2144	QY	GAAGCTGGGGAATGTGGGGCCCTTGGGGAGACTGTTTCGAGAACTGCGGTGTGAGGAGTCC	2203
1921	DB	GAAGCTGGGGAATGTGGGGCCCTTGGGGAGACTGTTTCGAGAACTGCGGTGTGAGGAGTCC	1980
2204	QY	AGTACACGATGGGGAATGTGACAAACCGACTCCCAAGAAATGGAAGGAAGTACTGTGGAAG	2263
1981	DB	AGTACACGATGGGGAATGTGACAAACCGACTCCCAAGAAATGGAAGGAAGTACTGTGGAAG	2040
2264	QY	GCMAACGAGTGGCTACAGATCTCTGTAACTGTAGGACTGTTCAGACAATAATGGAAGAAA	2323
2041	DB	GCMAACGAGTGGCTACAGATCTCTGTAACTGTAGGACTGTTCAGACAATAATGGAAGAAA	2100
2324	QY	CCTTTAGAGAGGAACAATGTGAAGCAACAACGAGTTTTCAAAAGCTCTCTTTGGGAGTG	2383
2101	DB	CCTTTAGAGAGGAACAATGTGAAGCAACAACGAGTTTTCAAAAGCTCTCTTTGGGAGTG	2160
2384	QY	GGCCTGGGTGGAATGTGATTTCCGAAGTACGCTGCGCTCTCACCAAGGACAGGTGCAAGC	2443
2161	DB	GGCCTGGGTGGAATGTGATTTCCGAAGTACGCTGCGCTCTCACCAAGGACAGGTGCAAGC	2220
2444	QY	TCATCTGCAAGCCAAAGGCATTGGCTACTTCTTCTGTTTTGCAGCCCAAGTGTGTAGATG	2503
2221	DB	TCATCTGCAAGCCAAAGGCATTGGCTACTTCTTCTGTTTTGCAGCCCAAGTGTGTAGATG	2280
2504	QY	GTACTCCATGTAGCCCGATTTCCACCTCTGTCTGTGTGCAAGGACAGTGTGAAAAGCTG	2563
2281	DB	GTACTCCATGTAGCCCGATTTCCACCTCTGTCTGTGTGCAAGGACAGTGTGAAAAGCTG	2340
2564	QY	GTTGTGATCGCATCATAGACTCCAAAAGAGTTTGTATTAATGTGGTGTGTTGCGGGGAA	2623
2341	DB	GTTGTGATCGCATCATAGACTCCAAAAGAGTTTGTATTAATGTGGTGTGTTGCGGGGAA	2400
2624	QY	ATGGATCTTACTTGTAAAAAATAATACAGATCAGTTTACTGTAGTGCAAAAACCTTGGATATCATG	2683
2401	DB	ATGGATCTTACTTGTAAAAAATAATACAGATCAGTTTACTGTAGTGCAAAAACCTTGGATATCATG	2460
2684	QY	ATATCATCACAAAATTCCAACTGGAGCCCAACATCGAAGTGTAAACAGCGGAACCCAGAGGG	2743

Db	2461	ATATCATCAAAATTCACATCTGGAGCCACCACATCGAAGTGAACAGCGGACCAGAGGG	2520
Qy	2744	GATCCAGGAAACAATGGCAGCTTTCTTGGCCATCAAAAGCTGCTGAATGGCACATATATCTTTA	2803
Db	2521	GATCCAGGAAACAATGGCAGCTTTCTTGGCCATCAAAAGCTGCTGAATGGCACATATATCTTTA	2580
Qy	2804	ATGGTGACTACACTTTGTCCACTTATAGACGACGACATTAATGACAAAGTGTTGTCCTGA	2863
Db	2581	ATGGTGACTACACTTTGTCCACTTATAGACGACGACATTAATGACAAAGTGTTGTCCTGA	2640
Qy	2864	GGTACAGCGGCTCCTCTGGGGCATTCGAAAGAAATTCGCAGCTTTAGCCCTCTCAAAAGAC	2923
Db	2641	GGTACAGCGGCTCCTCTGGGGCATTCGAAAGAAATTCGCAGCTTTAGCCCTCTCAAAAGAC	2700
Qy	2924	CCTTGACCATCCAGGTTCTTACTGTGGGCAATGCCCTTCGACCTTAAATATAACCT	2983
Db	2701	CCTTGACCATCCAGGTTCTTACTGTGGGCAATGCCCTTCGACCTTAAATATAACCT	2760
Qy	2984	ACTTCTAAAGAAGAAGAGGAATCTTCAATGCTATCCCCACTTTTTCAGCATGGGTCA	3043
Db	2761	ACTTCTAAAGAAGAAGAGGAATCTTCAATGCTATCCCCACTTTTTCAGCATGGGTCA	2820
Qy	3044	TTCAAGAGTGGGCGGAATGTTCTTAAGTCAATGCTAAATGGGTTGCGCAGAGAAGACTGGTAG	3103
Db	2821	TTCAAGAGTGGGCGGAATGTTCTTAAGTCAATGCTAAATGGGTTGCGCAGAGAAGACTGGTAG	2880
Qy	3104	AATGCCGAGACATTAATGGACAGCCTGCTTCCGAGTGTGCMAAGGAAGTGAAGCCAGCCA	3163
Db	2881	AATGCCGAGACATTAATGGACAGCCTGCTTCCGAGTGTGCMAAGGAAGTGAAGCCAGCCA	2940
Qy	3164	GCACGACACTTGTGCAGACCATCCCTGCCCCAGCTGGCGAGCTGGGGGAGTGGTCACTAT	3223
Db	2941	GCACGACACTTGTGCAGACCATCCCTGCCCCAGCTGGCGAGCTGGGGGAGTGGTCACTAT	3000
Qy	3224	GTTCGAAGCCTGTGGGAAGGGTTACAAAAAACAAGCTTGAAGTGCTCTGCCATCATG	3283
Db	3001	GTTCGAAGCCTGTGGGAAGGGTTACAAAAAACAAGCTTGAAGTGCTCTGCCATCATG	3060
Qy	3284	GAGGGTGTTATCTCATGACAGCTGTGATCCTTTAAAGAAACCTTAAACATTTTCATAGACT	3343
Db	3061	GAGGGTGTTATCTCATGACAGCTGTGATCCTTTAAAGAAACCTTAAACATTTTCATAGACT	3120
Qy	3344	TTTGCACAATGGCAGAAATGACGTTAAGTGGTGAAGTGGTGGTGGGAGTGGTCACTAT	3403
Db	3121	TTTGCACAATGGCAGAAATGACGTTAAGTGGTGAAGTGGTGGTGGGAGTGGTCACTAT	3180
Qy	3404	AAAGTGAAGAGGCTGTGTCAGGGAAGCAAGAGCTGAGGGATCCAGCGTATCTTC	3463
Db	3181	AAAGTGAAGAGGCTGTGTCAGGGAAGCAAGAGCTGAGGGATCCAGCGTATCTTC	3240
Qy	3464	CCAGTAACCAAGTGAAGTGTATCAGTAAGTGGGAATTAATGGGGGTAGATGAAGAGGAT	3523
Db	3241	CCAGTAACCAAGTGAAGTGTATCAGTAAGTGGGAATTAATGGGGGTAGATGAAGAGGAT	3300
Qy	3524	GAATCATCAGAGTAAACCTGCAGCTTGCAAAATTTGATAGGATAGTTAGTAGGATTATTA	3583
Db	3301	GAATCATCAGAGTAAACCTGCAGCTTGCAAAATTTGATAGGATAGTTAGTAGGATTATTA	3360
Qy	3584	CCTCTGAGCAGTGCATATAGCATTAATAAGCCCCGGGCATTAATTAATTAATTTCTTTTGT	3643
Db	3361	CCTCTGAGCAGTGCATATAGCATTAATAAGCCCCGGGCATTAATTAATTAATTTCTTTTGT	3420
Qy	3644	TACATCTACTACAAGTTTATAGAAAAAACAAGCAATTCCTCAAAAAAGCTTAGAATTTATC	3703
Db	3421	TACATCTACTACAAGTTTATAGAAAAAACAAGCAATTCCTCAAAAAAGCTTAGAATTTATC	3480
Qy	3704	AACCCCTGCTTCTGGTACTTATCAAAATCTTAGTATCATGGGGGTTGGGAAATGAAG	3763
Db	3481	AACCCCTGCTTCTGGTACTTATCAAAATCTTAGTATCATGGGGGTTGGGAAATGAAG	3540
Qy	3764	TAGGAGAAAGTGAGATTTTACTTAAGACCTGTTTTACTTTTACCTCACTAA	3813

Db 3541 TAGGAGAAAAGTACAGATTTTACTAGACCTGTGTTTACTTTACTCTCACTAA 3590

RESULT 7

US-10-159-563-192
; Sequence 192, Application US/10159563
; Publication No. US20040009154A1
; GENERAL INFORMATION:
; APPLICANT: Khan, Javed
; APPLICANT: Ringner, Markus
; APPLICANT: Peterson, Carsten
; APPLICANT: Meltzer, Paul
; TITLE OF INVENTION: SELECTIONS OF GENES AND METHODS OF USING THE SAME FOR
; TITLE OF INVENTION: DIAGNOSIS AND FOR TARGETING THE THERAPY OF SELECT CANCERS
; FILE REFERENCE: 11613.56US11
; CURRENT APPLICATION NUMBER: US/10/159,563
; CURRENT FILING DATE: 2002-12-09
; PRIOR APPLICATION NUMBER: US 10/133,937
; PRIOR FILING DATE: 2002-04-25
; NUMBER OF SEQ ID NOS: 444
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 192
; LENGTH: 4459
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-159-563-192

Query Match 64.0%; Score 2570; DB 17; Length 4459;
Best Local Similarity 99.5%; Pred. No. 0;
Matches 3470; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

QY	224	CTCTAGTCTCTCCAACTTTGGCTGGAAGAAAACCTCCCGCGCGCGCGAGAACTGCA 283
Db	1	CTCTAGTCTCTCCAACTTTGGCTGGAAGAAAACCTCCCGCGCGCGCGAGAACTGCA 60
QY	284	GGCGCTCTCTTAGTGACTCCGGAGCTTCGGGTGTAGCCGGCTCTGCGCGCCCTTCCAA 343
Db	61	GGCGCTCTCTTAGTGACTCCGGAGCTTCGGGTGTAGCCGGCTCTGCGCGCCCTTCCAA 120
QY	344	CGAATATAGAAATTTGTTAATTTTAAATCCAGACAGCCCAACAGAGCTTTGCTCTCC 403
Db	121	CGAATATAGAAATTTGTTAATTTTAAATCCAGACAGCCCAACAGAGCTTTGCTCTCC 180
QY	404	CGACCCGAATAAGCTCCCTCGCTCCGTCGTCTAGAGCGGTGTCTCTGGGGCTC 463
Db	181	CGACCCGAATAAGCTCCCTCGCTCCGTCGTCTAGAGCGGTGTCTCTGGGGCTC 240
QY	464	CAATGCAGCGAGCTGTGCCCGAGGGTTCCGGAAGCGCAAGCTGGGCGACATGGGGA 523
Db	241	CAATGCAGCGAGCTGTGCCCGAGGGTTCCGGAAGCGCAAGCTGGGCGACATGGGGA 300
QY	524	ACGCGAGCGGGTCCGGGGTCTCGAGCTTTGGGGCCCTACCGAGCTGTGCTGCTCG 583
Db	301	ACGCGAGCGGGTCCGGGGTCTCGAGCTTTGGGGCCCTACCGAGCTGTGCTGCTCG 360
QY	584	CGCGCGCTACTGGCCGTGTGGACGACTCGGGCGCCCTCCGAGGAGGACGAGGAC 643
Db	361	CGCGCGCTACTGGCCGTGTGGACGACTCGGGCGCCCTCCGAGGAGGACGAGGAGC 420
QY	644	TAGTGTGCGGAGCTGGAGCGCGTCCCGGGACACGGGACCAACGCGCCCTCCGCTGCA 703
Db	421	TAGTGTGCGGAGCTGGAGCGCGTCCCGGGACACGGGACCAACGCGCCCTCCGCTGCA 480
QY	704	CTTTGACAGAGCTGGATCTGGAGCTGCGCGCCGACAGAGCTTTTGGCGCCCGGT 763
Db	481	CTTTGACAGAGCTGGATCTGGAGCTGCGCGCCGACAGAGCTTTTGGCGCCCGGT 540
QY	764	TACGCTCCAGAACGTTGGGCGCAATCCGGGTCCGACACCCCGCTTCGGGAAACCGACC 823
Db	541	TACGCTCCAGAACGTTGGGCGCAATCCGGGTCCGAGACCGCGCTTCGGGAAACCGACC 600
QY	824	TGGCGCACTGCTTACTCTCGGCAACCGTGAATGGCGATCCAGCTCGGCTGCGCCCTCA 883

Db	601	TGGCGCACTGCTTACTCTCGGCACCGTGAATGGGATCCACAGCTCGGCTGCGCCCTCA 660
QY	884	GCCTCTGGAGGGCGTGGCGCGCTTACTCTGCTGGGGAGGAGTATTTTATCATCAGC 943
Db	661	GCCTCTGGAGGGCGTGGCGCGCTTACTCTGCTGGGGAGGAGTATTTTATCATCAGC 720
QY	944	CGCTGCCCGCCCGCAGCGAGCGCTTGGCCACCGCGCGCCCGCAGGGGAGAGCCCGCGCAC 1003
Db	721	CGCTGCCCGCCCGCAGCGAGCGCTTGGCCACCGCGCGCCCGCAGGGGAGAGCCCGCGCAC 780
QY	1004	CACTACAGTTCCACTCTCTGCGCGGGAATCGGACAGGGCGACGTAGCGGCACTGTCGGGG 1063
Db	781	CACTACAGTTCCACTCTCTGCGCGGGAATCGGACAGGGCGACGTAGCGGCACTGTCGGGG 840
QY	1064	TCGTGGACAGCAGCGCCCGCGCTGGGAAAGCGAGACCGAAGACGAGGAGGAGGA 1123
Db	841	TCGTGGACAGCAGCGCCCGCGCTGGGAAAGCGAGACCGAAGACGAGGAGGAGGA 900
QY	1124	CTGAGGGCGAGGACGAAAGGGCTCTAGTGTGTCGCCCGCAGGACCCGGCACTGCAAGGCTAG 1183
Db	901	CTGAGGGCGAGGACGAAAGGGCTCTAGTGTGTCGCCCGCAGGACCCGGCACTGCAAGGCTAG 960
QY	1184	GACAGCCACAGGAACTGGAAAGCAAGAAAGCGATTTGTCCAGTCAACCGCTATG 1243
Db	961	GACAGCCACAGGAACTGGAAAGCAAGAAAGCGATTTGTCCAGTCAACCGCTATG 1020
QY	1244	TGGAACCATGCTTGTGGCAGACAGTGTGATGGCAGAAATTCACGCGAGTGTCTAAAGC 1303
Db	1021	TGGAACCATGCTTGTGGCAGACAGTGTGATGGCAGAAATTCACGCGAGTGTCTAAAGC 1080
QY	1304	ATTACTCTTCTACGTTGTTTTCGGTGGCAGCAGATTTGTACAAACACCCCGACATTCGTA 1363
Db	1081	ATTACTCTTCTACGTTGTTTTCGGTGGCAGCAGATTTGTACAAACACCCCGACATTCGTA 1140
QY	1364	ATTAGTTAGCTGTGTGTGTGAAGATCTTGGTCAATCCAGATGAACAGAAAGGGGCCG 1423
Db	1141	ATTAGTTAGCTGTGTGTGTGAAGATCTTGGTCAATCCAGATGAACAGAAAGGGGCCG 1200
QY	1424	AGTCACTCCAACTGCTCCCTCACTCTGCGGAACTTTTGCAACTGGCAGAGAGCAGACA 1483
Db	1201	AGTCACTCCAACTGCTCCCTCACTCTGCGGAACTTTTGCAACTGGCAGAGAGCAGACA 1260
QY	1484	ACCCACCCAGTGCACCGGATGCAGAGCACTATGACACAGCAATTTCTTTTACCAGACAG 1543
Db	1261	ACCCACCCAGTGCACCGGATGCAGAGCACTATGACACAGCAATTTCTTTTACCAGACAG 1320
QY	1544	ACTGTGTGGTCCCGACATGTGATACTTTGGGATGGCTGATGTGGAACCTGTGTGTG 1603
Db	1321	ACTGTGTGGTCCCGACATGTGATACTTTGGGATGGCTGATGTGGAACCTGTGTGTG 1380
QY	1604	ATCCGAGCAGAGCTGCTCCGTCATAGAGATGATGTTTACAAGTGCCTTCAACACAG 1663
Db	1381	ATCCGAGCAGAGCTGCTCCGTCATAGAGATGATGTTTACAAGTGCCTTCAACACAG 1440
QY	1664	CCCATGAATTAGCCCACTGTTTAACTGATGATGATGATGATGATGATGATGATGATGAT 1723
Db	1441	CCCATGAATTAGCCCACTGTTTAACTGATGATGATGATGATGATGATGATGATGATGAT 1500
QY	1724	TTAATGGTGTGAACAGAGATCCCAATGATGGCGTCAATGTCTTCCAACTGGACCA 1783
Db	1501	TTAATGGTGTGAACAGAGATCCCAATGATGGCGTCAATGTCTTCCAACTGGACCA 1560
QY	1784	GCCAGCTTGTCTCTTTCAGTGGCTACATGATTTTACATCATTTCTTGGATATGTCATG 1843
Db	1561	GCCAGCTTGTCTCTTTCAGTGGCTACATGATTTTACATCATTTCTTGGATATGTCATG 1620
QY	1844	GGGAATGTTTGTATGACAGAGCTCAGAAATCCCATACAGCTCCCGAGCGCATCTCCCTGGCA 1903
Db	1621	GGGAATGTTTGTATGACAGAGCTCAGAAATCCCATACAGCTCCCGAGCGCATCTCCCTGGCA 1680
QY	1904	CCTCTGACGATCCCAACCGGCACTGCCATTTTACATTTTGGGGAGGAGCTCCTAACTGCG 1963
Db	1681	CCTCTGACGATCCCAACCGGCACTGCCATTTTACATTTTGGGGAGGAGCTCCTAACTGCG 1740

1964 CTGATCAGCCAGCACATGTAGCACCTTGTGTGTATCCGACACCTCTGTGTGGGTCTGG 2023
1741 CCGATCAGCCAGCACATGTAGCACCTTGTGTGTATCCGACACCTCTGTGTGGGTCTGG 1800
2024 TGTGTCAAAACCAACATCTCCGTGGGCGGATGGCACCGACTGTGGAAGGGAATGCT 2083
1801 TGTGTCAAAACCAACATCTCCGTGGGCGGATGGCACCGACTGTGGAAGGGAATGCT 1860
2084 GTATCAACGGCAAGTGTGTGAACAAACCAACAGAAAGCAATTTGATACGCCCTTTTCATG 2143
1861 GTATCAACGGCAAGTGTGTGAACAAACCAACAGAAAGCAATTTGATACGCCCTTTTCATG 1920
2144 GAAGCTGGGGAAATGTGGGGCCCTTGGGGAGACTGTTTCGAGAACGTCGCGTGGAGGAGTCC 2203
1921 GAAGCTGGGGAAATGTGGGGCCCTTGGGGAGACTGTTTCGAGAACGTCGCGTGGAGGAGTCC 1980
2204 AGTACAGATGAGGGAATGTGACAAACCCAGTCCCAAGAAATGGAAGGAAGTACTGTGAAG 2263
1981 AGTACAGATGAGGGAATGTGACAAACCCAGTCCCAAGAAATGGAAGGAAGTACTGTGAAG 2040
2264 GCAACGAGTGGCTACAGATCTGTAAACCTTGAGGACTGTCCAGACAAATAATGGAAGAA 2323
2041 GCAACGAGTGGCTACAGATCTGTAAACCTTGAGGACTGTCCAGACAAATAATGGAAGAA 2100
2324 CCTTTAGAGAGGAACAAATGTGAAGCACACAAACGAGTTCCTTTGGGAGTG 2383
2101 CCTTTAGAGAGGAACAAATGTGAAGCACACAAACGAGTTCCTTTGGGAGTG 2160
2384 GGCTCGGTGGAAATGGAATCCCAAGTACCGTGGCTGTCCAAAGGACAGGTGCAAGC 2443
2161 GGCTCGGTGGAAATGGAATCCCAAGTACCGTGGCTGTCCAAAGGACAGGTGCAAGC 2220
2444 TCATCTGCCAAGCCAAAGGCAATGGCTACTCTTCTGTTTGGAGCCCAAGTTGTAGATG 2503
2221 TCATCTGCCAAGCCAAAGGCAATGGCTACTCTTCTGTTTGGAGCCCAAGTTGTAGATG 2280
2504 GTACTCCATGTAGCCAGATTCACACCTCTGTGTGTGCAAGGACAGTGTGTAAGAGCTG 2563
2281 GTACTCCATGTAGCCAGATTCACACCTCTGTGTGTGCAAGGACAGTGTGTAAGAGCTG 2340
2564 GTTGTGATCGCATCATAGACTCAAAAGAAAGTTTGTGTAATGTGTGTTGGGGGGAA 2623
2341 GTTGTGATCGCATCATAGACTCAAAAGAAAGTTTGTGTAATGTGTGTTGGGGGGAA 2400
2624 ATGGATCTACTTGTAAAAAATAATCAGGATCAGTTACTAGTGCAAAACCTGGATATCATG 2683
2401 ATGGATCTACTTGTAAAAAATAATCAGGATCAGTTACTAGTGCAAAACCTGGATATCATG 2460
2684 ATATCATCAAAATTCAACTGGAGCCACCAACATCGAAGTGAACAGCGGAAACAGAGGG 2743
2461 ATATCATCAAAATTCAACTGGAGCCACCAACATCGAAGTGAACAGCGGAAACAGAGGG 2520
2744 GATCCAGGAACAAATGGCAGCTTTCTGGCCATCAAAAGCTGTGATGGCAATATATCTTA 2803
2521 GATCCAGGAACAAATGGCAGCTTTCTGGCCATCAAAAGCTGTGATGGCAATATATCTTA 2580
2804 ATGGTGAATACATCTTGTCCACCTTAGAGCAAGCAATATGTAACAAAGGTGTCTTGA 2863
2581 ATGGTGAATACATCTTGTCCACCTTAGAGCAAGCAATATGTAACAAAGGTGTCTTGA 2640
2864 GGTACAGCGCTCTCTCGCGGCAATGGAAAGAAATTCGACCTTTAGCCCTCTCAAAAGAGC 2923
2641 GGTACAGCGCTCTCTCGCGGCAATGGAAAGAAATTCGACCTTTAGCCCTCTCAAGAGC 2700
2924 CCTTGACCAATCCAGGTTCTTACTGTGGGCAATGCCCTTCGACCTAAATTAATACACCT 2983
2701 CCTTGACCAATCCAGGTTCTTACTGTGGGCAATGCCCTTCGACCTAAATTAATACACCT 2760
2984 ACTTGTAAAGAGAGGAAGGAATCTTTCAATGCTATCCCACTTTTTCAGCATGGGTCA 3043
2761 ACTTGTAAAGAGAGGAAGGAATCTTTCAATGCTATCCCACTTTTTCAGCATGGGTCA 2820

3044 TTGAAGAGTGGGGCGAAATGTTCTAAGTCATGTGAATTTGGTTGGCAGAGAAAGCTGGTAG 3103
2821 TTGAAGAGTGGGGCGAAATGTTCTAAGTCATGTGAATTTGGTTGGCAGAGAAAGCTGGTAG 2880
3104 AATGCCGAGACATTAATGACAGACCTGTTCCGAGTGTCAAAGGAAGTGAAGCCAGGCCA 3163
2881 AATGCCGAGACATTAATGACAGACCTGTTCCGAGTGTCAAAGGAAGTGAAGCCAGGCCA 2940
3164 GCACAGACCTTGTGTGCAGACCAATCCCTGCCAGTGGCAGCTGGGGAGTGGTCAATCAT 3223
2941 GCACAGACCTTGTGTGCAGACCAATCCCTGCCAGTGGCAGCTGGGGAGTGGTCAATCAT 3000
3224 GTTCTAAGACCTGTGGGAAGGGTTACAAAAAACAAGCTTGAAGTCTGTCTGCCATGATG 3283
3001 GTTCTAAGACCTGTGGGAAGGGTTACAAAAAACAAGCTTGAAGTCTGTCTGCCATGATG 3060
3284 GAGGGGTGTATCTCATGACAGCTGTGATCCTTTAAAGAAACCTAAACAATTTTCATAGACT 3343
3061 GAGGGGTGTATCTCATGAGCTGTGATCCTTTAAAGAAACCTAAACAATTTTCATAGACT 3120
3344 TTTGCAAAATGGCAGAAATCGAGTTAAAGTGGTGTAAAGTGGTGTAGCTTTGAGGGCAAGGC 3403
3121 TTTGCAAAATGGCAGAAATCGAGTTAAAGTGGTGTAAAGTGGTGTAGCTTTGAGGGCAAGGC 3180
3404 AAAGTGAAGAGGGCTGGTGCAGGGAAGCAAGAGCTGGAGGGATCCAGCGTATCTTC 3463
3181 AAAGTGAAGAGGGCTGGTGCAGGGAAGCAAGAGCTGGAGGGATCCAGCGTATCTTC 3240
3464 CCAGTAAACAGTGAAGTGTATCAGTAAAGTGGGATTAAGGGGTAGATAGAAAGGAGTT 3523
3241 CCAGTAAACAGTGAAGTGTATCAGTAAAGTGGGATTAAGGGGTAGATAGAAAGGAGTT 3300
3524 GAATCATCAGAGTAAACTGCCAGTTGCAAAATTTGATAGGATAGTGTAGGAGTATTAA 3583
3301 GAATCATCAGAGTAAACTGCCAGTTGCAAAATTTGATAGGATAGTGTAGGAGTATTAA 3360
3584 CCTCTGAGCAGTATATAGCATATTAAGCCCGCGGCATATTATTATTATTTCTTTTGT 3643
3361 CCTCTGAGCAGTATATAGCATATTAAGCCCGCGGCATATTATTATTATTTCTTTTGT 3420
3644 TACATCTACTACAAAGTTTAGAAAAACAAAGCAATTTGTCAAAAAAGTTAGAACTATTAC 3703
3421 TACATCTATTACAAAGTTTAGAAAAACAAAGCAATTTGTCAAAAAAGTTAGAACTATTAC 3480
3704 AACCCCTG 3711
3481 AACCCCTG 3488

RESULT 8

US-10-159-563-308
; Sequence 308, Application US/10159563
; Publication No. US20040009154A1
; GENERAL INFORMATION:
; APPLICANT: Khan, Javed
; APPLICANT: Ringner, Markus
; APPLICANT: Peterson, Carsten
; APPLICANT: Meltzer, Paul
; TITLE OF INVENTION: SELECTIONS OF GENES AND METHODS OF USING THE SAME FOR
; TITLE OF INVENTION: DIAGNOSIS AND FOR TARGETING THE THERAPY OF SELECT CANCERS
; FILE REFERENCE: 11613.560S11
; CURRENT APPLICATION NUMBER: US/10/159,563
; CURRENT FILING DATE: 2002-12-09
; PRIOR APPLICATION NUMBER: US 10/133,937
; PRIOR FILING DATE: 2002-04-25
; NUMBER OF SEQ ID NOS: 444
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 308
; LENGTH: 4459
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-159-563-308

Query Match 64.0%; Score 2570; DB 17; Length 4459; Best Local Similarity 99.5%; Pred. No. 0; Matches 3470; Conservative 0; Mismatches 18; Indels 0; Gaps 0;									
QY	224	CTCTCAGTGTCTCCAACTTTGGCTGGAGAGAAAACTTCCGCGCGCGCGGAGAACTGCA	283	Db	1021	TGGAACCATGCTTGTGGCAGACCACTGATGGCAGAAATTCACGCGCAGTGTCTTAAAGC	1080		
Db	1	CTCTCAGTGTCTCCAACTTTGGCTGGAGAGAAAACTTCCGCGCGCGCGGAGAACTGCA	60	QY	1304	ATTACCTTCTCAGCTTGTGTTTTCGGTGGCAGCAGATTGTACAAACACCCACGATTCGTA	1363		
QY	284	GGCGCTCTCTTAGTGACTCCGGGAGCTTTCGGCTGTAGCGGCTCTGGCGCGCTTCCAA	343	Db	1081	ATTACCTTCTCAGCTTGTGTTTTCGGTGGCAGCAGATTGTACAAACACCCACGATTCGTA	1140		
Db	61	GGCGCTCTCTTAGTGACTCCGGGAGCTTTCGGCTGTAGCGGCTCTGGCGCGCTTCCAA	120	QY	1364	ATTCACTTAGCTGGTGGTGAAGATCTTGGTCATCCAGATGAAACAGAGGGGCGCG	1423		
QY	344	CGAATAATAGAAATTTTAATTTTAACTATCAGAGCAGGCCAACAGAGGCTTTGCTCTCC	403	Db	1141	ATTCACTTAGCTGGTGGTGAAGATCTTGGTCATCCAGATGAAACAGAGGGGCGCG	1200		
Db	121	CGAATAATAGAAATTTTAATTTTAACTATCAGAGCAGGCCAACAGAGGCTTTGCTCTCC	180	QY	1424	AAGTCACTTCCAACTGCTCCCTCACTCTGGGAACTTTTGCAACTGCGCAGAGCAGACA	1483		
QY	404	CGACCCGAACTAAGCTCCTCGCTCGCTCGGCTGTACGAGCGGTGTCTCTCGGGCTC	463	Db	1201	AAGTCACTTCCAACTGCTCCCTCACTCTGGGAACTTTTGCAACTGCGCAGAGCAGACA	1260		
Db	181	CGACCCGAACTAAGCTCCTCGCTCGCTCGGCTGTACGAGCGGTGTCTCTCGGGCTC	240	QY	1484	ACCCACCACTGACCGGGATGACAGACATATGACACAGCAATCTTTTTCACAGACAGG	1543		
QY	464	CAATGACGAGCTGTGCCCGAGGGGTTCCGGAAGCGCAAGCTGGGCGACGACATGGGGA	523	Db	1261	ACCCACCACTGACCGGGATGACAGACATATGACACAGCAATCTTTTTCACAGACAGG	1320		
Db	241	CAATGACGAGCTGTGCCCGAGGGGTTCCGGAAGCGCAAGCTGGGCGACGACATGGGGA	300	QY	1544	ACTTGTGGGTCCCGACATGTGATACTCTTGGGATGGCTGATGTGGAACTGTGTGTG	1603		
QY	524	ACGCGAGCGGGCTCCGGGGTCTCGAGCTTTTGGGCGCGTACCCACGCTGTGTCTGTG	583	Db	1321	ACTTGTGGGTCCCGACATGTGATACTCTTGGGATGGCTGATGTGGAACTGTGTGTG	1380		
Db	301	ACGCGAGCGGGCTCCGGGGTCTCGAGCTTTTGGGCGCGTACCCACGCTGTGTCTGTG	360	QY	1604	ATCCGAGCAGAGCTGTCTCGTATAGAAATGATGTTTACAAGCTGCTTCAACACAG	1663		
QY	584	CGCGGGGCTACTGCGCGGTGTGCGAGCGACTCGGGGCGCCCTCCGAGGAGACGAGGAGC	643	Db	1381	ATCCGAGCAGAGCTGTCTCGTATAGAAATGATGTTTACAAGCTGCTTCAACACAG	1440		
Db	361	CGCGGGGCTACTGCGCGGTGTGCGAGCGACTCGGGGCGCCCTCCGAGGAGACGAGGAGC	420	QY	1664	CCCATGAATTAGGCCACCGTGTAAATGATGATGATGATGATGATGATGATGATGATG	1723		
QY	644	TAGTGTGTCGGAGCTGGAGCGGCTCCCGGACACGGGACACCGGCGCTCCGCTGTCAGG	703	Db	1441	CCCATGAATTAGGCCACCGTGTAAATGATGATGATGATGATGATGATGATGATGATG	1500		
Db	421	TAGTGTGTCGGAGCTGGAGCGGCTCCGGGACACGGGACACGGGCGCTCCGCTGTCAGG	480	QY	1724	TAAATGTGTGAAACAGGATTTCCACATGATGGCGTCAATGCTTTCCAACTGGACCA	1783		
QY	704	CTTTTGACAGAGCTGATCTGAGAGCTGCCCGCGGACAGAGCTTTTGGCGCGCGGCT	763	Db	1501	TAAATGTGTGAAACAGGATTTCCACATGATGGCGTCAATGCTTTCCAACTGGACCA	1560		
Db	481	CTTTTGACAGAGCTGATCTGAGAGCTGCCCGCGGACAGAGCTTTTGGCGCGCGGCT	540	QY	1784	GCAGGCTTGTGCTCTTGTGAGTGGCTACATGATTACATCATTTTCTGGATAATGGTCA	1843		
QY	764	TCAGGCTTCAGAACTGGGGCGCAATTCGGGTTCGACACCCCGCTTCGGGAAACCGAGC	823	Db	1561	GCAGGCTTGTGCTCTTGTGAGTGGCTACATGATTACATCATTTTCTGGATAATGGTCA	1620		
Db	541	TCAGCTTCAGAACTGGGGCGCAATTCGGGTTCGAGAGCGCGCTTCGGGAAACCGAGC	600	QY	1844	GGGATGTTTGTATGAGCAAGGCTCAGAAATCCCATACAGTCCCAAGGCGATCTCCCTGGCA	1903		
QY	824	TGGCGCACTGCTTCTACTCCGGCACCGTGAATGGCGATCCAGCTCGGCTCGCGCCCTCA	883	Db	1621	GGGATGTTTGTATGAGCAAGGCTCAGAAATCCCATACAGTCCCAAGGCGATCTCCCTGGCA	1680		
Db	601	TGGCGCACTGCTTCTACTCCGGCACCGTGAATGGCGATCCAGCTCGGCTCGCGCCCTCA	660	QY	1904	CCTCTAGCATGCCAAACCGGCGAGTCCCACTGATTTTACAATTTGGGGAGGACTCCAAACACTGCC	1963		
QY	884	GCCTCTGCGAGGCGGTGCGCGGCGCTTCTACTGTGTGGGAGGCGTATTTTATCCAGC	943	Db	1681	CCTCTAGCATGCCAAACCGGCGAGTCCCACTGATTTTACAATTTGGGGAGGACTCCAAACACTGCC	1740		
Db	661	GCCTCTGCGAGGCGGTGCGCGGCGCTTCTACTGTGTGGGAGGCGTATTTTATCCAGC	720	QY	1964	CTGATGACGACGACATGATGACCTTGTGGTGTACCGGCACTCTGTTGGGGTGTGG	2023		
QY	944	CGCTGCGCGCGCAGCGAGCGGCTCGCACCGCGCGCGCGCGCGCGCGCGCGCGCGC	1003	Db	1741	CCGATGACGACGACATGATGACCTTGTGGTGTACCGGCACTCTGTTGGGGTGTGG	1800		
Db	721	CGCTGCGCGCGCAGCGAGCGGCTCGCACCGCGCGCGCGCGCGCGCGCGCGCGCGC	780	QY	2024	TGTGTCAAACCAACACTTCCGCGGCGGATGGCAGCTGTGAGAGAGGAAATGTT	2083		
QY	1004	CACTACAGTTTCACTCTCGCGCGAATTCGGCAGGCGGCTAGCGCGGCTGGGGG	1063	Db	1801	TGTGTCAAACCAACACTTCCGCGGCGGATGGCAGCTGTGAGAGAGGAAATGTT	1860		
Db	781	CACTACAGTTTCACTCTCGCGCGAATTCGGCAGGCGGCTAGCGCGGCTGGGGG	840	QY	2084	GTATCAAACCGGAACTGTGTGAACAAAAACCAAGAAAGCATTTTTCATGATGATGATG	2143		
QY	1064	TCGTGGACGACGAGCGCGCGGCTGCGGAAAGCGGAGACCGAAGACGAGGACGAGGGA	1123	Db	1861	GTATCAAACCGGAACTGTGTGAACAAAAACCGACAGAGAAAGCATTTTTCATGATGATG	1920		
Db	841	TCGTGGACGACGAGCGCGCGGCTGCGGAAAGCGGAGACCGAAGACGAGGACGAGGGA	900	QY	2144	GAAGCTGGGGAATGGGGGCTTGGGGAGACTGTTTCAGAGAACTGTCGGGTGAGAGTCC	2203		
QY	1124	CTGAGGGCGAGGACGAGGGGCTCAGTGTGCGCGGAGGACCGGCGGCTGCGAGGCGGTAG	1183	Db	1921	GAAGCTGGGGAATGGGGGCTTGGGGAGACTGTTTCAGAGAACTGTCGGGTGAGAGTCC	1980		
Db	901	CTGAGGGCGAGGACGAGGGGCTCAGTGTGCGCGGAGGACCGGCGGCTGCGAGGCGGTAG	960	QY	2204	AGTACCATGAGGAAATGTGACAAACCCAGTCCCAAGAAATGAGAGGAAATGACTGTGAG	2263		
QY	1184	GACGCGCCACAGGAACTGGAGCATGAAGAAAGAGCGATTTGTCTCAGTACCGCTATG	1243	Db	1981	AGTACCATGAGGAAATGTGACAAACCCAGTCCCAAGAAATGAGAGGAAATGACTGTGAG	2040		
Db	961	GACGCGCCACAGGAACTGGAGCATGAAGAAAGAGCGATTTGTGTCTCAGTACCGCTATG	1020	QY	2264	GCAACGAGTGGCTTACAGATCTCTTAACCTTTGAGGACTGTCTCCAGACAAATATGAAAAA	2323		
QY	1244	TGGAACCATGCTTGTGGCAGACCACTCGATGGCAGAAATTCACGCGCAGTGGTCTTAAAGC	1303	Db	2041	GCAACGAGTGGCTTACAGATCTCTTAACCTTTGAGGACTGTCTCCAGACAAATATGAAAAA	2100		
Db				QY	2324	CTTTTAGAGAGAACTATGTGAGAGCACAACAGATTTTCAAAGCTTCTTTGGGAGTG	2383		

Db 2101 CCTTTAGAGAGAAACAATGTGAAGCACACACGAGTTTTTCAAAAGCTTCCTTTTGGAGTG 2160
Qy 2384 GGCCTGCGGTGGAATCGAATCCCAAGTACGCTGGGCTCTCACAAAGGACAGGTGCAAGC 2443
Db 2161 GGCCTGCGGTGGAATCGAATCCCAAGTACGCTGGGCTCTCACAAAGGACAGGTGCAAGC 2220
Qy 2444 TCATCTGCCAAGCCAAAGGCATTTGGCTACTCTTTCGTTTGCAGCCCAAGGTGTAGATG 2503
Db 2221 TCATCTGCCAAGCCAAAGGCATTTGGCTACTCTTTCGTTTGCAGCCCAAGGTGTAGATG 2280
Qy 2504 GTAATCCATGTAGCCAGATTCACCTCTGTCTGTGTGCAAGGACAGTGTGAAGAGCTG 2563
Db 2281 GTACTCCATGTAGCCAGATTCACCTCTGTCTGTGTGCAAGGACAGTGTGAAGAGCTG 2340
Qy 2564 GTTGTGATCGCATCATAGATCCCAAAAGAGTTCATAAATGTGTGTTTGGCGGGAA 2623
Db 2341 GTTGTGATCGCATCATAGATCCCAAAAGAGTTCATAAATGTGTGTTTGGCGGGAA 2400
Qy 2624 ATGGATCTACTTTGTAATAAATAATACAGGATCAGTTACTAGTGCATAAACCCTGGATATCATG 2683
Db 2401 ATGGATCTACTTTGTAATAAATAATACAGGATCAGTTACTAGTGCATAAACCCTGGATATCATG 2460
Qy 2684 ATATCATCAATTCACATGAGGACACCAACATCGAAGTGAAACAGCGGAACAGAGGG 2743
Db 2461 ATATCATCAATTCACATGAGGACACCAACATCGAAGTGAAACAGCGGAACAGAGGG 2520
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Db 2521 GATCCAGGACATGCGAGCTTCTTGGCCATCAAGCTGCTGATGCAACATATTTCTTGA 2580
Qy 2804 ATGGTGACTACACTTTGTCCACCTTAGAGCAAGACATATGTACAAAGGTGTGTCTTGA 2863
Db 2581 ATGGTGACTACACTTTGTCCACCTTAGAGCAAGACATATGTACAAAGGTGTGTCTTGA 2640
Qy 2864 GGTACAGCGGCTCCTCTGCGGCATTTGGAAAGATTCGAGCTTTAGCCCTCTCAAGAGC 2923
Db 2641 GGTACAGCGGCTCCTCTGCGGCATTTGGAAAGATTCGAGCTTTAGCCCTCTCAAGAGC 2700
Qy 2924 CTTTGACCATCCAGGTCTTACTGTGGGCAATCCCTTCGACCTAAATTAATACACCT 2983
Db 2701 CTTTGACCATCCAGGTCTTACTGTGGGCAATCCCTTCGACCTAAATTAATACACCT 2760
Qy 2984 ACTTCGTAAGAGAGAGAGGAATCTTTCAATGCTATCCCACTTTTTCAGCATGGGTCA 3043
Db 2761 ACTTCGTAAGAGAGAGAGGAATCTTTCAATGCTATCCCACTTTTTCAGCATGGGTCA 2820
Qy 3044 TTGAAGAGTGGGCGAATGTTCTAAGTCATGTGAATTTGGGTTGCGAGAGAGCTGGTAG 3103
Db 2821 TTGAAGAGTGGGCGAATGTTCTAAGTCATGTGAATTTGGGTTGCGAGAGAGCTGGTAG 2880
Qy 3104 AATGCCGAGACATTAATGGACAGCTCTTCCGAGTGTGCAAGGAGTGAAGCCAGCCA 3163
Db 2881 AATGCCGAGACATTAATGGACAGCTCTTCCGAGTGTGCAAGGAGTGAAGCCAGCCA 2940
Qy 3164 GCACCAAGCTTGTGCAGACATCCCTCGCCCAAGTGGCAGCTGGGGAGTGGTTCATCAT 3223
Db 2941 GCACCAAGCTTGTGCAGACATCCCTCGCCCAAGTGGCAGCTGGGGAGTGGTTCATCAT 3000
Qy 3224 GTTCTAAGACTGTGGGAAGGTTTACAAAACCAAGCTTGAAGTGTCTGTCCCATGATG 3283
Db 3001 GTTCTAAGACTGTGGGAAGGTTTACAAAACCAAGCTTGAAGTGTCTGTCCCATGATG 3060
Qy 3284 GAGGGGTGTTATCTCATGACAGCTGTGATCTTTTAAAGAACCTTAACATTTTCATAGACT 3343
Db 3061 GAGGGGTGTTATCTCATGACAGCTGTGATCTTTTAAAGAACCTTAACATTTTCATAGACT 3120
Qy 3344 TTTTGCAATGTGGCAGATTCAGTGAAGTGTGTTTAAAGTGTGTAGCTTTGAGGCGCAGGC 3403
Db 3121 TTTTGCAATGTGGCAGATTCAGTGAAGTGTGTTTAAAGTGTGTAGCTTTGAGGCGCAGGC 3180
Qy 3404 AAAGTGAAGGAGGCTGTGTGAGGGAAGCAAGAGGCTGGAGGATTCAGCGGTATCTTC 3463
Db 3181 AAAGTGAAGGAGGCTGTGTGAGGGAAGCAAGAGGCTGGAGGATTCAGCGGTATCTTC 3240

Qy 3464 CCAGTAACCAAGTGAAGTGTATCAGTAAGTGGGATTATGGGGGTAGATAGAAAAAGAGTT 3523
Db 3241 CCAGTAACCAAGTGAAGTGTATCAGTAAGTGGGATTATGGGGGTAGATAGAAAAAGAGTT 3300
Qy 3524 GAATCATCAGAGTAACCTGCCAGTTTGCAAATTTGATAGGATAGTTAGTGAGGATTATTAA 3583
Db 3301 GAATCATCAGAGTAACCTGCCAGTTTGCAAATTTGATAGGATAGTTAGTGAGGATTATTAA 3360
Qy 3584 CCTCTGAGCAGTATATAGCATATAAAGCCCGGGCAATTATTATTATTATTCTTTTGT 3643
Db 3361 CCTCTGAGCAGTATATAGCATATAAAGCCCGGGCAATTATTATTATTATTCTTTTGT 3420
Qy 3644 TACATCTACTACAGTTTAAAAAACAAGCAATTTGTCAAAAAAGTTAGAACCTATTAC 3703
Db 3421 TACATCTATTACAAGTTTAAAAAACAAGCAATTTGTCAAAAAAGTTAGAACCTATTAC 3480
Qy 3704 AACCCCTG 3711
Db 3481 AACCCCTG 3488

RESULT 9

US-10-473-974-98
; Sequence 98, Application US/10473974
; Publication No. US2004026580A1
; GENERAL INFORMATION:
; APPLICANT: GARCIA, TERESA
; APPLICANT: ROMAN, ROMAN, SERGIO
; APPLICANT: BARON, ROLAND
; APPLICANT: CALL, KATHERINE
; APPLICANT: THEILHABER, JOACHIM
; APPLICANT: CONNOLLY, TIMOTHY
; APPLICANT: JACKSON, AMANDA
; APPLICANT: BUSHNELL, STEVEN
; APPLICANT: RAWADI, GEORGES
; TITLE OF INVENTION: GENES INVOLVED IN OSTEOGENESIS, AND METHODS OF USE
; FILE REFERENCE: 37991-0023
; CURRENT APPLICATION NUMBER: US/10/473,974
; CURRENT FILING DATE: 2003-10-03
; PRIOR APPLICATION NUMBER: PCT/IB02/02211
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: 60/281,400
; PRIOR FILING DATE: 2001-04-05
; NUMBER OF SEQ ID NOS: 246
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 98
; LENGTH: 3430
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (3332)
; OTHER INFORMATION: a, c, g, t, other or unknown
US-10-473-974-98

Query Match 63.5%; Score 2548; DB 18; Length 3430;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 3318; Conservative 0; Mismatches 13; Indels 1; Gaps 1;
Qy 280 TGAGCGGCTCTCTTTAGTGACTCCCGGAGCTTCGCGCTGTAGCGGCTCTGCGGCGCTT 339
Db 1 TGAGCGGCTCTCTTTAGTGACTCCCGGAGCTTCGCGCTGTAGCGGCTCTGCGGCGCTT 60
Qy 340 CCAACCAATTAAGAAATTTAAATTTTAAATCCAGACAGCCCAACAGAGCTTTGCT 399
Db 61 CCAACCAATTAAGAAATTTAAATTTTAAATCCAGACAGCCCAACAGAGCTTTGCT 120
Qy 400 CTCCGACCCGAACTAAAGCTCCCTCGCTCGCTCGCTGTCTACGAGCGGTGTCTCTGGG 459
Db 121 CTCCGACCCGAACTAAAGCTCCCTCGCTCGCTGTCTACGAGCGGTGTCTCTGGG 180
Qy 460 GCTTCAATGCAGCGAGCTGTGTCGCGAGGGGTTCCGAAGGCGCAAGCTGGGCGAGCATG 519

181 GCTCCAAATGACGAGCTGTGCCCCGAGGGGTTCGGAAGSCGCAAGCTGGCGAGCGACATG 240
520 GGGAAAGCGGAGCGGGCTCCGGGGTCTCGGAGCTTTTGGGCCGTACACCGCTGCTGCTG 579
241 GGGAAAGCGGAGCGGGCTCCGGGGTCTCGGAGCTTTTGGGGCCGTACCCACGCTGCTGCTG 300
580 CTCGCCGCGGGCTACTGCGCGCTGTCGAGCGCACTCGGGCGCCCTCCGAGGAGACGAG 639
301 CTCGCCGCGGGCTACTGCGCGCTGTCGAGCGCACTCGGGCGCCCTCCGAGGAGACGAG 360
640 GAGCTAGTGGTCCCGAGCTGAGAGCGGTCCCGGGACACGCGACCAACGCGCTCCGCGCTG 699
361 GAGCTAGTGGTCCCGAGCTGAGAGCGGTCCCGGGACACGCGACCAACGCGCTCCGCGCTG 420
700 CAGCGCTTTGACAGAGCTGATCTGAGCTGCGCGCGCGCGCGAGCAGCAGCTTTTGGGGCC 759
421 CAGCGCTTTGACAGAGCTGATCTGAGCTGCGCGCGCGCGCGAGCAGCAGCTTTTGGGGCC 480
760 GGGTTACGCTCCAGAACTGGGGCGCAATCCGGGTCCGACACCGCTCCGGAAC 819
481 GGGTTACGCTCCAGAACTGGGGCGCAATCCGGGTCCGAGACGCGCTTCGGAAC 540
820 GACCTGGCGCACTGCTTCTACTCCGGCACCGTGAATGGCGATCCAGCTCGGCTCCGCGC 879
541 GACCTGGCGCACTGCTTCTACTCCGGCACCGTGAATGGCGATCCAGCTCGGCTCCGCGC 600
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601 CTCAGCTCTGCGAGGCGTGGCGCGCTTCTACTGCTGGGGAGCGCTATTTCATC 660
940 CAGCGCTGCCCGCGCAGCAGCGCTTCGCCACCGCGCCCGCGGAGAGCGCGC 999
661 CAGCGCTGCCCGCGCAGCAGCGCTTCGCCACCGCGCCCGCGGAGAGCGCGC 720
1000 GCACCACTACAGTTCCACTCTCTGCGGGGGAATCGGCAGGGCGAGTAGGGCGCACGTGC 1059
721 GCACCACTACAGTTCCACTCTCTGCGGGGGAATCGGCAGGGCGAGTAGGGCGCACGTGC 780
1060 GGGGTCTGGACGACGAGCGCCCGCGCTGCGGAAGCGGAGACCGAGACGAGACGAA 1119
781 GGGGTCTGGACGACGAGCGCCCGCGCTGCGGAAGCGGAGACCGAGACGAGACGAA 840
1120 GGGGTCTGGAGGAGGAGGAGGAGGCTCAGTGGTCCGCGAGGACCGCGCACTGCAAGC 1179
841 GGGGTCTGGAGGAGGAGGAGGAGGCTCAGTGGTCCGCGAGGACCGCGCACTGCAAGC 900
1180 GTAGGACAGCCCAAGGAACTGGAAGCATAGAAAGAGCGATTTGTGTCAGTCAACGCG 1239
901 GTAGGACAGCCCAAGGAACTGGAAGCATAGAAAGAGCGATTTGTGTCAGTCAACGCG 960
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961 TATGTGGAACCATGCTGTGTGCGAGACGAGTCGATGGCGAATTCACGGCAGTGGTCTA 1020
1300 AAGCAATTACTTCTCAGCTGTTTTCGGTGGCAGCAGATGTCACAAACACCCAGCATTT 1359
1021 AAGCAATTACTTCTCAGCTGTTTTCGGTGGCAGCAGATGTCACAAACACCCAGCATTT 1080
1360 CGTAATTCAATTAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1419
1081 CGTAATTCAATTAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1140
1420 CCGGAGTGAACCTCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1479
1141 CCGGAGTGAACCTCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1200
1480 CACAAACCCACCCAGTGAACCGGATGACAGCAGTATGACACAGCAATTTCTTTTCCACGA 1539
1201 CACAAACCCACCCAGTGAACCGGATGACAGCAGTATGACACAGCAATTTCTTTTCCACGA 1260
1540 CAGGACTTGTGTGGGTCCAGACATGTGATATCTTTGGGATGGCTGATGTTGGAACTGTG 1599

1261 CAGGACTTGTGTGGGTCCAGACATGTGATATCTCTTGGGATGGCTGATGTTGGAACTGTG 1320
1600 TGTGATCCGACGAGAGCTGCTCGTCAATAGAGATGATGTTTACAGAGCTGCCCTTCACC 1659
1321 TGTGATCCGACGAGAGCTGCTCGTCAATAGAGATGATGTTTACAGAGCTGCCCTTCACC 1380
1660 ACAGCCCATGAATTAAGGCGAGCTGTTTAAATGCCACATGATGATGATGATGATGATGATG 1719
1381 ACAGCCCATGAATTAAGGCGAGCTGTTTAAATGCCACATGATGATGATGATGATGATGATG 1440
1720 AGCTTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1779
1441 AGCTTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1500
1780 CACAGCCAGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1839
1501 CACAGCCAGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1560
1840 CATGGGGAATGTTGATGGAACAAGCTCCAGATCCATACAGCTCCAGGGCGATCTCCCT 1899
1561 CATGGGGAATGTTGATGGAACAAGCTCCAGATCCATACAGCTCCAGGGCGATCTCCCT 1620
1900 GGCACCTCGTACGATGCGCAACCGGCGAGTCCAGTTTATCATTTTGGGAGGAGCTCCAAAC 1959
1621 GGCACCTCGTACGATGCGCAACCGGCGAGTCCAGTTTATCATTTTGGGAGGAGCTCCAAAC 1680
1960 TGCCCTGATGCGAGCAGCAGCATGTAGCACCTTGTGCTGCTGCTGCTGCTGCTGCTGCTG 2019
1681 TGCCCTGATGCGAGCAGCAGCATGTAGCACCTTGTGCTGCTGCTGCTGCTGCTGCTGCTG 1740
2020 CTGCTGTCTCAAAACCAACACTTCCCGTGGGCGGATGGCACAGCTGTGGAGAAAGGAAA 2079
1741 CTGCTGTCTCAAAACCAACACTTCCCGTGGGCGGATGGCACAGCTGTGGAGAAAGGAAA 1800
2080 TGTGTTATCAACCGCAAGTGTGTGAAACAAACCAACAGAGCATTTTGTATAGCGCTTTT 2139
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2140 CATGGAAGCTGGGGAATGTTGGGGCTTGGGGAGACTGTTGAGAAACGTTGGGCTGGAGA 2199
1861 CATGGAAGCTGGGGAATGTTGGGGCTTGGGGAGACTGTTGAGAAACGTTGGGCTGGAGA 1920
2200 GTCCAGTACAGATGAGGGAATGTGACAAACCGCTCCCAAGAAATGGAAGGGAAGTACTGT 2259
1921 GTCCAGTACAGATGAGGGAATGTGACAAACCGCTCCCAAGAAATGGAAGGGAAGTACTGT 1980
2260 GAAGCAACAGAGTGGCTCAGATCTCTGTAACCTTGAGGAGTGTCCAGACATATATGGA 2319
1981 GAAGCAACAGAGTGGCTCAGATCTCTGTAACCTTGAGGAGTGTCCAGACATATATGGA 2040
2320 AAAACCTTTAGAGAGAAACAATGTGAAGCACAACAGAGTTCCTTCAAAAGCTTCTTTGGG 2379
2041 AAAACCTTTAGAGAGAAACAATGTGAAGCACAACAGAGTTCCTTCAAAAGCTTCTTTGGG 2100
2380 AGTGGGCTCGCGTGGGAATGGAATCCCAAGTACGCTGCTCTCAACCAAGGACAGGTGC 2439
2101 AGTGGGCTCGCGTGGGAATGGAATCCCAAGTACGCTGCTCTCAACCAAGGACAGGTGC 2160
2440 AAGCTCATCTGCAAGCAACCAAGGAGTGGCTACTTCTTCTGTTTTCAGCCCAAGGTTGTA 2499
2161 AAGCTCATCTGCAAGCAACCAAGGAGTGGCTACTTCTTCTGTTTTCAGCCCAAGGTTGTA 2220
2500 GATGTTACTCTCATGTAGCCAGATTCACCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2559
2221 GATGTTACTCTCATGTAGCCAGATTCACCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2280
2560 GCTGTTGTGATTCGATCATAGACTCCAAAGAAAGTGTGATAAATGTTGTTTTCGCGGG 2619
2281 GCTGTTGTGATTCGATCATAGACTCCAAAGAAAGTGTGATAAATGTTGTTTTCGCGGG 2340
2620 GGAATGATCTACTTGTGTAATAAATATCAGATCAGTTACTAGTGCAAAACCTCGATAT 2679
2341 GGAATGATCTACTTGTGTAATAAATATCAGATCAGTTACTAGTGCAAAACCTCGATAT 2400

Qy	2680	CATGATATCATCAAAATCCAAATCGAGTGAACCAACATCGAAGTGAAACAGCGGAACCCAG	2739
Db	2401	CATGATATCATCAAAATCCAAATCGAGTGAACCAACATCGAAGTGAAACAGCGGAACCCAG	2460
Qy	2740	AGGGGATCCAGGAACAATGGCAGCTTCTTTGCCATCAAAGCTCTGTATGCGCACATATATT	2799
Db	2461	AGGGGATCCAGGAACAATGGCAGCTTCTTTGCCATCAAAGCTCTGTATGCGCACATATATT	2520
Qy	2800	CTTAAATGGTGACATACACTTTTGTCACACTTAGACGAAGACATATATGTAACAAGGTGTGTC	2859
Db	2521	CTTAAATGGTGACATACACTTTTGTCACACTTAGACGAAGACATATATGTAACAAGGTGTGTC	2580
Qy	2860	TTGAGGTACAGCGGCTCCTCTGGCGCAATCGGAAGAAATTCGCAGCTTTAGCCCTCTCAAA	2919
Db	2581	TTGAGGTACAGCGGCTCCTCTGGCGCAATCGGAAGAAATTCGCAGCTTTAGCCCTCTCAAA	2640
Qy	2920	GAGCCCTTGACATCAGAGTTCTTACTGTGGGCAATGCCCTTCGACCTAAATTAATATAC	2979
Db	2641	GAGCCCTTGACATCAGAGTTCTTACTGTGGGCAATGCCCTTCGACCTAAATTAATATAC	2700
Qy	2980	ACCTACTTCTGAAGAAGAAAGGAATCTTTCAATGCTATCCCACTTTTTCAGCATGG	3039
Db	2701	ACCTACTTCTGAAGAAGAAAGGAATCTTTCAATGCTATCCCACTTTTTCAGCATGG	2760
Qy	3040	GTCAATTGAAGTGGGGCGAATGTTCTAAGTCTATGTGAATGGGTGGCAGAGAAGCTG	3099
Db	2761	GTCAATTGAAGTGGGGCGAATGTTCTAAGTCTATGTGAATGGGTGGCAGAGAAGCTG	2820
Qy	3100	GTGAATGCCGAGACATTAATGGCAGCCTGCTTCGAGTGTGCAAAAGGAAGTGAAGCCA	3159
Db	2821	GTGAATGCCGAGACATTAATGGCAGCCTGCTTCGAGTGTGCAAAAGGAAGTGAAGCCA	2880
Qy	3160	GCCAGCACAGACCTTGTGCAGACCATCCCTGCCCCAGTGGCAGCTGGGGGAGTGGTCA	3219
Db	2881	GCCAGCACAGACCTTGTGCAGACCATCCCTGCCCCAGTGGCAGCTGGGGGAGTGGTCA	2940
Qy	3220	TCATGTTCTTAAGACCTGTGGGAGGGGTTACAAAAAACAAGCTTGAAGTGTCTGTGCCAT	3279
Db	2941	TCATGTTCTTAAGACCTGTGGGAGGGGTTACAAAAAACAAGCTTGAAGTGTCTGTGCCAT	3000
Qy	3280	GATGGAGGGGTGTTATCTCATGACAGCTGTGATCCTTTAAAGAAACCTAAACATTTTCA	3339
Db	3001	GATGGAGGGGTGTTATCTCATGAGAGCTGTGATCCTTTAAAGAAACCTAAACATTTTCA	3060
Qy	3340	GACTTTTGGCACAATGGCAGAATGAGTGGTTTAAGTGGTGTAGCTTTTGAAGGCCA	3399
Db	3061	GACTTTTGGCACAATGGCAGAATGAGTGGTTTAAGTGGTGTAGCTTTTGAAGGCCA	3119
Qy	3400	AGGCAAGTGTAGGAGGGCTGGTGCAGGGAAGCAAGAGCTTGAGGGATCCAGCGTAT	3459
Db	3120	AGGCAAGTGTAGGAGGGCTGGTGCAGGGAAGCAAGAGCTTGAGGGATCCAGCGTAT	3179
Qy	3460	CTTCCCAAGTAACAGTGAAGGTGATCAGTAAGGTGGGATTTATGGGGGTAGATAGAAAAGG	3519
Db	3180	CTTCCCAAGTAACAGTGAAGGTGATCAGTAAGGTGGGATTTATGGGGGTAGATAGAAAAGG	3239
Qy	3520	AGTTGAATCATCAGAGTAAACTGCCAGTTGCAAAATTTGATAGGATAGTTAGTGAGGATTA	3579
Db	3240	AGTTGAATCATCAGAGTAAACTGCCAGTTGCAAAATTTGATAGGATAGTTAGTGAGGATTA	3299
Qy	3580	TTAACTCTGTAGCAGTGAATAGCATTAATAA	3611
Db	3360	TTAACTCTGTAGCAGTGAATAGCATTAATAA	3331

RESULT 10

REF ID: A667281

09-10-087-281-1
: Sequence 1. Application US/10667281

; Publication No. US20050100916A1

GENERAL INFORMATION:

APPLICANT: Klonowski, Paul

: APPLICANT: Allard, John

Db 738 GAACTGGAAGCATAAAGAAAGACGATTTGTGTCCAGTCCACCGCTATGTGGAACCATGC 797
Qy 1256 TTGTGGCAGACCAAGTCGATGGCAGAAATTCACGGCAGATGGTCTAAAGCATTTACCTTCTCA 1315
Db 798 TTGTGGCAGACCAAGTCGATGGCAGAAATTCACGGCAGATGGTCTAAAGCATTTACCTTCTCA 857
Qy 1316 CGTTGTTTTCGGTGGCAGCAGATTTGTACAAACACCCACAGCATTCGTAAATTCAGTTAGCC 1375
Db 858 CGTTGTTTTCGGTGGCAGCAGATTTGTACAAACACCCACAGCATTCGTAAATTCAGTTAGCC 917
Qy 1376 TGGTGGTGGTGAAGATCTTTGGTCATCCACGATGAACAGAAAGGGGCCGGAAGTGACCTCCA 1435
Db 918 TGGTGGTGGTGAAGATCTTTGGTCATCCACGATGAACAGAAAGGGGCCGGAAGTGACCTCCA 977
Qy 1436 ATGCTGGCCTCACTCTGGGGAATTTTGGCACTGSCAGNAGCAGCAACCCACCCAGTG 1495
Db 978 ATGCTGGCCTCACTCTGGGGAATTTTGGCACTGSCAGNAGCAGCAACCCACCCAGTG 1037
Qy 1496 ACCGGGATGCAGACACTATGACACAGCAATTTCTTTTACCAGACAGGACTTGTGTGGGT 1555
Db 1038 ACCGGGATGCAGACACTATGACACAGCAATTTCTTTTACCAGACAGGACTTGTGTGGGT 1097
Qy 1556 CCCAGACATGTGATACTCTTGGGATGGCTGATGTTGGAACTGTGTGATCCGAGCAGAA 1615
Db 1098 CCCAGACATGTGATACTCTTGGGATGGCTGATGTTGGAACTGTGTGATCCGAGCAGAA 1157
Qy 1616 GCTGCTCGTGTAGAAAGATGATGTTTACAGCTGCTTACCAAGCCCATGAAATTAG 1675
Db 1158 GCTGCTCGTGTAGAAAGATGATGTTTACAGCTGCTTACCAAGCCCATGAAATTAG 1217
Qy 1676 GCCAGTGTAAACATGCCACATGATGACAAAGCAGTGTGCCAGCCTTAATGTGTGA 1735
Db 1218 GCCAGTGTAAACATGCCACATGATGACAAAGCAGTGTGCCAGCCTTAATGTGTGA 1277
Qy 1736 ACCAGGATTTCCACATGATGGCGTCAATGCTTTCCAACTCGACACACAGCCCTTGGT 1795
Db 1278 ACCAGGATTTCCACATGATGGCGTCAATGCTTTCCAACTCGACACACAGCCCTTGGT 1337
Qy 1796 CTCCTTGCAAGTGGCTACATGATTTACATCATTTCTGGATTAAGTCAATGGGAAATGTTGA 1855
Db 1338 CTCCTTGCAAGTGGCTACATGATTTACATCATTTCTGGATTAAGTCAATGGGAAATGTTGA 1397
Qy 1856 TGGACAAGCTCCAGAAATCCATACAGCTCCAGGCGATCTCCCTGCGCACTCGTACGATG 1915
Db 1398 TGGACAAGCTCCAGAAATCCATACAGCTCCAGGCGATCTCCCTGCGCACTCGTACGATG 1457
Qy 1916 CCAACCGGCAGTGCAGATTTACATTTGGGGAGGACTCCAAACACTGCCCTGATGACGCA 1975
Db 1458 CCAACCGGCAGTGCAGATTTACATTTGGGGAGGACTCCAAACACTGCCCTGATGACGCA 1517
Qy 1976 GCACATGTAGCACTTGTGGTGTACGGGACCTCTGTTGGGTGCTGTTGTGTCAACCA 2035
Db 1518 GCACATGTAGCACTTGTGGTGTACGGGACCTCTGTTGGGTGCTGTTGTGTCAACCA 1577
Qy 2036 AACACTTCCGTTGGGCGGATGCAACAGCTGTGGAGAGGAAATGTTGTATCAACGGCA 2095
Db 1578 AACACTTCCGTTGGGCGGATGCAACAGCTGTGGAGAGGAAATGTTGTATCAACGGCA 1637
Qy 2096 AGTGTGTGAACAAAAACCAAGAAAGCAATTTTGATACGCTTTTTCATGGAAGCTGGGAA 2155
Db 1638 AGTGTGTGAACAAAAACCAAGAAAGCAATTTTGATACGCTTTTTCATGGAAGCTGGGAA 1697
Qy 2156 TGTGGGGGCTTGGGAGACTGTTTCAGAAACAGTGGGTGGAGAGTCCAGTACAGATGA 2215
Db 1698 TGTGGGGGCTTGGGAGACTGTTTCAGAAACAGTGGGTGGAGAGTCCAGTACAGATGA 1757
Qy 2216 GGGAAATGTCAACACCAAGTCCCAAGAAATGGAGGAAAGTACTGTGAAGCCAAACAGATGC 2275
Db 1758 GGGAAATGTCAACACCAAGTCCCAAGAAATGGAGGAAAGTACTGTGAAGCCAAACAGATGC 1817
Qy 2276 GCTACAGATCTGTAAACCTTGGAGACTGTCCAGACAATAATGAAACCTTTAGAGAGG 2335
Db 1818 GCTACAGATCTGTAAACCTTGGAGACTGTCCAGACAATAATGAAACCTTTAGAGAGG 1877

Qy 2336 AACATGTGAAGCACACAAACGAGTTTTCAAAAGCTTCTCTTTGGGAGTGGCTCGGTGG 2395
Db 1878 AACATGTGAAGCACACAAACGAGTTTTCAAAAGCTTCTCTTTGGGAGTGGCTCGGTGG 1937
Qy 2396 AATGATTTCCCAAGTACGCTGCGCTCTCACAAAGGACAGGTGCAAGCTCATCTGCCAAG 2455
Db 1938 AATGATTTCCCAAGTACGCTGCGCTCTCACAAAGGACAGGTGCAAGCTCATCTGCCAAG 1997
Qy 2456 CCAAGGCAATTTGGCTACCTTCTGTTTTCGAGCCCAAGTTGTAGATGGTACTCATGTA 2515
Db 1998 CCAAGGCAATTTGGCTACCTTCTGTTTTCGAGCCCAAGTTGTAGATGGTACTCATGTA 2057
Qy 2516 GCCCAGATTTCCACCTCTGCTGTGTGCAAGACAGTGTGTAAGCTGCTGTGTGATCGCA 2575
Db 2058 GCCCAGATTTCCACCTCTGCTGTGTGCAAGACAGTGTGTAAGCTGCTGTGTGATCGCA 2117
Qy 2576 TCATAGACTCCAAAAGAAAGTTTGATAAATGTGGTGTGTTGCGGGGAAATGGATCTACTT 2635
Db 2118 TCATAGACTCCAAAAGAAAGTTTGATAAATGTGGTGTGTTGCGGGGAAATGGATCTACTT 2177
Qy 2636 GTAAAAAATATCAGGATCAGTTACTAGTGCAAAACCTTGGATATCATGATATCATCAAA 2695
Db 2178 GTAAAAAATATCAGGATCAGTTACTAGTGCAAAACCTTGGATATCATGATATCATCAAA 2237
Qy 2696 TTCCAACTGGAGCCACCAACATCGAAGTGAACACAGCGGAAACAGAGGGATCCAGAAACA 2755
Db 2238 TTCCAACTGGAGCCACCAACATCGAAGTGAACACAGCGGAAACAGAGGGATCCAGAAACA 2297
Qy 2756 ATGGCAGCTTTCTTGGCCATCAAAAGCTGTGATGGCAATATTTCTTAATGGTGACTACA 2815
Db 2298 ATGGCAGCTTTCTTGGCCATCAAAAGCTGTGATGGCAATATTTCTTAATGGTGACTACA 2357
Qy 2816 CTTTGTCCACCTTAGAGCAAGACATTTATGTACAAAGTGTGTTCTTGTAGAGTACAGCGCT 2875
Db 2358 CTTTGTCCACCTTAGAGCAAGACATTTATGTACAAAGTGTGTTCTTGTAGAGTACAGCGCT 2417
Qy 2876 CTTCTGCGGCAATGGAAAGAAATTCGACGCTTTAGCCCTCTCAAAAGAGCCCTTGACATCC 2935
Db 2418 CTTCTGCGGCAATGGAAAGAAATTCGACGCTTTAGCCCTCTCAAAAGAGCCCTTGACATCC 2477
Qy 2936 AGTTTCTTACTGTGGGCAATGCCCTTCGACCTTAAATTAATAACCTTTCGTAAGA 2995
Db 2478 AGTTTCTTACTGTGGGCAATGCCCTTCGACCTTAAATTAATAACCTTTCGTAAGA 2537
Qy 2996 AGAAGAGAAATCTTTCAATGCTATCCCCCTTTTTCGACATGGGTCAATGAGAGTGGG 3055
Db 2538 AGAAGAGAAATCTTTCAATGCTATCCCCCTTTTTCGACATGGGTCAATGAGAGTGGG 2597
Qy 3056 GCGAATGTTCTAAGTCATGTGAATTTGGGTTCGACAGAAAGCTGTAGAAATGCCGAGACA 3115
Db 2598 GCGAATGTTCTAAGTCATGTGAATTTGGGTTCGACAGAAAGCTGTGTAGAAATGCCGAGACA 2657
Qy 3116 TTAATGAGCAGCTGCTTTCCGAGTGTGCAAAAGAAAGTGAAGCCAGCCAGCAGACCTT 3175
Db 2658 TTAATGAGCAGCTGCTTTCCGAGTGTGCAAAAGAAAGTGAAGCCAGCCAGCAGACCTT 2717
Qy 3176 GTGAGACCATCTTCCGCCCCAGTGGGAGTGGTGCATCATGTTCTAAGACCT 3235
Db 2718 GTGAGACCATCTTCCGCCCCAGTGGGAGTGGTGCATCATGTTCTAAGACCT 2777
Qy 3236 GTGGGAAGGGTTTACAAAAAACAAGCTTGAAGTGTCTGTCCCATGATGAGGGGTGTTAT 3295
Db 2778 GTGGGAAGGGTTTACAAAAAACAAGCTTGAAGTGTCTGTCCCATGATGAGGGGTGTTAT 2837
Qy 3296 CTCATGACAGCTGTGATCTTTTAAAGAAACCTTAAACATTTTCATAGACTTTTGCACAAATGG 3355
Db 2838 CTCATGACAGCTGTGATCTTTTAAAGAAACCTTAAACATTTTCATAGACTTTTGCACAAATGG 2897
Qy 3356 CAGAAATGACAGTTAAGTGGTGTAAAGTGGTGTAGCTTTTGGGGCAAGGCAAGGTGAGGAG 3415
Db 2898 CAGAAATGACAGTTAAGTGGTGTAAAGTGGTGTAGCTTTTGGGGCAAGGCAAGGTGAGGAG 2957

Db 1461 AACTGGCAGAAGCAGCAGCAACCCACCAGTCAGCGGATGCAGAGCACTATGACACAGCA 1520
Qy 1525 ATTCTTTTCCACAGACAGGACTTGTGTGGTCCGAGACATGTGATACCTTTGGGATGGCT 1584
Db 1521 ATTCTTTTCCACAGACAGGACTTGTGTGGTCCGAGACATGTGATACCTTTGGGATGGCT 1580
Qy 1585 GATGTTGGAATGTGTGTGATCCGAGCAGAAAGCTGCTCCGTATAGAAAGATGATGGTTTA 1644
Db 1581 GATGTTGGAATGTGTGTGATCCGAGCAGAAAGCTGCTCCGTATAGAAAGATGATGGTTTA 1640
Qy 1645 CAAAGTGCCTTCCACACAGCCCATGAAATAGGCCACGCTGTTTAAACATGCCATGATGAT 1704
Db 1641 CAAAGTGCCTTCCACACAGCCCATGAAATAGGCCACGCTGTTTAAACATGCCATGATGAT 1700
Qy 1705 GCAAGCAGTGTGCGAGCCCTTAATGGTGTGAACCAAGGATCCCAATGATGCGCTCAATG 1764
Db 1701 GCAAGCAGTGTGCGAGCCCTTAATGGTGTGAACCAAGGATCCCAATGATGCGCTCAATG 1760
Qy 1765 CTTTCCAACTGGACACACAGCCAGCTTGTGCTCTCTGAGTGGCTTACATGATTACATCA 1824
Db 1761 CTTTCCAACTGGACACACAGCCAGCTTGTGCTCTCTGAGTGGCTTACATGATTACATCA 1820
Qy 1825 TTTCTGGAATATGGTCATGGGAATGTTTGATGGAACAAGCCCTCAGAAATCCCATACAGCTC 1884
Db 1821 TTTCTGGAATATGGTCATGGGAATGTTTGATGGAACAAGCCCTCAGAAATCCCATACAGCTC 1880
Qy 1885 CCAGCGATCTCCCTGGACACCTGTCAGATGCCACACCGCAGTGCAGTTTACATTTGGG 1944
Db 1881 CCAGCGATCTCCCTGGACACCTGTCAGATGCCACACCGCAGTGCAGTTTACATTTGGG 1940
Qy 1945 GAGGACTCCAAACACTGCCCTGATGCAGCCACACATGTAGCACCTTGTGGTGTACCGGC 2004
Db 1941 GAGGACTCCAAACACTGCCCTGATGCAGCCACACATGTAGCACCTTGTGGTGTACCGGC 2000
Qy 2005 ACCTCTGTGGGGTCTGTGTGTCAAAACCAACACTTCCCGTGGCGGATGGCACCCAGC 2064
Db 2001 ACCTCTGTGGGGTCTGTGTGTCAAAACCAACACTTCCCGTGGCGGATGGCACCCAGC 2060
Qy 2065 TGTGAGAAGGAATGTTATCAACGGCAGTGTGTGAACAAACCAACCAAGAGCAT 2124
Db 2061 TGTGAGAAGGAATGTTATCAACGGCAGTGTGTGAACAAACCAACCAAGAGCAT 2120
Qy 2125 TTTGATAGCCCTTTTCATGGAAGCTGGGAATGTGGGGCCCTTGGGGAGACTGTTTCGAGA 2184
Db 2121 TTTGATAGCCCTTTTCATGGAAGCTGGGAATGTGGGGCCCTTGGGGAGACTGTTTCGAGA 2180
Qy 2185 ACGTCGGTGGAGGAGTCCAGTACACGATGAGGGAATGTGACAAACCCAGTCCCAAGAAAT 2244
Db 2181 ACGTCGGTGGAGGAGTCCAGTACACGATGAGGGAATGTGACAAACCCAGTCCCAAGAAAT 2240
Qy 2245 GGAGGGAAGTACTGTGAAGGGAACGAGTGCCTACAGATCCTGTAACTTTGAGGACTGT 2304
Db 2241 GGAGGGAAGTACTGTGAAGGGAACGAGTGCCTACAGATCCTGTAACTTTGAGGACTGT 2300
Qy 2305 CCAGACAAATATGGAAGAAACCTTTAGAGAGGAACAAATGTGAAGACACAAACGAGTTTCA 2364
Db 2301 CCAGACAAATATGGAAGAAACCTTTAGAGAGGAACAAATGTGAAGACACAAACGAGTTTCA 2360
Qy 2365 AAAAGTTCCTTTGGAGTGGGCTCGGTGGAAATGGATTCGCAAGTACGCTGGCCTCTCA 2424
Db 2361 AAAAGTTCCTTTGGAGTGGGCTCGGTGGAAATGGATTCGCAAGTACGCTGGCCTCTCA 2420
Qy 2425 CCAAGGACAGTGCAGCTCATCTCCCAAGCCCAAGGATTTGGCTTCTTCGTTTGG 2484
Db 2421 CCAAGGACAGTGCAGCTCATCTCCCAAGCCCAAGGATTTGGCTTCTTCGTTTGG 2480
Qy 2485 CAGCCCAAGTTGTAGATGTTACTCCTAGTACCCAGATTTCCACCTCTGTCTGTGTGCA 2544
Db 2481 CAGCCCAAGTTGTAGATGTTACTCCTAGTACCCAGATTTCCACCTCTGTCTGTGTGCA 2540
Qy 2545 GGAACAGTGTGAAAAGCTGGTTGTGATCGCATCATAGACTCCAAAGAAAGTTTGATAAA 2604
Db 2541 GGAACAGTGTGAAAAGCTGGTTGTGATCGCATCATAGACTCCAAAGAAAGTTTGATAAA 2600

Qy 2605 TGTGTTGTTTTCGGGGGAAATGGATCTACTTTGTAAGAAATATCAGGATCAGTTACTAGT 2664
Db 2601 TGTGTTGTTTTCGGGGGAAATGGATCTACTTTGTAAGAAATATCAGGATCAGTTACTAGT 2660
Qy 2665 GCAAAACCTCGGATATCATGATATCATCAAAATCCAACTGGAGCCACCAACATCGAAGTG 2724
Db 2661 GCAAAACCTCGGATATCATGATATCATCAAAATCCAACTGGAGCCACCAACATCGAAGTG 2720
Qy 2725 AAAACGCGGAACGAGGGGATCCAGGAACAAATGGCAGCTTTCTTGCCATCAAGCTGCT 2784
Db 2721 AAAACGCGGAACGAGGGGATCCAGGAACAAATGGCAGCTTTCTTGCCATCAAGCTGCT 2780
Qy 2785 GATGSCACATATTTCTTAATGTTGACTACACTTTGTCCACTTAGACCAAGACATTATG 2844
Db 2781 GATGSCACATATTTCTTAATGTTGNTCTACACTTTGTCCACTTAGACCAAGACATTATG 2840
Qy 2845 TACAAAGTGTGTTCTTGAGGTACAGCGGCTCCTCTGCGGCATTTGGAAGAAATTCGACG 2904
Db 2841 TACAAAGTGTGTTCTTGAGGTACAGCGGCTCCTCTGCGGCATTTGGAAGAAATTCGACG 2900
Qy 2905 TTTAGCCCTCTCAAAGAGCCCTTGACCATCCAGGTTCTTACTGTGGGCAATGCCCTTCGA 2964
Db 2901 TTTAGCCCTCTCAAAGAGCCCTTGACCATCCAGGTTCTTACTGTGGGCAATGCCCTTCGA 2960
Qy 2965 CCTAAATTTAAATACACCTACTTCTGTAAGGAAGAAAGGAATCTTTCAATGCTATCCCC 3024
Db 2961 CCTAAATTTAAATACACCTACTTCTGTAAGGAAGAAAGGAATCTTTCAATGCTATCCCC 3020
Qy 3025 ACTTTTTCAGCATGGGTCAITTAAGAGTGGGCGGAATGTTCTAACTCATGTGAATGGGT 3084
Db 3021 ACTTTTTCAGCATGGGTCAITTAAGAGTGGGCGGAATGTTCTAACTCATGTGAATGGGT 3080
Qy 3085 TGGCAGAGAAGACTGGTGTAGAAATGCCAGACATTAATGACAGCCCTGCTTCCGAGTGTGA 3144
Db 3081 TGGCAGAGAAGACTGGTGTAGAAATGCCAGACATTAATGACAGCCCTGCTTCCGAGTGTGA 3140
Qy 3145 AAGGAAGTGAAGCCAGCCAGCACAGACTTGTGTGAGACCACTCCCTGCCCCCAGTGGCAG 3204
Db 3141 AAGGAAGTGAAGCCAGCCAGCACAGACTTGTGTGAGACCACTCCCTGCCCCCAGTGGCAG 3200
Qy 3205 CTGGGGAGTGGTCAATCATGTTCTAAGACCTGTGTGGGAAGGTTTACAAAAACAAGCTTG 3264
Db 3201 CTGGGGAGTGGTCAATCATGTTCTAAGACCTGTGTGGGAAGGTTTACAAAAACAAGCTTG 3260
Qy 3265 AAGTGTCTGTCCCATGATGGAGGGGTGTATCTCATGACAGCTGTGATCCTTTAAGAAA 3324
Db 3261 AAGTGTCTGTCCCATGATGGAGGGGTGTATCTCATGAGAGCTGTGATCCTTTAAGAAA 3320
Qy 3325 CCTAAACATTTTCATAGACTTTTGCACAAATGGCAGAAATGCAGTTAAGTGGTTTAAAGTGG 3384
Db 3321 CCTAAACATTTTCATAGACTTTTGCACAAATGGCAGAAATGCAGTTAAGTGGTTTAAAGTGG 3380
Qy 3385 TTAGCTTTGAGGGCAAGGCAAGAGTGGAGAGGGCTGTGTGCAAGGAAAGCAAGAGCTGG 3444
Db 3381 TTAGCTTTGAGGGCAAGGCAAGAGTGGAGAGGGCTGTGTGCAAGGAAAGCAAGAGCTGG 3440
Qy 3445 AGGATCCAGCGTATCTTCCAGTAAACAGTGAAGGTATCAGTAAGGTGGATTTATGGG 3504
Db 3441 AGGATCCAGCGTATCTTCCAGTAAACAGTGAAGGTATCAGTAAGGTGGATTTATGGG 3500
Qy 3505 GGTAGATAGAAAAGGAGTTGAATCATCAGAGTAAACTGCCAGTTCCAAATTTGATAGGAT 3564
Db 3501 GGTAGATAGAAAAGGAGTTGAATCATCAGAGTAAACTGCCAGTTCCAAATTTGATAGGAT 3560
Qy 3565 AGTTAGTCAGGATTAATAACCTCTGAGCAGTGATATAGCAATAAAGCCCCGGGCATTA 3624
Db 3561 AGTTAGTCAGGATTAATAACCTCTGAGCAGTGATATAGCAATAAAGCCCCGGGCATTA 3620
Qy 3625 TTATTTATTTCTTTCTTTCTTACATCTACTACAGTTTGAAGAAAACAAGCAATTTGTCAA 3684
Db 3621 TTATTTATTTCTTTCTTTCTTACATCTACTACAGTTTGAAGAAAACAAGCAATTTGTCAA 3680

Db 1581 GATGTGGAACTGTGTGTGATCCGAGCAGAAGCTGCTCCGTCAATAGAAATGATGGTTTA 1640
Qy 1645 CAAAGTGCCTTTCACACAGCCCCATGAATTTAGGCCAGCTGTTTTAAACATGSCCAATGATGAT 1704
Db 1641 CAAAGTGCCTTTCACACAGCCCCATGAATTTAGGCCAGCTGTTTTAAACATGSCCAATGATGAT 1700
Qy 1705 GCAAAAGCAGTGTGCGAGCCCTTAATGTGTGGAACCCAGGATTTCCACATGATGCGTCAATG 1764
Db 1701 GCNAGCAGTGTGCGAGCCCTTAATGTGTGGAACCCAGGATTTCCACATGATGCGTCAATG 1760
Qy 1765 CTTTCCAACTCGAACACAGCCAGCCCTTGGTCTCCTTGCAGTGGCTACATGATTAATCA 1824
Db 1761 CTTTCCAACTCGAACACAGCCAGCCCTTGGTCTCCTTGCAGTGGCTACATGATTAATCA 1820
Qy 1825 TTTCTGGTAATGTCATGGGAATGTTTGATGGACAAGCCCTCAGAAATCCCATACAGCTC 1884
Db 1821 TTTCTGGTAATGTCATGGGAATGTTTGATGGACAAGCCCTCAGAAATCCCATACAGCTC 1880
Qy 1885 CCAGCGATCTCCCTGGCACCTCGTACGATGCCAACCGGCAGTGGCCAGTTTACATTTGGG 1944
Db 1881 CCAGCGATCTCCCTGGCACCTCGTACGATGCCAACCGGCAGTGGCCAGTTTACATTTGGG 1940
Qy 1945 GAGGACTCCAAACACTGCTGATCGAGCAGCACATGAGCACCTTGTGTGTACCCGCG 2004
Db 1941 GAGGACTCCAAACACTGCTGATCGAGCAGCACATGAGCACCTTGTGTGTACCCGCG 2000
Qy 2005 ACCTCTGTGGGGTGTGTGTGTCAACCAACACCTTCCGTGGCGGATGGCACCAGC 2064
Db 2001 ACCTCTGTGGGGTGTGTGTGTCAACCAACACCTTCCGTGGCGGATGGCACCAGC 2060
Qy 2065 TGTGAGAGGAGAAATGTTGATCAACGCCAGTGTGGAACAAAAACACAGAAAGCAT 2124
Db 2061 TGTGAGAGGAGAAATGTTGATCAACGCCAGTGTGGAACAAAAACACAGAAAGCAT 2120
Qy 2125 TTTGTACGCCCTTTTCATGAAAGCTGGGGAATGTGGGGCCCTTGGGGAGCTGTTTCGAGA 2184
Db 2121 TTTGTACGCCCTTTTCATGAAAGCTGGGGAATGTGGGGCCCTTGGGGAGCTGTTTCGAGA 2180
Qy 2185 AGTGGGTGGAGGAGTCCAGTACAGATGAGGGAATGTGACAAACCCAGTCCCAAGAT 2244
Db 2181 AGTGGGTGGAGGAGTCCAGTACAGATGAGGGAATGTGACAAACCCAGTCCCAAGAT 2240
Qy 2245 GGAGGGAAGTACTGTGAAGGCCAAACAGTGCCTACAGATCTGTAACTTCAGGACTGT 2304
Db 2241 GGAGGGAAGTACTGTGAAGGCCAAACAGTGCCTACAGATCTGTAACTTCAGGACTGT 2300
Qy 2305 CCAGACAATTAATGGAAAAACCTTTAGAGAGGAACAATGTGAAGCACAACAACGAGTTTCA 2364
Db 2301 CCAGACAATTAATGGAAAAACCTTTAGAGAGGAACAATGTGAAGCACAACAACGAGTTTCA 2360
Qy 2365 AAAGCTTCTTTGGGAGTGGGCTCGGTTGGAAATGGATTTCCAGTACGCTGGCTCTCA 2424
Db 2361 AAAGCTTCTTTGGGAGTGGGCTCGGTTGGAAATGGATTTCCAGTACGCTGGCTCTCA 2420
Qy 2425 CCAAGGACAGGTGCAAGCTCATCTGCCAAGCCAAAGCATTTGGCTACTTCTCGTTTGG 2484
Db 2421 CCAAGGACAGGTGCAAGCTCATCTGCCAAGCCAAAGCATTTGGCTACTTCTCGTTTGG 2480
Qy 2485 CAGCCCAAGGTTGTAGATGGTACTCAGTGTAGCCCAAGATTTCCACCTCTGTGTGTGCAA 2544
Db 2481 CAGCCCAAGGTTGTAGATGGTACTCAGTGTAGCCCAAGATTTCCACCTCTGTGTGTGCAA 2540
Qy 2545 GGACAGTGTGTAAGCTGGTTGTGATCGCATCATAGACTCCAAAGAGTTTGTATAA 2604
Db 2541 GGACAGTGTGTAAGCTGGTTGTGATCGCATCATAGACTCCAAAGAGTTTGTATAA 2600
Qy 2605 TGTGTGTTTTCGGGGGAATGGATCTACTGTGTAAGAAATATCAGGATCAGTTACTGT 2664
Db 2601 TGTGTGTTTTCGGGGGAATGGATCTACTGTGTAAGAAATATCAGGATCAGTTACTGT 2660
Qy 2665 GCAAAACCTGGATATCATGATATCATCAAAATTCAACTGGAGCCCAACATCGAAGTG 2724
Db 2661 GCAAAACCTGGATATCATGATATCATCAAAATTCAACTGGAGCCCAACATCGAAGTG 2720

Qy 2725 AAACAGCGGAACCCAGAGGGGATCCAGGAACAATGCGAGCTTTCTTGCCATCAAAGCTGCT 2784
Db 2721 AAACAGCGGAACCCAGAGGGGATCCAGGAACAATGCGAGCTTTCTTGCCATCAAAGCTGCT 2780
Qy 2785 GATGCGACATATATTTCTTAATGGTGACTACACTTTGTCCACCTTAGAGCAAGACATTTATG 2844
Db 2781 GATGCGACATATATTTCTTAATGGTGACTACACTTTGTCCACCTTAGAGCAAGACATTTATG 2840
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Db 2841 TACAAAGGTGTTGTTCTTGAGGTACAGCGCTCTCTGCGGCAATTTGGAAGAATTTGCGAGC 2900
Qy 2905 TTTTACCCCTCTCAAGAGCCCTTGACCATCCAGGTTCTTACTGTGGCAATGCCCTTCCA 2964
Db 2901 TTTTACCCCTCTCAAGAGCCCTTGACCATCCAGGTTCTTACTGTGGCAATGCCCTTCCA 2960
Qy 2965 CTTAAATTTAAATACACCTACTTTCTGTAAGAGAAAGAAAGAAATCTTTCAATGCTATCCCC 3024
Db 2961 CTTAAATTTAAATACACCTACTTTCTGTAAGAGAAAGAAAGAAATCTTTCAATGCTATCCCC 3020
Qy 3025 ACTTTTTCAGCATGGGTCAATTTGAAGTGGGCGCAATGTTCTAAGTCATGTGAATTTGGGT 3084
Db 3021 ACTTTTTCAGCATGGGTCAATTTGAAGTGGGCGCAATGTTCTAAGTCATGTGAATTTGGGT 3080
Qy 3085 TGGCAGAGAACTGTTAGAAATGCCAGACATTAATGGACAGCCTGCTTCCAGGTGTGCA 3144
Db 3081 TGGCAGAGAACTGTTAGAAATGCCAGACATTAATGGACAGCCTGCTTCCAGGTGTGCA 3140
Qy 3145 AAGGAAGTGAAGCCAGCCAGCACAGACTGTTGTGAGACACCATCCCTGCCCCAGTGGCAG 3204
Db 3141 AAGGAAGTGAAGCCAGCCAGCCAGCACAGACTGTTGTGAGACACCATCCCTGCCCCAGTGGCAG 3200
Qy 3205 CTGGGGAGTGTCTCATGTTCTAAGACCTGTGGGAAGGGTTTACAAAAACAAGCTTG 3264
Db 3201 CTGGGGAGTGTCTCATGTTCTAAGACCTGTGGGAAGGGTTTACAAAAACAAGCTTG 3260
Qy 3265 AAGTCTCTGCCATGATGGAGGGTGTATCTCATGACAGCTGTATGATCTTTAAAGAAA 3324
Db 3261 AAGTCTCTGCCATGATGGAGGGTGTATCTCATGAGAGCTGTATGATCTTTAAAGAAA 3320
Qy 3325 CTTAAACATTTTCATAGACTTTTTCACAATGGCAGAAATGAGTTAAGTGGTTTAAAGTGTG 3384
Db 3321 CTTAAACATTTTCATAGACTTTTTCACAATGGCAGAAATGAGTTAAGTGGTTTAAAGTGTG 3380
Qy 3385 TTAGCTTTGAGGGCAAGGCAAAAGTGAAGAGGGCTGTGTCAGGGAAGCAAGAGCTGG 3444
Db 3381 TTAGCTTTGAGGGCAAGGCAAAAGTGAAGAGGGCTGTGTCAGGGAAGCAAGAGCTGG 3440
Qy 3445 AGGGATCCAGCGTATCTTCCAGTAAACAGTGAAGTGTATCAGTAAGTGGGATTTATGG 3504
Db 3441 AGGGATCCAGCGTATCTTCCAGTAAACAGTGAAGTGTATCAGTAAGTGGGATTTATGG 3500
Qy 3505 GGTAGATGAAAGAGGTTGAATCATCAGAGTAAACTGTCAGTTGCAAAATTTGATAGAT 3564
Db 3501 GGTAGATGAAAGAGGTTGAATCATCAGAGTAAACTGTCAGTTGCAAAATTTGATAGAT 3560
Qy 3565 AGTTAGTGAGGATTAATTAACCTCTGAGCAGTGAATAGCATTAATTAAGCCCCGGGCAATTA 3624
Db 3561 AGTTAGTGAGGATTAATTAACCTCTGAGCAGTGAATAGCATTAATTAAGCCCCGGGCAATTA 3620
Qy 3625 TTATTTATTTCTTTTGTGTATCTATTAAGTTTGAAGAAAAACAAGCAATTTGTCAA 3684
Db 3621 TTATTTATTTCTTTTGTGTATCTATTAAGTTTGAAGAAAAACAAGCAATTTGTCAA 3680
Qy 3685 AAAAAAGTTAGAACTATTACACCCCTGCTTCTGCTACTTATCAAAATCTTAGTATCATG 3744
Db 3681 AAAAAAGTTAGAACTATTACACCCCTGCTTCTGCTACTTATCAAAATCTTAGTATCATG 3740
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Db 3741 GGGGTTGGGAATGAAAGTAGGAGAAAAGTGAGATTTTACTAAGACCTGTTTTACTTTA 3800

Qy 3805 CCTCACTAA 3813
Db 3801 CCTCACTAA 3809

RESULT 13

US-10-210-120-57

: Sequence 57, Application US/10210120

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: GENERAL INFORMATION:

: APPLICANT: Chinnaiyan, Arul M.

: APPLICANT: Rubin Mark A.

APPLICANT: RUDITH, MARK A.
APPLICANT: Sreekumar Arun

APPLICANT: SREEKUMAR, ARUN
TITLE OF INVENTION: Expression Profile of Prostate Cancer

FILE OF INVENTION: EXPLO
FILE REFERENCE: UM-07221

FILE REFERENCE: UM-0721
CURRENT APPLICATION NUMBER: IIS/10/210.120

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 ;
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; NUMBER OF SEQ ID NOS: 123

; SOFTWARE: Pa

; SEQ ID NO 57

; LENGTH: 4309

; TYPE: DNA

; ORGANISM: HOM

Query Match 60.9%; Score 2443; DB 16; Length 4309;

Query match	00.50;	00.50;
Best Local Similarity	99.48;	99.48;
Best Local Similarity	99.48;	99.48;
pred. No. 0;	pred. No. 0;	pred. No. 0;

BEST LOCAL SIMILARITY 55.4%, FREQ. NO: 0,
 Matches 3443: Conservative 0: Mismatches 20: Indels 0: Gaps 0:

351	Qy	TAGNAATTGTTAAATTTTAA	CNAATCCAGAGCAGGCAACGAGGCTTTCCTCTCCCGACCCG	410
1	Db	TAGAAATTTGTTAAATTTTAA	CAATCCAGAGCAGGCAACGAGGCTTTCCTCTCCCGACCCG	60
411	Qy	AACTAAAGCTCCCTCGCTCCGTC	CGCTGCTACAGAGCGGTCTCCTCGGGCTCCAAATGCA	470
61	Db	AACTTAAAGGTCCTTCGCTCCGTC	CGCTGCTACAGAGCGGTCTCCTCGGGCTCCAAATGCA	120
471	Qy	GCAGAGCTGTGCGCCGAGGGGTT	CGAAGCGCAAGCTGGGCAAGCAATATGGGAAACGGCGGA	530
121	Db	GCAGAGCTGTGCGCCGAGGGGTT	CGAAGCGCAAGCTGGGCAAGCAATATGGGAAACGGCGGA	180
531	Qy	CGGGGCTCCGGGGTCTCGGAGCT	TTGGGCCCGTACCCACGCTGTGCTCTCGCGCGCGGC	590
181	Db	CGGGGCTCCGGGGTCTCGGAGCT	TTGGGCCCGTACCCACGCTGTGCTCTCGCGCGCGGC	240
591	Qy	GCTACTCGCGGTGTCGGAACGCA	CTCGGCGGCCCTCCGAGGAGGACGAGAGCTAGTGGT	650
241	Db	GCTACTCGCGGTGTCGGAACGCA	CTCGGCGGCCCTCCGAGGAGGACGAGAGCTAGTGGT	300
651	Qy	GCCGGAGCTGAGGCGGCTCCGGG	ACACGGGACCAAGCGCTTCGCTGCAAGCGCTTTTGA	710
301	Db	GCCGGAGCTGAGGCGGCGCCCG	GAGACACGGGACCAAGCGCTTCGCTGCAAGCGCTTTTGA	360
711	Qy	CCAGCAGCTGGAATCTGGAGCTG	CGCCCGCACAGCAGCTTTTGGGCGCCCGGCTTCACGCT	770
361	Db	CCAGCAGCTGGAATCTGGAGCTG	CGCCCGCACAGCAGCTTTTGGGCGCCCGGCTTCACGCT	420
771	Qy	CCAGAACTGGGGCGCAAACTCGG	GTCCGACACCCCGCTTCGGGAAACCGACCTTGGCGCA	830
421	Db	CCAGAACTGGGGCGCAAACTCGG	GTCCGACACCCCGCTTCGGGAAACCGACCTTGGCGCA	480
831	Qy	CTGCTTTCTACTCCGCGCACCG	GTGAATGGCGAATCCAGCTCGGCTGCGGCCCTCAGCCTCTG	890
481	Db	CTGCTTTCTACTCCGCGCACCG	GTGAATGGCGAATCCAGCTCGGCTGCGGCCCTCAGCCTCTG	540
891	Qy	CGAGGGCGGTGCGCGCGCTTCT	CTACTGCTGGGGGAGGCGTAATTTTCATCAGCGCGCTGCC	950
541	Db	CGAGGGCGGTGCGCGCGCTTCT	CTACTGCTGGGGGAGGCGTAATTTTCATCAGCGCGCTGCC	600

Db 1681 AACCAAACTTCCCGTGGCGGATGGCACAGCTGTGTGAGAAAGGCAATGGTATCAA 1740
QY 2091 CGGCAAGTGTGTGAACAAAAACACAGAAAGCATTTTGTATAGCCCTTTTCATGGAGCTG 2150
Db 1741 CGGCAAGTGTGTGAACAAAAACACAGAAAGCATTTTGTATAGCCCTTTTCATGGAGCTG 1800
QY 2151 GGGAAATGTGGGGCCCTTGGGGAGACTGTTTCGAGAACGTCGGGTGGAGGAGTCCAGTACAC 2210
Db 1801 GGGAAATGTGGGGCCCTTGGGGAGACTGTTTCGAGAACGTCGGGTGGAGGAGTCCAGTACAC 1860
QY 2211 GATGAGGGAATGTGAACAAACCCAGTCCCAAAGAAATGGAGGGAAGTACTGTGAAGGCCAAAGC 2270
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Db 1921 AGTGGCTACAGATCCTGTAACTTTGAGGACTGTCCAGCAATATGGAAGAAACCTTTAG 1980
QY 2331 AGAGGAACAATGTGAAGCACACAAACGAGTTTCAAAAGCTTCTTTGGGAGTGGGCTGC 2390
Db 1981 AGAGGAACAATGTGAAGCACACAAACGAGTTTCAAAAGCTTCTTTGGGAGTGGGCTGC 2040
QY 2391 GGTGGAATGGATTCACCAAGTACGCTGGCTCTCACCAAAAGGACAGGTGCAAGCTCATCTG 2450
Db 2041 GGTGGAATGGATTCACCAAGTACGCTGGCTCTCACCAAAAGGACAGGTGCAAGCTCATCTG 2100
QY 2451 CCAAGCCAAAGCATTTGGCTACTTCTTCTTTGAGGAGTGGGCTGC 2510
Db 2101 CCAAGCCAAAGCATTTGGCTACTTCTTCTTTGAGGAGTGGGCTGC 2160
QY 2511 ATGTAGCCAGATTCACCTCTGTCTGTGCAAGGACAGTGTGAAAAGCTGGTGTGA 2570
Db 2161 ATGTAGCCAGATTCACCTCTGTCTGTGCAAGGACAGTGTGAAAAGCTGGTGTGA 2220
QY 2571 TCGCATCATAGACTCCAAAAGAAAGTTTGATAAATGTGGTGTGGGGGAAAATGGATC 2630
Db 2221 TCGCATCATAGACTCCAAAAGAAAGTTTGATAAATGTGGTGTGGGGGAAAATGGATC 2280
QY 2631 TACTTTGAAAAAATATCAGGATCAGTTACTAGTGCNAACCTGGATATCATGATCAT 2690
Db 2281 TACTTTGAAAAAATATCAGGATCAGTTACTAGTGCNAACCTGGATATCATGATCAT 2340
QY 2691 CACAAATTCACCTGGAGCCACCAACATCGAAGTGAACACAGCGGAACACAGAGGGGATCCAG 2750
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QY 2751 GAACAAATGGCAGCTTCTTTGCCATCAAAAGCTGCTGATGGCAATATATTTTAAATGGTGA 2810
Db 2401 GAACAAATGGCAGCTTCTTTGCCATCAAAAGCTGCTGATGGCAATATATTTTAAATGGTGA 2460
QY 2811 CTACACTTTGTCACCTTTAGACAGACATATATGTACAAAGTGTGTCTTGAGGTACAG 2870
Db 2461 CTACACTTTGTCACCTTTAGACAGACATATATGTACAAAGTGTGTCTTGAGGTACAG 2520
QY 2871 CGGCTCTCTGGGCAATGGAAGAAATTCGAGCTTTAGCCCTCTCAAGAGCCCTTGAC 2930
Db 2521 CGGCTCTCTGGGCAATGGAAGAAATTCGAGCTTTAGCCCTCTCAAGAGCCCTTGAC 2580
QY 2931 CATCCAGGTTCTTACTGTGGCAATGCCCTTCGACCTTAAATTAATACACTTCTGT 2990
Db 2581 CATCCAGGTTCTTACTGTGGCAATGCCCTTCGACCTTAAATTAATACACTTCTGT 2640
QY 2991 AAAGAGAGAGAGGAATCTTTCAATGCTATCCCACTTTTTCAGCATGGGTCAATGAAGA 3050
Db 2641 AAAGAGAGAGAGGAATCTTTCAATGCTATCCCACTTTTTCAGCATGGGTCAATGAAGA 2700
QY 3051 GTGGGCGGAATGTCTTAAGTCAATGTGAATGGTGGCAGAGAAGACTGTTAGAAATCGCG 3110
Db 2701 GTGGGCGGAATGTCTTAAGTCAATGTGAATGGTGGCAGAGAAGACTGTTAGAAATCGCG 2760
QY 3111 AGACATTAATGACAGCTGCTTCCAGTGTGCAAGGAAGTGAAGCCAGCCAGCACCCAG 3170

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QY 3231 GACCTGTGGGAGGTTTACAAAAACAAGCTTTGAAGTGTCTGTGCCATGATGGAGGGT 3290
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QY 3291 GTTATCTCATGACAGCTGTGATCCTTTAAAGAAACCTTAAACAATTTTCATAGACTTTTGCAC 3350
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Db 3061 GGAAGGGCTGTGTCAGGGGAAAGCAAGAGGCTTGGAGGATCCAGGCTATCTTCCAGTAA 3120
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RESULT 14

US-09-373-658-1
; Sequence 1, Application US/09373658
; Publication No. US20030092900A1
; GENERAL INFORMATION:
; APPLICANT: Iruela-Arispe, Luisa
; APPLICANT: Hastings, Gregg A.
; APPLICANT: Ruben, Steven M.
; APPLICANT: Jonak, Zdenka L.
; APPLICANT: Trulli, Stephen H.
; APPLICANT: Fronwald, James A.
; APPLICANT: Terrett, Jonathan A.
; TITLE OF INVENTION: Meth1 and Meth2 Polynucleotides and Polypeptides
; FILE REFERENCE: 1488.107006
; CURRENT APPLICATION NUMBER: US/09/373,658
; CURRENT FILING DATE: 1999-08-13
; NUMBER OF SEQ ID NOS: 125
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 1
; LENGTH: 3261
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(2853)
; NAME/KEY: UNSURE

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Db 2269 GATGGCACATATATCTTAATGGTGACATACATTTGTGTCACCTTGTGACCAAGACATATATG 2328
QY 2845 TACAAAGGTGTTGCTTGAAGGTACAGCGCTCTCTGCGGCATTCGAAAGAAATTCGCAGC 2904
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RESULT 15

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US-09-989-687-1
; Sequence 1, Application US/09989687
; Publication No. US20040002449A1
; GENERAL INFORMATION:
; APPLICANT: Hastings, Gregg A.
; APPLICANT: Ruben, Steven M.
; TITLE OF INVENTION: Meth1 and Meth2 Polynucleotides and Polypeptides
; FILE REFERENCE: 1488.107000D
; CURRENT APPLICATION NUMBER: US/09/989,687
; CURRENT FILING DATE: 2001-11-21
; NUMBER OF SEQ ID NOS: 126
; SOFTWARE: PatentIn Ver. 2.0
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; ORGANISM: Homo sapiens
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; LOCATION: (1)..(2853)
; NAME/KEY: misc feature
; LOCATION: (3195)
; OTHER INFORMATION: n is any nucleic acid
; NAME/KEY: misc feature
; LOCATION: (3248)
; OTHER INFORMATION: n is any nucleic acid
; NAME/KEY: misc feature
; LOCATION: (3255)
; OTHER INFORMATION: n is any nucleic acid
; NAME/KEY: misc feature
; LOCATION: (3261)
; OTHER INFORMATION: n is any nucleic acid
US-09-989-687-1
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Db 649 CCGGCACCTGCAAGGCGTAGGACAGCCACAGGAACCTGGAAGCATAGAAAGAGCGATT 708
QY 1225 GTGTCAGTCAACCGCTATGTGAAACCAATGTTGTGGCAGACCACTGCGATGCGAAATTC 1284
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QY	1585	GATGTTGGAACCTGTGTGTGATCCGAGCAGAGAGTGTCTCGTCAATAGAGATGATGTTTA	1644
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QY	1645	CAAGCTGCCCTTACACAGCCCATGATTAATAGGCACTGTGTTTAAATGCCACATGATGAT	1704
Db	1129	CAAGCTGCCCTTACACAGCCCATGATTAATAGGCACTGTGTTTAAATGCCACATGATGAT	1188
QY	1705	GCAAAGCAGTGTCCAGCCCTTAATGTTGTAACACAGGATTTCCACATGATGGCGTCAATG	1764
Db	1189	GCAAAGCAGTGTCCAGCCCTTAATGTTGTAACACAGGATTTCCACATGATGGCGTCAATG	1248
QY	1765	CTTTCCAACTGTGACACAGCCAGCTTGTCTCTTGCAGTGGCTACATGATACATCA	1824
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QY	1825	TTTCTCGATAATGTCATGCGGAATGTTTGAATGCAAGCTCAGAAATCCCATACAGCTC	1884
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QY	1885	CCAGGCGATCTCCCTGGCACTCGTACGATGCCAACCAGGAGTCCAGTTTTACATTTGGG	1944
Db	1369	CCAGGCGATCTCCCTGGCACTCGTACGATGCCAACCAGGAGTCCAGTTTTACATTTGGG	1428
QY	1945	GAGGACTCCAAAACCTGCCCTGATGACGACGACATGTATAGCACTTGTGTGGTACCGGC	2004
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QY	2005	ACCTCTGTTGGGTGTGTGTGTCTCAACCAACACATTTCCCTGGGCGGATGACCCAGC	2064
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Db	1969	CAGCCCAAGGTTGTAGATGGTACTCCATGTAGCCCAAGATTCACCTCTGTCTGTGTGCAA	2028
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QY	2605	TGTGGTGTGTTGGGGGGAATGGATCTACTTTGTAATAAAAAATATCAGGATCAGTTACTAGT	2664

Db	2089	TGTGGTGTGTTGGGGGGAATGGATCTACTTGTATAAAAAATATCAGGATCAGTTACTAGT	2148
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Db	2149	GCAAAACCTGGATATCATGATATCATCAATATTCACAACTGGAGCCACCAACATCGAAGTG	2208
QY	2725	AAACAGCGGAAACAGAGGGGATCCAGGAACAATGCGAGCTTTCTTGCCCATCAAGCTGCT	2784
Db	2209	AAACAGCGGAAACAGAGGGGATCCAGGAACAATGCGAGCTTTCTTGCCCATCAAGCTGCT	2268
QY	2785	GATGGCACAATATTTCTTAATGTTGACTACACTTTGTCCACCTTAGAGCAAGACATTTATG	2844
Db	2269	GATGGCACAATATTTCTTAATGTTGACTACACTTTGTCCACCTTAGAGCAAGACATTTATG	2328
QY	2845	TACAAAGTGTGTTCTTGTGAGGTACAGCGCTCTCTGCGGCAATGGAAAGAAATTCGCAGC	2904
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QY	2905	TTTAGCCCTCTCAAAGAGCCCTTGAACCATCCAGGTTCTTACTGTGGGCAATGCCCTTCGA	2964
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Db	2449	CTTAAATTAATTAACACCTACTTCTGTAAGAAGAGAGGAATCTTTCAATGCTATCCCC	2508
QY	3025	ACTTTTTCAGCATGGTCTCAATGAAAGAGTGGGGCGAATGTTCTAAGTCATGTGAATTTGGGT	3084
Db	2509	ACTTTTTCAGCATGGTCTCAATGAAAGAGTGGGGCGAATGTTCTAAGTCATGTGAATTTGGGT	2568
QY	3085	TGSCAGAGAGACTGTGTAGAAATCCGAGACATTAATGGAAGAGCTGTCCGAGTGTGCA	3144
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QY	3145	AAGGAAGTGAAGCCAGCAGCACAGACCTTGTGCAAGCCATCCCTGCCCCAGTGGCAG	3204
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Db	2809	CCTAAACATTTTCATAGACTTTTGCACAAATGGCAGAAATGCAAGTTAAGTGGTTAAGTGGTG	2868
QY	3385	TTAGCTTTGAGGGCAAGGCAAGTGAAGAGGGCTGTGTGAGGAAAGCAAGAGGCTGG	3444
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GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: May 23, 2005, 18:53:57 ; Search time 381 Seconds
(without alignments)

4152.965 Million cell updates/sec

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Perfect score: 5287

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Ygapop 10.0 , Ygapext 0.5
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Searched: 1202784 seqs, 818138359 residues

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Database :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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2	5230	98.9	3889	4	US-09-568-559-1
3	5219	98.7	4858	3	US-09-392-184-1
4	4262	80.6	3706	3	US-09-484-970B-58
5	3922	74.2	2184	4	US-09-445-023A-2
6	3652	69.1	2184	4	US-09-445-023A-13
7	2472	46.8	2853	4	US-10-009-332-2
8	2271.5	43.0	3638	3	US-09-369-364A-8
9	2165	40.9	3126	3	US-09-392-184-7
10	2156	40.8	4192	3	US-09-132-126B-1
11	2156	40.8	4192	4	US-09-634-286A-1
12	2156	40.8	4192	4	US-10-247-685-1

13	1926.5	36.4	3250	3	US-09-122-126B-14	Sequence 14, Appl
14	1926.5	36.4	3250	4	US-09-634-286A-14	Sequence 14, Appl
15	1926.5	36.4	3250	4	US-10-247-685-14	Sequence 14, Appl
16	1909.5	36.1	3002	3	US-09-369-364A-1	Sequence 1, Appl
17	1751.5	33.1	5804	3	US-09-369-364A-12	Sequence 12, Appl
18	1613	30.5	2825	3	US-09-369-364A-14	Sequence 14, Appl
19	1608.5	30.4	6659	4	US-09-321-987B-1	Sequence 1, Appl
20	1406	26.6	2114	3	US-09-130-491-7	Sequence 7, Appl
21	1333.5	25.2	5357	3	US-09-392-184-5	Sequence 5, Appl
22	1295	24.5	3377	4	US-09-981-953A-3	Sequence 3, Appl
23	1293	24.5	3571	4	US-09-799-451-411	Sequence 411, Appl
24	1278.5	24.2	3675	3	US-09-930-872-3	Sequence 3, Appl
25	1278.5	24.2	3675	4	US-10-217-774-3	Sequence 3, Appl
26	1278.5	24.2	4042	3	US-09-930-872-5	Sequence 5, Appl
27	1278.5	24.2	4042	4	US-10-217-774-5	Sequence 1, Appl
28	1270	24.0	3766	4	US-09-981-953A-1	Sequence 1, Appl
29	1217	23.0	3218	3	US-09-369-364A-6	Sequence 6, Appl
30	1214.5	23.0	2727	4	US-09-963-791-1	Sequence 1, Appl
31	1203	22.8	3885	3	US-09-369-364A-16	Sequence 16, Appl
32	1151.5	21.8	2274	4	US-09-963-791-23	Sequence 23, Appl
33	1112	21.0	3636	4	US-09-949-016-5530	Sequence 5530, Ap
34	1112	21.0	6692	3	US-09-491-522-1	Sequence 1, Appl
35	1096	20.7	4580	3	US-09-491-522-8	Sequence 8, Appl
36	1066.5	20.2	3860	4	US-09-963-791-25	Sequence 25, Appl
37	1040.5	19.7	1520	3	US-09-369-364A-3	Sequence 3, Appl
38	1038.5	19.6	2848	3	US-09-369-364A-4	Sequence 4, Appl
39	1003.5	19.0	3158	4	US-09-949-016-1988	Sequence 1988, Ap
40	950.5	18.0	2450	3	US-09-491-522-2	Sequence 2, Appl
41	949.5	18.0	2450	3	US-09-491-522-9	Sequence 9, Appl
42	781	14.8	1770	4	US-09-963-791-11	Sequence 11, Appl
43	718	13.6	1317	4	US-09-963-791-21	Sequence 21, Appl
44	712.5	13.5	739	3	US-09-369-364A-10	Sequence 10, Appl
45	607.5	11.5	703	3	US-09-392-184-6	Sequence 6, Appl

ALIGNMENTS

RESULT 1

US-09-130-491-1
Sequence 1, Application US/09130491
Patent No. 6416974
GENERAL INFORMATION:
APPLICANT: Holtzman, Douglas A.
APPLICANT: Goodearl, Andrew D.J.
TITLE OF INVENTION: TANGO-71, TANGO-73, TANGO-74, TANGO-76, AND TANGO-83
FILE REFERENCE: 09404/041001
CURRENT APPLICATION NUMBER: US/09/130,491
EARLIER FILING DATE: 1998-08-07
EARLIER FILING DATE: 1997-09-05
EARLIER FILING DATE: 1997-08-06
NUMBER OF SEQ ID NOS: 16
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 1
LENGTH: 4676
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (460)...(3360)
US-09-130-491-1

Alignment Scores:
Pred. No.: 0
Score: 5232.00
Percent Similarity: 99.38%
Best Local Similarity: 98.97%
Query Match: 98.96%
DB: 3
Length: 4676
Matches: 957
Conservative: 4
Mismatch: 6
Indels: 0
Gaps: 0

US-09-373-658C-126 (1-967) x US-09-130-491-1 (1-4676)

QY 1 MetGlnArgAlaValProGluGlyPheGlyArgGlyLeuGlySerAspMetGlyAsn 20
DB 460 ATGCAAGCGAGCTGTGCCGAGGGGTTCCGAAGCGCAGCTGGGACGACATGGGGAC 519
QY 21 AlaGluArgAlaProGlySerArgSerPheGlyProValProThrLeuLeuLeuAla 40
DB 520 GCGGAGCGGGCTCCGGGGTCTCGGAGCTTTGGGCGGTACCCACGCTGCTGCTCGCC 579
QY 41 AlaAlaLeuLeuAlaValSerAspAlaLeuGlyArgProSerGluGluAspGluLeu 60
DB 580 GCGGGGCTACTGGCGGTGTGCGAGCGACTTCGGGCGCCCTCCGAGGAGACGAGAGCTA 639
QY 61 ValValProGluLeuGluArgValProGlyHisGlyThrThrArgLeuArgLeuHisAla 80
DB 640 GTGGTCCCGGAGCTGAGGCGCCCGCGGACACGGACCCAGCGCTCCCGCTGACAGCC 699
QY 81 PheAspGlnGlnLeuAspLeuAspValProProAspSerSerPheLeuAlaProGlyPhe 100
DB 700 TTTGACGACGCTGGATCTGGAGCTGGCGGCCGCGACAGCAGCTTTTGGCGCGCGCTTC 759
QY 101 ThrLeuGlnAsnValGlyArgLysSerGlySerAspThrProLeuProGluThrAspLeu 120
DB 760 ACGCTCCGAACGTGGGGCGCAATCCGGGTCCGAGACCGCGCTTCGGGAACCGACCTG 819
QY 121 AlaHisCysPheTyrSerGlyThrValAsnGlyAspProSerSerAlaAlaAlaLeuSer 140
DB 820 GCGCACTGTTCTACTCCGGCACCGTGATGGGATCCGAGCTCGGCTCCGCCCTCAGC 879
QY 141 LeuCysGluGlyValArgGlyAlaPheTyrLeuLeuGlyGluAlaTyrPheIleGlnPro 160
DB 880 CTCGCGAGGCGGTGCGCGCGCTTCTACCTGCTGGGGGAGCGGTATTTCATCCAGCG 939
QY 161 LeuProAlaAlaSerGluArgLeuAlaThrAlaAlaProGlyGluLysProProAlaPro 180
DB 940 CTGCGCGCGCGAGCGAGCGCTCGCCACCGCGCGCCCGCGAGGAGCGCGCGCACCA 999
QY 181 LeuGlnPheHisLeuLeuArgArgAsnArgGlnGlyAspValGlyGlyThrCysGlyVal 200
DB 1000 CTACAGTTCACCTCTCGCGGGGATTCGGGAGGGCGAGTGGCGGACGTGCGGGGTC 1059
QY 201 ValAspAspGluProArgProThrGlyLysAlaGluThrGluAspGluAspGluGlyThr 220
DB 1060 GTGGACGACGACCGCGCGGCTCGGAAAGCGGAGACCGCAAGACGAGGAGGACT 1119
QY 221 GluGlyGluAspGluGlyProGlnTrpSerProGlnAspProAlaLeuGlnGlyValGly 240
DB 1120 GAGGGCGAGGACGAAGGGCTTCAGTGGTCCGCGCAGGACCCGCGACTGCAAGGCGTAGGA 1179
QY 241 GlnProThrGlyThrGlySerIleArgLysLysArgPheValSerSerHisArgTyrVal 260
DB 1180 CAGCCCAAGGAACCTGGAAAGCATAGAAAGAACCGATTTGTTCAGTCCCGCTATGTG 1239
QY 261 GluThrMetLeuValAlaAspGlnSerMetAlaGluPheHisGlySerGlyLeuLysHis 280
DB 1240 GAAACCATCTTGTGGCAGACCACTCGATGGCAGAAATCCACGGCAGTGGTCTAAGACAT 1299
QY 281 TyrLeuLeuThrLeuPheSerValAlaAlaArgLeuTyrLysHisProSerIleArgAsn 300
DB 1300 TACCTTCTCACGTGTTTTTGGTGGCAGCCAGATTGTACAAACACCCCGCAGCATTCGTAAT 1359
QY 301 SerValSerLeuValValLysIleLeuValIleHisAspGluGlnLysGlyProGlu 320
DB 1360 TCAGTTAGCTGTGTGTGAGATCTTTGGTTCATCCAGATGAAAGGGGGCGGAA 1419
QY 321 ValThrSerAsnAlaAlaLeuThrLeuArgAsnPheCysAsnTrpGlnLysGlnHisAsn 340
DB 1420 GTGACCTCCATGCTGCCCTCACTCGCGAACTTTTGGCAACTGGCAGAGCAGCACAAAC 1479
QY 341 ProProSerAspArgAspAlaGluHisTyrAspThrAlaIleLeuPheThrArgGlnAsp 360
DB 1480 CCACCCAGTGACCGGATCAGAGCACTATGACACAGCAATTTCTTTTCCACGACAGGAC 1539
QY 361 LeuCysGlySerGlnThrCysAspThrThrLeuGlyMetAlaAspValGlyThrValCysAsp 380

DB 1540 TTGTGTGGGTCCGACCATGTGATACTCTTGGATGGCTGATGTTGGAACCTGTGTGTGAT 1599
QY 381 ProSerArgSerCysSerValIleGluAspAspGlyLeuGlnAlaAlaPheThrThrAla 400
DB 1600 CCGAGCAGAAGCTGCTCCGTCTATAGAAGATGATGTTTACAAGCTGCCCTTCCACGAGC 1659
QY 401 HisGluLeuGlyHisValPheAsnMetProHisAspAspAlaLysGlnCysAlaSerLeu 420
DB 1660 CATGAATTAGGCCACCGTGTTTAACTGCCACATGATGATGCAAGCAGTGTGCCAGCCTT 1719
QY 421 AsnGlyValAsnGlnAspSerHisMetMetAlaSerMetLeuSerAsnLeuAspHisSer 440
DB 1720 AATGTTGTGAACGAGATTCCACATGATGGCGTCAATGCTTTCCAACTCGACACAGC 1779
QY 441 GlnProTrpSerProCysSerGlyTyrMetIleThrSerPheLeuAspAsnGlyHisGly 460
DB 1780 CAGCCTTGGTCTCTCTTGCAGTGCCTACATGATTACATCATTTCTGGATAAATGTCATGG 1839
QY 461 GluCysLeuMetAspLysProGlnAsnProIleGlnLeuProGlyAspLeuProGlyThr 480
DB 1840 GAATGTTTGTATGGACAGGCTCAGAAATCCATACAGCTCCGAGGCAATCTCCTGGCACC 1899
QY 481 SerTyrAspAlaAsnArgGlnCysGlnPheThrPheGlyGluAspSerLysHisCysPro 500
DB 1900 TCGTACGATGCCAACCGGCGAGTCCAGTTTACATTTGGGGAGGACTCCAAACACTGCCCC 1959
QY 501 AspAlaAlaSerThrCysSerThrLeuTrpCysThrGlyThrSerGlyGlyValLeuVal 520
DB 1960 GATGCGAGCAGCACATGTAGCACCTTGTGTGTATCCGGCACCCTCTGGTGGGGTGTGGT 2019
QY 521 CysGlnThrLysHisPheProTrpAlaAspGlyThrSerCysGlyGluGlyLysTrpCys 540
DB 2020 TGTCAAAACCAACACTTCCCGTGGCGGATGGCACCAAGCTGTGGAGAGGGAATGCTGT 2079
QY 541 IleAsnGlyLysCysValAsnLysAsnHisArgLysHisPheAspThrProPheHisGly 560
DB 2080 ATCAACGCGCAAGTGTGTGAACAAACCGACAGAAAGCATTTTGTATACGCTTTTCATGA 2139
QY 561 SerTrpGlyMetTrpGlyProTrpGlyAspCysSerArgThrCysGlyGlyValGln 580
DB 2140 AGCTGGGAATGTGGGGCTTTGGGGAGACTGTTCCAGAACCTGGCGGTGGAGAGTCCAG 2199
QY 581 TyrThrMetArgGluCysAspAsnProValProLysAsnGlyLysLysTyrCysGluGly 600
DB 2200 TACACGATGAGGAATGTGACAAACCGCTCCCAAGAAATGGAGGAGTACTGTGAAGC 2259
QY 601 LysArgValArgTyrArgSerCysAsnLeuGluAspCysProAspAsnAsnGlyLysThr 620
DB 2260 AAACGAGTGGCTACAGATCTCTGTAACCTTGAGGACTGTCCAGACAAATAATGGAAAAAC 2319
QY 621 PheArgGluGluGlnCysGluAlaHisAsnGluPheSerLysAlaSerPheGlySerGly 640
DB 2320 TTTAGAGAGGAACAATGTGAAGCACACACGAGTTTTCAAAAGCTTCTTTGGGAGTGG 2379
QY 641 ProAlaValGluTrpIleProLysTyrAlaGlyValSerProLysAspArgCysLysLeu 660
DB 2380 CTTGGGTGGAATGATTTCCCAAGTACGCTGGCTCTCAACAAAGGACAGGTGCAAGCTC 2439
QY 661 IleCysGlnAlaLysGlyIleGlyTyrPhePheValLeuGlnProLysValValAspGly 680
DB 2440 ATCTGCCAAGCAAAAGGCAATGGCTACTTCTTCTGTTTTCAGCCCAAGGTTGTAGATGT 2499
QY 681 ThrProCysSerProAspSerThrSerValCysValGlnGlyCysValLysAlaGly 700
DB 2500 ACTCATGTAGCCCAAGATTCCACCTCTGTCTGTGTGCAAGGACAGGTGTAAAGCTGGT 2559
QY 701 CysAspArgIleIleAspSerLysLysLysPheAspLysCysGlyValCysGlyGlyAsn 720
DB 2560 TGTGATCGCATATAGACTCCAAAGAAAGTTTGTATAATGTGTGTGTTCGGGGGAAAT 2619
QY 721 GlySerThrCysGlyLysLysSerGlySerValThrSerAlaLysProGlyTyrHisAsp 740

Db 2620 GGATCTACTTTGTAATAAATAATCATGAGTACGATTTACTAGTGCACAAACCTGGATATCATGAT 2679
Qy 741 IletleThrileProThrGlyValaThrAsnilleGluVallysGlnArgAsnGlnArgGly 760
Db 2680 ATCATCAATTCNACTGGAGCCACCAACATCGAAGTGAACACGCGAACCAGAGGGGA 2739
Qy 761 SetArganhenGlySerPheLeuAlaileLysAlaaleAspGlyThrlyrileLeuAsn 780
Db 2740 TCCAGGAACAATGGCAGCTTCTTGCCATCAAGCTGCTGATGGCACATATATCTTAAT 2799
Qy 781 GlyAspTyrThrLeuSerThrLeuGluClnAspileMetTyrLysGlyValValLeuArg 800
Db 2800 GGTGACTACACTTTGTCCACCTTAGACCAAGACATATATGACAAAGGTGTGTCTTGAG 2859
Qy 801 TyrSerGlySerSerAlaAlaLeuGluArgLearSerPheSerProLeuLysGluPro 820
Db 2860 TACAGCGGCTCCTCTGGGCANATTGGAAGAATTCGAGCTTTAGCCCTCTCAAGAGACCC 2919
Qy 821 LeuThrileGlnValLeuThrValGlyAsnAlaLeuArgProLysilleLysTyrThrTyr 840
Db 2920 TTGACCATCCAGGTTCCTTACTGTGGCAATGCCCTTCGACCTAAATTTAAATACACCTAC 2979
Qy 841 PheVallysLysLysLysGluSerPheAsnAlaileProThrPheSerAlaTrpValile 860
Db 2980 TTCGTAAGAAGAAGAGGAATCTTCAATGCTATCCCACTTTTTCAGCATGGGTCAAT 3039
Qy 861 GluGluTrpGlyGluCysSerLysSerCysGluLeuGlyTrpGlnArgArgLeuValGlu 880
Db 3040 GAAGAGTGGGCGAATGTTCTAAGTCATGTGAATGGTTGGCAGAGAACTGGTAGAA 3099
Qy 881 CysArgAspileAsnGlyGlnProAlaSerGluCysAlaLysGluValLysProAlaSer 900
Db 3100 TGCCGAGACATTAATGACAGCCTGCTCCGAGTGTGCAAGGAAGTGAAGCCAGCCAGC 3159
Qy 901 ThrArgProCysAlaAspHisProCysProGlnTrpGlnLeuGlyGluTrpSerSerCys 920
Db 3160 ACCAGACTTGTGCAGACCATCCCTGCCCGCCAGTGGCAGCTGGGGAGTGTGCATCATGT 3219
Qy 921 SerLysThrCysGlyLysGlyTyrLysLysThrSerLeuLysCysLeuSerHisAspPhe 940
Db 3220 TCTAAGACCTGTGGGAAGGGTACAAAGAAAGAGCTTGAAGTGTCTGTCCATGATGGA 3279
Qy 941 GlyValLeuSerHisAspSerCysAspProLeuLysLysProLysHisPheileAspPhe 960
Db 3280 GGGGTGTATCTCATGAGAGCTGTGATCCITTAAGAAACCTTAACATTTTCATAGACTTT 3339
Qy 961 CysThrMetAlaGluCysSer 967
Db 3340 TGCAATGGCAGATGCAGT 3360

RESULT 2

US-09-568-559-1
; Sequence 1, Application US/09568559
; Patent No. 6649377
; GENERAL INFORMATION:
; APPLICANT: Klonowski, Paul
; APPLICANT: Allard, John
; APPLICANT: Heller, Renu
; APPLICANT: Van Wart, Harold
; TITLE OF INVENTION: Human Aggrecanase and Nucleic Acid
; TITLE OF INVENTION: Compositions Encoding the Same
; FILE REFERENCE: ROCH-002
; CURRENT APPLICATION NUMBER: US/09/568,559
; CURRENT FILING DATE: 2000-05-09
; PRIOR APPLICATION NUMBER: 60/133,343
; PRIOR FILING DATE: 1999-05-10
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 3889
; TYPE: DNA
; ORGANISM: human
US-09-568-559-1

Alignment Scores:

Pred. No.: 0 Length: 3889
Score: 5230.00 Matches: 956
Percent Similarity: 99.38% Conservatives: 5
Best Local Similarity: 98.86% Mismatches: 6
Query Match: 98.92% Indels: 0
DB: 4 Gaps: 0

US-09-373-658C-126 (11-967) x US-09-568-559-1 (11-3889)

Qy 1 MetGlnArgAlaValProGluGlyPheGlyArgArgLysLysLeuGlySerAspMetGlyAsn 20
Db 8 ATGCAGCGATCTGTGCCCGAGGGGTTTCGAAGCGCGAAGCTGGCGACGACATATGGGGAAC 67
Qy 21 AlaGluArgAlaProGlySerArgSerPheGlyProValProThrLeuLeuLeuAla 40
Db 68 GCGAGCGGGCTCGGGGCTCTCGAGCTTTGGGCCCTGACCCAGCTGTCTGTCTGTCTGCC 127
Qy 41 AlaAlaLeuLeuAlaValSerAspAlaLeuGlyArgProSerGluGluAspGluLeu 60
Db 128 GCGCGCTACTGGCGGTGTGCGACGCACTCGGGCGCCCTCCGAGGAGGACGAGAGCTA 187
Qy 61 ValValProGluLeuArgValProGlyHisGlyThrThrArgLeuArgLeuHisAla 80
Db 188 GTGTGCGGAGCTGGAGCGCGCCCGGAGACACGGGACACGCGCCTCCGCTGCACGCC 247
Qy 81 PheAspGlnGlnLeuAspLeuAspValProProAspSerSerPheLeuAlaProGlyPhe 100
Db 248 TTTGACGACGAGCTGGAGCTCGGGCTCGGGCCCGACAGCAGCTTTTGGGCCCGGCTTC 307
Qy 101 ThrLeuGlnAsnValGlyArgLysSerGlySerAspThrProLeuProGluThrAspLeu 120
Db 308 ACCTCCAGAACGTGGGGCGCAATCCGGGTCCGAGACGCGCTTCCGGAACCGACCTG 367
Qy 121 AlaHisCysPheTyrSerGlyThrValAsnGlyAspProSerSerAlaAlaAlaLeuSer 140
Db 368 GCGCAGCTGTCTACTCCGCGACCGTGAATGGCGATCCAGCTCGGCTCGCGCTCCAGC 427
Qy 141 LeuCysGluGlyValArgGlyAlaPheTyrLeuLeuGlyGluAlaTyrPheileGlnPro 160
Db 428 CTCTGCGAGGCGGTGCGCGCGGCTTCTACTCTGGGGGAGGGGTATTTTATCCAGCCG 487
Qy 161 LeuProAlaAlaSerGluArgLeuAlaThrAlaAlaProGlyGluLysProAlaPro 180
Db 488 CTGCCCCCGCCAGCGAGCGCTCGCCACCGCCCGCCCGAGGAGAGCGCGCGCACCA 547
Qy 181 LeuGlnPheHisLeuLeuArgArgAsnArgGlnGlyAspValGlyThrCysGlyVal 200
Db 548 CTACAGTTCACCTCTCTGCGCGGAATCGGCGAGGCGACGTCGCGCGCACGTGCGGGGTC 607
Qy 201 ValAspAspGluProArgProThrGlyLysAlaGluThrGluAspGluAspGluGlyThr 220
Db 608 GTGAGCAGCAGCGCCCGCGCTCTGGGAAAGCGGAGACCCGAAAGACGAGGAGGACT 667
Qy 221 GluGlyGluAspGluGlyProGlnTrpSerProGlnAspProAlaLeuGlnGlyValGly 240
Db 668 GAGGCGAGGACGAGGGGCTCAGTGTGCGCGCAGGACCCCGGCTGCAAGGGGTAGGA 727
Qy 241 GlnProThrGlyThrGlySerileArgLysArgPheValSerSerHisArgTyrVal 260
Db 728 CAGCCACAGGAACTGGAAGCATAAAGAGCGATTTGTGTCCAGTTCACCGCTATGTG 787
Qy 261 GluThrMetLeuValAlaAspGlnSerMetAlaGluPheHisGlySerGlyLeuLysHis 280
Db 788 GAAACCATGTTGTGGCAGACCACTGATGGCAATTCACACGCGAGTGGTCTTAAGGAT 847
Qy 281 TyrLeuLeuThrLeuPheSerValAlaAlaArgLeuTyrLysHisProSerileArgAsn 300
Db 848 TACCTTCTCAGTGTGTTTGTGGCGACCCAGATTGTACAAACACCCCGAGCATTCGTAT 907
Qy 301 SerValSerLeuValValLysileLeuValleHisAspGluGlnLysGlyProGlu 320

Db 908 TCAGTTAGCCTGGTGGTGAAGATCTTTGGTTCATCCAGATCAACAGAAAGGGCCGGAA 967
QY 321 ValThrSerAsnAlaAlaLeuThrLeuArgAsnPheCysAsnTrpGlnLysGlnHisAsn 340
Db 968 GTGACCTCAATGCTGCCCTCACTCTGCGGAATCTTTGCAACTGGCAGAGCAGCAAC 1027
QY 341 ProProSerAspArgAspAlaGluHisTyrAspThrAlaIleLeuPheThrArgGlnAsp 360
Db 1028 CCACCCAGTGACCGGATCCAGAGCCTATGACACAGCAATCTTTTCCACAGAGGAC 1087
QY 361 LeuCysGlySerGlnThrCysAspThrLeuGlyMetAlaAspValGlyThrValCysAsp 380
Db 1088 TTGTGTGGCTCCACAGATGTGATATCTCTTGGGATGGCTGATTTGGAACTGTGTGTGAT 1147
QY 381 ProSerArgSerCysSerValIleGluAspAspGlyLeuGlnAlaAlaPheThrAla 400
Db 1148 CCGAGCAGAAGCTGCTCCGTCTAGAGAATGATGGTTTACAAGCTGCCTTCCACACAGCC 1207
QY 401 HisGluLeuGlyHisValPheAsnMetProHisAspAspAlaLysGlnCysAlaSerLeu 420
Db 1208 CATGAATTAGGCCACGTGTTTAACATGCCACATGATGATGCAAGCAGTGTGCCAGCCTT 1267
QY 421 AsnGlyValAsnGlnAspSerHisMetMetAlaSerMetLeuSerAsnLeuAspHisSer 440
Db 1268 AATGTGTGAACCCAGGATTCACATGATGGCGTCAATGCTTTCCAACTGGACACACAGC 1327
QY 441 GlnProTrpSerProCysSerGlyTyrMetIleThrSerPheIleuAspAsnGlyHisGly 460
Db 1328 CAGCCTTGCTCTCCTTGGCAGTGCCTACATGATTTACATCATCTTTCTGGATTAATGGTCATGGG 1387
QY 461 GluCysLeuMetAspLysProGlnAsnProIleGlnLeuProGlyAspLeuProGlyThr 480
Db 1388 GAATGTTTATGGACAGAGCTCAGATCCATCCATACAGCTCCAGGCGATCTCCTTGGCACC 1447
QY 481 SerTyrAspAlaAsnArgGlnCysGlnPheThrPheGlyGluAspSerLysHisCysPro 500
Db 1448 TCGTACGATGCCAACCCGCGAGTGCCAGTTTACATTTGGGGAGAGCTCCAAAACACTGCCCT 1507
QY 501 AspAlaAlaSerThrCysSerThrLeuTrpCysThrGlyThrSerGlyGlyValLeuVal 520
Db 1508 GATGACGACGACACATGTATGACCTTTGTGGTGTACCGGACCTCTGTGGTGGGTGGTGGT 1567
QY 521 CysGlnThrLysHisPheProTrpAlaAspGlyThrSerCysGlyGluGlyLysTrpCys 540
Db 1568 TGTCAACCAACAACTTCCCGTGGCGGATGGCACCATGCTGTGGAGAGGAAATGGTGT 1627
QY 541 IleAsnGlyLysCysValAsnLysAsnHisArgLysHisPheAspThrProPheHisGly 560
Db 1628 ATCAACGGCAAGTGTGTGAACAAACCCACAGAAAGCATTTTGATACGGCTTTTCATGGA 1687
QY 561 SerTrpGlyMetTrpGlyProTrpGlyAspCysSerArgThrCysGlyGlyValGln 580
Db 1688 AGCTGGGGAATGTGGGGCTTTGGGAGACTGTTCAGAACGTGGCGGTGGAGAGTCCAG 1747
QY 581 TyrThrMetArgGluCysAspAsnProValProLysAsnGlyLysLysTyrCysGluGly 600
Db 1748 TACACGATGAGGGAATGTGCAACCCAGTCCCAAGAAATGGAGGAGTACTGTGNAGCC 1807
QY 601 LysArgValArgTyrArgSerCysAsnLeuGluAspCysProAspAsnAsnGlyLysThr 620
Db 1808 AAACGAGTGGCTACAGATCTGTAACTTGAACCTTGAGGACTGTCCAGACAAATTAATGGAAAAACC 1867
QY 621 PheArgGluGlnCysGluAlaHisAsnGluPheSerLysAlaSerPheGlySerGly 640
Db 1868 TTTAGAGAGGAACAATGTGAAGCACACACAGAGTTTTCAAAAGCTTCTTTGGGAGTGGG 1927
QY 641 ProAlaValGluTrpIleProLysTyrAlaGlyValSerProLysAspArgCysLysLeu 660
Db 1928 CTGCGGTGGATGGATTTCCCAAGTACGCTGGCGTCTCCAAAGACAGAGTGCAGACTC 1987
QY 661 IleCysGlnAlaLysGlyIleGlyTyrPheValLeuGlnProLysValValAspGly 680
Db 1988 ATCTGCCAAGCCAAAGGCATGGCTACTCTTCTGTTTTCAGCCCAAGGTTGTAGATGTT 2047

QY 681 ThrProCysSerProAspSerThrSerValCysValGlnGlnCysValLysValGly 700
Db 2048 ACTCCATGTAGCCCCAGATTCCACCTCTGTCTGTGTGCAAGGACAGTGTGTAAGAGTGT 2107
QY 701 CysAspArgIleIleAspSerLysLysPheAspLysCysGlyValCysGlyGlyAsn 720
Db 2108 TGTGATCGATCATAGACTCCAAAAGAAGTTTGATAATGTGTGTGTTTCCGGGGAAAT 2167
QY 721 GlySerThrCysLysLysIleSerGlySerValThrSerAlaLysProGlyTyrHisAsp 740
Db 2168 GGATCTACTTGTAAAAAATAATCAGGATCAGTTACTAGTGCAAAAACCTGGATATCATGAT 2227
QY 741 IleIleThrIleProThrGlyAlaThrAsnIleGluValLysGlnArgAsnGlnArgGly 760
Db 2228 ATCATCACAATTTCCAACTGGAGCCCAACATCGAAGTGAACAGCGGAACAGAGGGA 2287
QY 761 SerArgAsnAsnGlySerPheLeuAlaIleLysAlaAlaAspGlyThrTyrIleLeuAsn 780
Db 2288 TCCAGGAACAATGGCAGCTTTCTTGGCATCAAGCTGCTGATGGCACATATATCTTAT 2347
QY 781 GlyAspTyrThrLeuSerThrLeuGlnAspIleMetTyrLysGlyValValLeuArg 800
Db 2348 CGTGACTACACTTTGTCCACCTTAGAGCAAGACATATGTACAAAGGTGTGTCTTGAGG 2407
QY 801 TyrSerGlySerSerAlaAlaLeuGluArgIleArgSerPheSerProLeuLysGluPro 820
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QY 821 LeuThrIleGlnValLeuThrValGlyAsnAlaLeuArgProLysIleLysTyrThrTyr 840
Db 2468 TTGACCATCCAGTCTTACTGTGGCAATGCCCTTCGACCTAAAAATTAATACACCTAC 2527
QY 841 PheValLysLysLysGluSerPheAsnAlaIleProThrPheSerAlaTrpValIle 860
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Db 2588 GAAGAGTGGGGCAATGTTCTAAGTCATGTGAATTTGGGTGGCAGAGAAGACTGGTAGAA 2647
QY 881 CysArgAspIleAsnGlyGlnProAlaSerGluCysAlaLysGluValLysProAlaSer 900
Db 2648 TCCCGAGACATTAATGGACAGCTCTCTCCGAGTGTGCAAGGAAGTGAAGCCAGCCAGC 2707
QY 901 ThrArgProCysAlaAspHisProCysProGlnTrpGlnLeuGlyLysTrpSerSerCys 920
Db 2708 ACCAGACCTTGTGCAGACCATCCCTGCCCGAGTGGCAGCTGGGGAGTGGTCATCATGT 2767
QY 921 SerLysThrCysGlyLysGlyTyrLysLysThrSerLeuLysCysLeuSerHisAspGly 940
Db 2768 TCTAAGACTGTGGAGAGGTTACAAAAGAAAGCTTGAAGTGTCTGCCCATGATGA 2827
QY 941 GlyValLeuSerHisAspSerCysAspProLeuLysLysProLysHisPheIleAspPhe 960
Db 2828 GGGGTGTTATCTCATGAGAGCTGTGATCCTTTAAAGAAACCTTAAACATTTTCATAGACT 2887
QY 961 CysThrMetAlaGluCysSer 967
Db 2888 TGCACAATGGCAGAATGCAGT 2908

RESULT 3

US-09-392-184-1
; Sequence 1, Application US/09392184
; Patent No. 6395889
; GENERAL INFORMATION:
; APPLICANT: Robison, Keith E.
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN
; TITLE OF INVENTION: PROTEASE HOMOLOGS
; FILE REFERENCE: 5800-55
; CURRENT APPLICATION NUMBER: US/09/392,184
; CURRENT FILING DATE: 1999-09-09
; NUMBER OF SEQ ID NOS: 33

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FASTA: FASTA for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 4858
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(4858)
; OTHER INFORMATION: reprotolysin (ADAM family of metalloprotease)
; NAME/KEY: misc feature
; LOCATION: (1)...(4858)
; OTHER INFORMATION: n = A,T,C or G
US-09-392-184-1

Alignment Scores:
Pred. No.: 0 Length: 4858
Score: 5219.00 Matches: 957
Percent Similarity: 99.28% Conservative: 4
Best Local Similarity: 98.86% Mismatches: 6
Query Match: 98.71% Indels: 1
DB: 3 Gaps: 0

US-09-373-658C-126 (1-967) x US-09-392-184-1 (1-4858)
QY 1 MetGlnArgAlaValProGluGlyPheGlyArgArgLysLeuGlySerAspMetGlyAsn 20
DB 454 ATCCAGCAGCTGTGCCGAGGGGTTCCGAAGAGCGCAAGCTGGGCGAGCAGCATGGGGAAC 513
QY 21 AlaGluArgAlaProGlySerArgSerPheGlyProValProThrLeuLeuLeuLeuLeu 40
DB 514 GCGGAGCGGCTCCGGGGTCTCGAGCTTTGGGCGGCTATCCACGCTGCTGCTCGCC 573
QY 41 AlaAlaLeuLeuAlaValSerAspAlaLeuGlyArgProSerGluGluAspGluGluLeu 60
DB 574 GCGGCGCTACTGCGCGGTCTCGAGCGACTCGGGCGGCCCCCGGACACGCGCTCCGCGCTGCGAGCTA 633
QY 61 ValValProGluLeuGluArgValProGlyPheGlyThrThrArgLeuArgLeuHisAla 80
DB 634 GTGGTCCGCGAGCTGGAGCGCGCCCCCGGACACGCGGACACGCGCTCCGCGCTGCGAGCC 693
QY 81 PheAspGlnGlnLeuAspLeuAspValProProAspSerSerPheLeuAlaProGlyPhe 100
DB 694 TTTGACGAGCAGCTGGATCTCGAGCTCGGCGCGGACAGCAGCTTTTGGCGCGCGGCTTC 753
QY 101 ThrLeuGlnAsnValGlyArgLysSerGlySerAspThrProLeuProGluThrAspLeu 120
DB 754 ACCTCCAGAACGTGGGGCGCAATCCGGTCCGAGACGCGCTTCGGAACCGACCTG 813
QY 121 AlaHisCysPheTyrSerGlyThrValAsnGlyAspProSerSerAlaAlaLeuSer 140
DB 814 GCGCACTGCTTACTCCGCGCAGCGTGAATGGCGATCCCAAGCTCGGCTGCGCGCTCAGC 873
QY 141 LeuCysGluGlyValArgGlyAlaPheTyrLeuLeuGlyGluAlaTyrPheIleGlnPro 160
DB 874 CTCTGCGAGGCGGTGCGCGCGCTTCTACCTGCTGGGGAGGCGTATTTTCATCCAGCGC 933
QY 161 LeuProAlaAlaSerGluArgLeuAlaThrAlaAlaProGlyGlyLysProProAlaPro 180
DB 934 CTGCCCCCGCCAGCAGCGCTCGCCACCGCGCCCCCGGAGAGCGCCGCGCACCA 993
QY 181 LeuGlnPheHisLeuLeuArgAsnArgGlnGlyAspValGlyGlyThrCysGlyVal 200
DB 994 CTACAGTTTCCACTCTCGCGGGAATCGGCGAGCGGCGACGTAGCGCGCACGTGCGGGTTC 1053
QY 201 ValAspAspGluProArgProThrGlyAlaGluThrGluAspGluAspGluGlyThr 220
DB 1054 GTGACGACGAGCGCGCGCTGCGGAAACGCGAGACCGAAGACGAGGAGGACT 1113
QY 221 GluGlyGluAspGluGlyProGlnTrpSerProGlnAspProAlaLeuGlnGlyValGly 240
DB 1114 GAGGGCGAGGACGAGGCGCTCAGTGTGCGCGGACCGCGGCTGCAAGGCGTAGGA 1173
QY 241 GlnProThrGlyThrGlySerIleArgLysLysArgPheValSerSerHisArgTyrVal 260

1174 CAGCCACAGGAACCTGGAAGCATAGAAAGAGCGATTTGTGTCCAGTCCCGCTATGTG 1233
261 GluThrMetLeuValAlaAspGlnSerMetAlaGluPheHisGlySerGlyLeuLysHis 280
1234 GAAACCATGCTTGTGGCAGACCATGTCAGTGGCAGAAATTCACCGCAGTGTCTAAAGCAT 1293
281 TyrLeuLeu-ThrLeuPheSerValAlaAlaArgLeuTyrLysHisProSerIleArgAs 300
1294 TACCTTCTCAACGCTTGTTCGGTGGCAGCCAGATTTGTATCAAAACACCCAGCATTCGTAA 1353
300 nSerValSerLeuValValLysLysLeuValLysLeuValLysLeuValLysGlyProG 320
1354 TTCAGTTAGCTGCTGGTGGTGAAGATCTTGGTCAATCCAGATGAACAGAGGGCGCGGA 1413
320 uValThrSerAsnAlaAlaLeuThrLeuArgAsnPheCysAsnTrpGlnLysGlnHisAs 340
1414 AGTGACCTCCATGCTGCCCTCACTCTGGGAACTTTTGGCACTTGGCAGGAGCAGCAAA 1473
340 nProProSerAspArgAspAlaGluHisTyrAspThrAlaIleLeuPheThrArgGlnAs 360
1474 CCCACCCAGTGACCGGGATGCGAGCACATATGACACAGCAATTTCTTTTCCACGACAGGA 1533
360 pLeuCysGlySerGlnThrCysAspThrLeuGlyMetAlaAspValGlyThrValCysAs 380
1534 CTTGTGTGGTCCCGACATGTGATCTCTTGGGATGGCTGTGTTGGAACTGTGTGTGA 1593
380 pProSerArgSerCysSerValIleGluAspAspGlyLeuGlnAlaAlaPheThrThrAl 400
1594 TCCAGGACGAGAGCTGCTCCGTCATAGAGATGATGTTTACAAGCTGCTTCCACGACG 1653
400 aHisGluLeuGlyHisValPheAsnMetProHisAspAspAlaLysGlnCysAlaSerLe 420
1654 CCATGAATTAGGCCACGCTGTTTAAATGATGCCACATGATGATGATGATGATGATGATG 1713
420 uAsnGlyValAsnGlnAspSerHisMetMetAlaSerMetLeuSerAsnLeuAspHisSe 440
1714 TAATGTGTGAACAGGATTTCCACATGATGATGGGCTCAATGCTTTTCCAACCTGGACCA 1773
440 xGlnProTrpSerProCysSerGlyTyrMetIleThrSerPheLeuAspAsnGlyHisG 460
1774 CCAGCTTGTGTCTCTTTCAGTGCCTTACATGATGATGATGATGATGATGATGATGATG 1833
460 yGluCysLeuMetAspLysProGlnAsnProIleGlnLeuProGlyAspLeuProGlyTh 480
1834 GGAATGTTTGTATGAGCAAGCTCAGAAATCCATACAGCTCCAGGCGATCTCCCTGGCAC 1893
480 rSerTyrAspAlaAsnArgGlnCysGlnPheThrPheGlyGluAspSerLysHisCysPr 500
1894 CTCGTACGATGCCAACCGGCGAGTCCAGATTTTACATTTTGGGGAGGACTCCAAACACTG 1953
500 oAspAlaAlaSerThrCysSerThrLeuTyrCysThrGlyThrSerGlyGlyValLeuVa 520
1954 TGATGACGACGACATGATGACACCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2013
520 lCysGlnThrLysHisPheProTrpAlaAspGlyThrSerCysGlyGluGlyLysTrpCy 540
2014 GTGTCAAAACCAACACTTCCGCTGGGCGGATGCGACAGCTGTGAGAGAGGAATGGTG 2073
540 sIleAsnGlyLysCysValAsnLysAsnHisArgLysHisPheAspThrProPheHisG 560
2074 TATCAACCGGAGTGTGTGAACAAAACCGACAGAAAGCATTTTGTATCGCTTTTTCATGG 2133
560 ySerTrpGlyMetTrpGlyProTrpGlyAspCysSerArgThrCysGlyGlyValG 580
2134 AAGTGGGGAATGTGGGGGCTTTGGGGAGACTGTTTCCAGAACGTCGCGGTGGAGAGTCCA 2193
580 nTyrThrMetArgGluCysAspAsnProValProLysAsnGlnGlyLysTyrCysGluG 600
2194 GTACACGATGAGGGAATGTGACAAACCCAGTCCCAAGAAATGGAGGGAAGTACTGTGAAG 2253
600 yLysArgValArgTyrArgSerCysAsnLeuGluAspCysProAspAsnGlnGlyLysTh
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Db 2254 CAACAGGTGGCTACAGATCCTGTAACTTGGAGCTGTCCAGACAATAATGTAAGAAAAC 2313
Qy 620 rPheArgGluGluGlnCysGluAlaHisAsnGluPheSerIysAlaSerPheGlySerG1 640
Db 2314 CTTTATAGAGGAAACAATGTGAAGACACACACAGATTTTCAAAAGCTTCTCTTTGGGAGTGG 2373
Qy 640 yProAlaValGluTTPilleProLysTyrAlaGlyValSerProLysAspArgCysLysle 660
Db 2374 GCCTGGGTGGATGGATTCACAGTAGCTGGCGCTCTCACCAAGAGCAGGTGCAAGCT 2433
Qy 660 uileCysGlnAlaLysGlyIleGlyTyrPhePheValLeuGlnProLysValValAspG1 680
Db 2434 CATCTGCCAAGCAAGGATTTGGCTTCTTCTGTTTGGAGCCCAAGGTTGTAGATGG 2493
Qy 680 yThrProCysSerProAspSerThrSerValCysValGlnGlnGlnCysValLysAlaG1 700
Db 2494 TACTCCATGTAGCCAGATTCACCTCTGTCTGTGTGCAAGGACAGGTGTGTAAGAGCTGG 2553
Qy 700 yCysAspArgIleIleAspSerLysLysLysPheAspLysCysGlyValCysGlyGlyAs 720
Db 2554 TTGTGATGCATCATAGACTCCAAAAGAGTTTGATTAATGTGTGTGTTGGCGGGGAAA 2613
Qy 720 nGlySerThrCysLysLysIleSerGlySerValThrSerAlaLysProGlyTyrHisAs 740
Db 2614 TGGATCTACTTGTAAAAAATATCAGGATCAGTTACTAGTGCAAAACCTGGATATCATGA 2673
Qy 740 pileIleThrIleProThrGlyAlaThrAsnIleGluValLysGlnArgAsnGluArgG1 760
Db 2674 TATCATCAATTCACCTGGAGCCCAACCAATCGAAGTGAACAGCGCAACAGAGGGG 2733
Qy 760 ySerArgAsnAngLysSerPheLeuAlaIleLysAlaAlaAspGlyThrTyrIleLeuAs 780
Db 2734 ATCCAGGAACAATGCGAGCTTTCTTGCCATCAAACTGCTGATGGACATATTTCTTAA 2793
Qy 780 nGlyAspTyrThrLeuSerThrLeuGluGlnAspIleMetTyrLysGlyValValLeuAr 800
Db 2794 TGGTGACTACACTTTGTCCACCTTAGAGCAAGACATTTATGACAAAGGTGTTGTCTTGA 2853
Qy 800 gTyrSerGlySerSerAlaAlaLeuGluArgIleArgSerPheSerProLeuLysGluPr 820
Db 2854 GTACAGCGCTCTCTCGGCAATGGAAAGAAATTCGACGCTTTAGCCCTCTCAAGAGCC 2913
Qy 820 oleuThrIleGlnValLeuThrValGlyAsnAlaLeuArgProLysIleLysTyrThrTy 840
Db 2914 CTTGACCATCCAGGTTCTTACGTGGGCAATGCCCTTCGACCTAAATTAATACACCTA 2973
Qy 840 rPheValLysLysLysGluSerPheAsnAlaIleProThrPheSerAlaTrpValI1 860
Db 2974 CTTGTAAAGAAAGAAAGGAATCTTTCAATGCTATCCCACTTTTTCAGCATGGTCA 3033
Qy 860 eGluGluTrpGlyGluCysSerLysSerCysGluLeuGlyTyrGlnArgArgLeuValG1 880
Db 3034 TGAAGAGTGGGCGCAATGTTCTTAAGTCATGTGAATGGTGGTGGCAGAGAAGACTGGTGA 3093
Qy 880 uCysArgAspIleAsnGlyGlnProAlaSerGluCysAlaLysGluValLysProAlase 900
Db 3094 ATGCCGAGACATTAATGACACCTGCTTCCAGGTGTGCAAGGAAGTGAACCCAGCCAG 3153
Qy 900 rThrArgProCysAlaAspHisProCysProGlnTrpGlnLeuGlyGluTrpSerSerCy 920
Db 3154 CACCAACCTTGTGCAGACCATCCCTGCCCCCAGTGGCAGCTGGGGAGTGTGTATCATG 3213
Qy 920 sSerLysThrCysGlyLysGlyTyrIlyLysThrSerLeuLysCysLeuSerHisAspG1 940
Db 3214 TTCTAAGACCTGTGGAGGGTTACAAAAAAGAGCTTGAAGTGTCTGTCCCATGATGG 3273
Qy 940 yGlyValLeuSerHisAspSerCysAspProLeuLysLysProLysHisPheIleAspPh 960
Db 3274 AGGGGTGTATCTCATGAGAGCTGTGATCTTTTAAGAAACCTTAACATTTCTATGACTT 3333
Qy 960 eCysThrMetAlaGluCysSer 967
Db 3334 TTGCACAAATGGCAGATGTCAGT 3355

RESULT 4

US-09-484-970B-58
; Sequence 58, Application US/09484970B
; Patent No. 6426186
; GENERAL INFORMATION:
; APPLICANT: Jones, Karen A.
; APPLICANT: Volkmar, Wayne
; APPLICANT: Walker, Michael G.
; TITLE OF INVENTION: BONE REMODELING GENES
; FILE REFERENCE: PB-0014 US
; CURRENT APPLICATION NUMBER: US/09/484,970B
; CURRENT FILING DATE: 2000-01-18
; NUMBER OF SEQ ID NOS: 172
; SOFTWARE: PERL Program
; SEQ ID NO 58
; LENGTH: 3706
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; NAME/KEY: unsure
; LOCATION: 3634, 3638-3639, 3642-3643, 3647-3648, 3652, 3654-3658, 3664, 3674, 3681
; OTHER INFORMATION: a, t, c, g, or other
US-09-484-970B-58

Alignment Scores:

Pred. No.:	0	Length:	3706
Score:	4262.00	Matches:	772
Percent Similarity:	99.36%	Conservative:	1
Best Local Similarity:	99.23%	Mismatches:	4
Query Match:	80.61%	Indels:	1
DB:	3	Gaps:	0

US-09-373-658C-126 (1-967) x US-09-484-970B-58 (1-3706)

Qy	191	GlnGluAspValGlyGlyThrCysGlyValValAspAspGluProArgProThrGlyLys	210
Db	3	CAGGCGACGTAGGCGGCACGTGCGGGTCTGTGGACGACGAGCCCGCGGCTGGGAAA	62
Qy	211	AlaGluThrGluAspGluAspGluGlyThrGluGlyGluAspGluGlyProGlnTrpSer	230
Db	63	GCGAGACCGAAGACGAGGAGCTGAGGCGGAGGACGAGGCGCTCAGTGTGCG	122
Qy	231	ProGlnAspProAlaLeuGlnGlyValGlyGlnProThrGlyThrGlySerIleArgLys	250
Db	123	CGCAGGACCCGCGCATGCAAGGCGTAGGACAGCCACAGGAACTGGAGGCATAGAAG	182
Qy	251	LysArgPheValSerSerHisArgTyrValGluThrMetLeuValAlaAspGlnSerMet	270
Db	183	AMGCAATTTGTCTCAGTCACCGCTATGTGGAAACCATGCTTGTGGCAGACCATGCGATG	242
Qy	271	AlaGluPheHisGlySerGlyLeuLysHisTyrLeuLeuThrLeuPheSerValAlaAla	290
Db	243	GCAGAAATTCACGCGCAGTGTCTAAAGCATTTACCTTCTCACGTTGTTTCGGTGGCAGCC	302
Qy	291	ArgLeuTyrLysHisProSerIleArgAsnSerValSerLeuValValLysIleLeu	310
Db	303	AGATTGTCAAAACACCCCAAGTTCGTAATTCAGTTAGCTGTGGTGGTGAAGATCTTG	362
Qy	311	ValIleHisAspGluGlnLysGlyProGluValThrSerAsnAlaAlaLeuThrLeuArg	330
Db	363	GTCAATCCAGATGAACAGAGGGCGGAGTAGCTCCATGCTGCTCTCTCTCTCTCTCT	422
Qy	331	AsnPheCysAsnTrpGlnLysGlnHisAsnProProSerAspArgAspAlaGluHisTyr	350
Db	423	AACTTTTGGCAACTGGCAGAAAGCAGCAACACCCAGTACCCGAGTGCAGGACTAT	482
Qy	351	AspThrAlaIleLeuPheThrArgGlnAspLeuCysGlySerGlnThrCysAspThrLeu	370
Db	483	GACACAGCAATTTCTTTTCCACAGACGAGGACTTGTGTGGTCCACAGATGTGATCTCT	542

371 GlyMetAlaAspValGlyThrValCysAspProSerArgSerCysSerValIleGluAsp 390
543 GGGATGGCTGATGTTGGAACTGTGTGATCCGAGCAGAAAGCTGCTCCGTCATAGAAGAT 602
391 AspGlyLeuGlnAlaAlaPheThrThrAlaHisGluLeuGlyHisValPheAsnMetPro 410
603 GATGGTTTAAAGCTGCTCCACAGAGCCCATGAATTAGGCCACAGCTGTTTAAACATGCCA 662
411 HisAspAlaAlaGlyGlnCysAlaSerLeuAsnGlyValAsnGlnAspSerHisMetMet 430
663 CATGATGATGCAAGCAGTGTGCCACCTTAATGTTGTGACACAGGATTTCCACATGATG 722
431 AlaSerMetLeuSerAsnLeuAspHisSerGlnProTrpSerProCysSerGlyTyrMet 450
723 GGGTCAATGCTTTCCAACTGGACACAGCAGCCCTTGGTCTCTCTTGCAGTGCCTACATG 782
451 IleThrSerPheLeuAspAsnGlyHisGlyGluCysLeuMetAspLysProGlnAsnPro 470
783 ATTACATCATTTCTGGATAATGTCATGGGAATGTTTGTATGACCAAGCCTTCAGAAATCCC 842
471 IleGlnLeuProGlyAspLeuProGlyThrSerTyrAspAlaAsnArgGlnCysGlnPhe 490
843 ATACAGCTCCAGCGCATCTCCCTGGCAGCTCTGTAGATGCCAACCCGGCAGTGCAGTTT 902
491 ThrPheGlyGluAspSerLysHisCysProAspAlaAsnSerThrCysSerThrLeuTrp 510
903 ACATTTGGGGAGGACTCCAAACACTGCCCGCATGCAGCCAGCACATGTAGCACCTTGTGG 962
511 CysThrGlyThrSerGlyValLeuValCysGlnThrLysHisPheProTrpAlaAsp 530
963 TGTACCGGACCTCTGGTGGGTGCTGGTGTGTCAAAACCAACACTTCCCGTGGCGGAT 1022
531 GlyThrSerCysGlyGluGlyLysTrpCysIleAsnGlyLysCysValAsnLysAsnHis 550
1023 GGCACAGCTGTGGAGAGGAATGTTGTATCAAGCGCAAGTGTGAACAAACCCGAC 1082
551 ArgLysHisPheAspThrProPheHisGlySerTrpGlyMetTrpGlyProTrpGlyAsp 570
1083 AGAAGCATTTTTCATACGCTTTTTCATGAAGCTGGGGAATGTGGGGCTTGGCGAGAC 1142
571 CysSerArgThrCysGlyGlyValGlnTyrThrMetArgGluCysAspAsnProVal 590
1143 TGTTCAGAACCTGCGGTGGAGAGTCCAGTACACGATGAGGAATGTGACAAACCCAGTC 1202
591 ProLysAsnGlyGlyLysTrpCysGluGlyLysArgValArgTyrArgSerCysAsnLeu 610
1203 CCNAGAAATGGAGGAAGTACTGTGAAGCGAAGCGAGTGGCTACAGATCTGTAACTT 1262
611 GluAspCysProAspAsnAsnGlyLysThrPheArgGluGlnCysGluAlaHisAsn 630
1263 GAGGACTGTCCAGACAATAATGAAACCTTTTAGAGAGGAACAATGTGAAGCACACAAC 1322
631 GluPheSerLysAlaSerPheGlySerGlyProAlaValGluTrpIleProLysTyrAla 650
1323 GAGTTTTCAAAGCTTCTTGGAGTGGGCTCGCGTGGAAATGGATTTCCAAAGTACGCT 1382
651 GlyValSerProLysAspArgCysLysLeuIleCysGlnAlaLysGlyIleGlyTyrPhe 670
1383 GGGCTCTCCAAAGGACAGTGCAGCTCATCTGCCAGCCAAAGCATTTGGCTACTTTC 1442
671 PheValLeuGlnProLysValValAspGlyThrProCysSerProAspSerThrSerVal 690
1443 TTCGTTTTCAGCCCAAGGTTGTAGATGGTACTCCATGTAGCCAGCATTCACCTCTGTC 1502
691 CysValGlnGlyGlnCysValLysAlaGlyCysAspArgIleIleAspSerLysLysLys 710
1503 TGTGTGCAAGGACAGTGTGTAAGGCTGGTGTGATCGCATCATAGACTCCAAAGAAAG 1562
711 PheAspLysCysGlyValCysGlyGlyAsnGlySerThrCysValLysIleSerGlySer 730
1563 TTTGATAAATGTGTGTTTGGGGGGAATGGATCTACTTGTATAAATAATATCAGGATCA 1622
731 ValThrSerAlaLysProGlyTyrHisAspIleIleThrIleProThrGlyAlaThrAsn 750

1623 GTTACTAGTGCAAAACCTGGATATCATGATATCATCACAAATTCCTCAATGGAGCCACAAC 1682
751 IleGluValLysGlnArgAsnGlnArgGlySerArgAsnAsn-GlySerPheLeuAlaIle 770
1683 ATCGAAGTGAACAGCGGAACCCAGAGGATCCAGGAACATGGGAGCTTCTTGGCAT 1742
770 elysAlaAlaAspGlyThrTyrIleLeuAsnGlyAspTyrThrLeuSerThrLeuGlu 790
1743 CAAAGCTGCTGATGGCACATATATTCTTAATGGTACTACACTTTGTCACCTTAGAGCA 1802
790 nAspIleMetTyrLysGlyValValLeuArgTyrSerGlySerSerAlaAlaLeuGlu 810
1803 AGACATTAATGTACAAAGGTGTTGCTGTGAGGTACAGCGCTCTCTGCGCATTTGAAAG 1862
810 gIleArgSerPheSerProLeuLysGluProLeuThrIleGlnValLeuThrValGlyAs 830
1863 AATTCGACCTTTAGCCCTCTCAAGAGCCCTTGACCATCCAGGTTCTTACTGTGGGCAA 1922
830 nAlaLeuArgProLysIleLysTyrThrPheValLysLysLysLysLysLysSerPheAs 850
1923 TGGCTTTCGACCTAAATTAATACACTTCTGTAAGAGAGGAAGAAATCTTTCAA 1982
850 nAlaIleProThrPheSerAlaTrpValIleGluGluTrpGlyGluCysSerLysSerCy 870
1983 TGCTATCCCCACTTTTTCAGCATGGGTCAATTGAAGAGTGGGCGAATGTTCTTAAGTCATG 2042
870 sGluLeuGlyTrpGlnArgArgLeuValGluCysArgAspIleAsnGlyGlnProAlaSe 890
2043 TGAAATGGGTGGCAGAGAGACTGGTAGATGCCAGACATTAATGGACAGCTGCTTTC 2102
890 rGluCysAlaLysGluValLysProAlaSerThrArgProCysAlaAspHisProCysPr 910
2103 CGAGTGTGCAAGGAAGTGAAGCCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 2162
910 oGlnTrpGlnLeuGlyGluTrpSerSerCysSerLysThrCysGlyLysGlyTyrLysLy 930
2163 CCAGTGGCAGCTGGGGAGTGGTCACTGTTCTTAAGACCTGTGGGAAGGTTACAAAA 2222
930 sThrSerLeuLysCysLeuSerHisAspGlyValLeuSerHisAspSerCysAspPr 950
2223 AGAACCTTGAAGTGTCTGTCCATGATGGAGGGGTGTTATCTCATGAGAGCTGTGATCC 2282
950 oLeuLysLysProLysHisPheIleAspPheCysThrMetAlaGluCysSer 967
2283 TTTAAAGAAACCTTAACATTTTCATAGACTTTTGCACAATGGCAGAAATGCAGT 2334

RESULT 5
US-09-445-023A-2
; Sequence 2, Application US/09445023A
; Patent No. 6565858
; GENERAL INFORMATION:
; APPLICANT: Hirose, Kunitaka
; APPLICANT: Inoguchi, Eiji
; APPLICANT: Hakozaaki, Michinori
; APPLICANT: Ishioka, Keiko
; APPLICANT: Ishida, Yukako
; APPLICANT: Matsuhashi, Kouji
; APPLICANT: Kuno, Kouji
; TITLE OF INVENTION: Human ADAMTS-1 protein, gene encoding the same, pharmaceutical
; FILE REFERENCE: 057092
; CURRENT APPLICATION NUMBER: US/09/445, 023A
; CURRENT FILING DATE: 1999-12-03
; PRIOR APPLICATION NUMBER: JP 9-160422
; PRIOR FILING DATE: 1997-06-03
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 2184
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:

QY 908 ProCysProGlnTrpGlnLeuGlyGluTrpSerSerCysSerLysThrCysGlyLysGly 927
DB 2002 CCTGCCCCCAGTGGCAGCTGGGGAGTGGTCAATGTTCTAAGACCTGTGGGAGGGT 2061
QY 928 TyrLysLysThrSerLeuLysCysLeuSerHisAspGlyGlyValLeuSerHisAspSer 947
DB 2062 TACAAAAAAGAGCTTGAAGTGTCTGCTCCCATGATGGAGGGGTGTATCTCATGAGAGC 2121
QY 948 CysAspProLeuLysLysProLysHisPheIleAspPheCysThrMetAlaGluCysSer 967
DB 2122 TGTGATCCCTTTAAGAAACCTAAACATTTCTAGACTTTTGGCACACTGACAGTGCAT 2181

RESULT 6
US-09-445-023A-13
Sequence 13, Application US/09445023A
Patent No. 6565858
GENERAL INFORMATION:
APPLICANT: Hirose, Kunitaka
APPLICANT: Inoguchi, Biiji
APPLICANT: Hakozaaki, Michinori
APPLICANT: Ishioka, Keiko
APPLICANT: Ishida, Yukako
APPLICANT: Matsushima, Kouji
APPLICANT: Kuno, Kouji
TITLE OF INVENTION: Human ADAMTS-1 protein, gene encoding the same, pharmaceutical.
FILE REFERENCE: Q57092
CURRENT APPLICATION NUMBER: US/09/445, 023A
CURRENT FILING DATE: 1999-12-03
PRIOR APPLICATION NUMBER: JP 9-160422
PRIOR FILING DATE: 1997-06-03
NUMBER OF SEQ ID NOS: 14
SOFTWARE: PatentIn version 3.0
SEQ ID NO 13
LENGTH: 2184
TYPE: DNA
ORGANISM: Mus sp.
FEATURE:
NAME/KEY: exon
LOCATION: (1)..(2184)
US-09-445-023A-13

Alignment Scores:
Pred. No.: 0 Length: 2184
Score: 3652.00 Matches: 646
Percent Similarity: 94.77% Conservatives: 43
Best Local Similarity: 88.86% Mismatches: 38
Query Match: 69.08% Indels: 0
DB: 4 Gaps: 0

US-09-373-658C-126 (1-967) x US-09-445-023A-13 (1-2184)

QY 241 GlnProThrGlyThrGlySerIleArgLysLysArgPheValSerSerHisArgTyrVal 260
DB 1 AAGCCATCAGGACGAGCAGCATAAGAGAGAGCGATTTGTGTCCAGCCCCCGTTATGTG 60
QY 261 GluThrMetLeuValAlaAspGlnSerMetAlaGluPheHisGlySerGlyLeuLysHis 280
DB 61 GAAACCATGCTCGTAGTCGACCGATCCATGGCCGATTCACCGCAGCGGTCTAAAGCAT 120
QY 281 TyrLeuLeuThrLeuPheSerValAlaAlaArgLeuTyrLysHisProSerIleArgAsn 300
DB 121 TACCTTCTAACCTGTCTCGGTGGCAGCCAGCTTTTACAAGCATCCAGCATTTAGGAAT 180
QY 301 SerValSerLeuValValLysIleLeuValIleHisAspGluGlnLysGlyProGlu 320
DB 181 TCAATTAGCCTGTGTGTGTGAAGATCTTGGTCTATATACGAGGAGCAGAGGAGCCAGAA 240
QY 321 ValThrSerAsnAlaAlaLeuThrLeuAtcAsnPheCysAsnTrpGlnLysGlnHisAsn 340
DB 241 GTTACCTCCAATGAGCTCTCACCCCTTCGGAATTTCTGACGCTGGCAGAAACCAAC 300
QY 341 ProProSerAspArgAspAlaGluHisTyrAspThrAlaIleLeuPheThrArgGlnAsp 360

DB 301 AGCCCCAGTGCAGCGGATCCAGAGCAGCTATGACACCTGCAATTCGTGTCCAGACAGGAT 360
QY 361 LeuCysGlySerGlnThrCysAspThrLeuGlyMetAlaAspValGlyThrValCysAsp 380
DB 361 TTATGTGGCTCCACACAGTGTGACACTCTCGGAATGGCAGATGTTGGACCGTATGTGAC 420
QY 381 ProSerArgSerCysSerValIleGluAspAspGlyLeuGlnAlaAlaPheThrThrAla 400
DB 421 CCCAGCAGGAGCTGTCTCAGTCATAGAAGATGATGGTTTGCAGCTGCCCTTCCACACAGCC 480
QY 401 HisGluLeuGlyHisValPheAsnMetProHisAspAspAlaLysGlnCysAlaSerLeu 420
DB 481 CATGAATTGGGCCATGTGTTTAAACATGCCCACGATGATGCTAAGCAGCTGTGCAGCTTG 540
QY 421 AsnGlyValAsnGlnAspSerHisMetMetAlaSerMetLeuSerAsnLeuAspHisSer 440
DB 541 AATGGTGTGAGTGGCGATTTCTCATGTATGGCTCGATGCTCTCCAGCTTAGACCATAGC 600
QY 441 GlnProTrpSerProCysSerGlyTyrMetIleThrSerPheLeuAspAsnGlyHisGly 460
DB 601 CAGCCCTGTCTACCTTGCAGTGCCTACATGGTCACGCTCTCTAGATAATGGACACGGG 660
QY 461 GluCysLeuMetAspLysProGlnAsnProIleGlnLeuProGlyAspLeuProGlyThr 480
DB 661 GAATGTTGATGGACAAAGCCAGATCAATCAAGCTCCCTTCTGATCTTCCCGGTACC 720
QY 481 SerTyrAspAlaAsnArgGlnCysGlnPheThrPheGlyGluAspSerLysHisCysPro 500
DB 721 TTGTAGTAGCCCAACCCGCGAGTGTCACTTACATTCGAGAGGAAATCCAGACACTGCCCT 780
QY 501 AspAlaAlaSerThrCysSerThrLeuTrpCysThrGlyThrSerGlyGlyValLeuVal 520
DB 781 GATGACGACGACACATGTACTACCTGTGTGCTGCTGACCTCCGCTGGCTTACTGGTG 840
QY 521 CysGlnThrLysHisPheProTrpAlaAspGlyThrSerCysGlyGluGlyLysTrpCys 540
DB 841 TGCCAAACAAACACTTCCCTTTGGGCAGATGGCAGCAGCTGTGGAGAGGAAAGTGGTGT 900
QY 541 IleAsnGlyLysCysValAsnLysAsnHisArgLysHisPheAspThrProPheHisGly 560
DB 901 GTCAGTGGCAAGTGTGTGAACAGACAGACATGTAAGCATTTTGTACTCTCTGTTCATGGA 960
QY 561 SerTrpGlyMetTrpGlyProTrpGlyAspCysSerArgThrCysGlyGlyGlyValGln 580
DB 961 AGCTGGGACCATGGGACCGTGGGAGACTGTCTCAAGAACCTGTGGTGGTGGAGTCAA 1020
QY 581 TyrThrMetArgGluCysAspAsnProValProLysAsnGlyGlyLysTrpCysGluGly 600
DB 1021 TACACAATGAGAGAAATGTGACAAACCCAGTCCCAAGAACGAGGGAAGTACTGTGAAGGC 1080
QY 601 LysAtqValArgTyrArgSerCysAsnLeuGluAspCysProAspAsnAsnGlyLysThr 620
DB 1081 AAACGAGTCCGCTACAGGTCCTGTACATCGAGGACTGTCCAGACATTAACGGAAACG 1140
QY 621 PheArgGluGlnCysGluAlaHisAsnGluPheSerLysAlaSerPheGlySerGly 640
DB 1141 TTCAGAGAGGAGCAGTGCAGGCGCAGCAATGAGTTTTTCCAAAGCTTCTTTGGGAATGAG 1200
QY 641 ProAlaValGluTrpIleProLysTyrAlaGlyValSerProLysAspArgCysLysLeu 660
DB 1201 CCCACTGTAGAGTGGACACCCAGTACGCGCGGCTCTCGCCAAAGGACAGTGCAGCTC 1260
QY 661 IleCysGlnAlaLysGlyIleGlyTyrPhePheValLeuGlnProLysValValAspGly 680
DB 1261 ACCTGTGAAGCCAAAGCATTTGGCTACTTTTCTTACAGCCCAAGGTTGTAGATGGC 1320
QY 681 ThrProCysSerProAspSerThrSerValCysValGlnGlyGlnCysValLysAlaGly 700
DB 1321 ACTCCCTGTAGTCCAGACTCTACTCTGTGTGTGCAAGGGCAGTGTGTGAAAGCTGGC 1380
QY 701 CysAspArgIleIleAspSerLysLysPheAspLysCysGlyValCysGlyGlyAsn 720

310 LeuValIleHisAspGluGlnLysGlyProGluValThrSerAsnAlaIleLeuThrLeu 329
 808 CTGCTTCTAGAGATCGTGAATCGGGCCCAAGGTACCGGCCTGAGCGCTG 867
 330 ArgAspPheCysAsnTrpGlnLysGlnHisAsnProProSerAspArgAspAlaGluHis 349
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 350 TyrAspThrAlaIleLeuPheThrArgGlnAspLeuCysGlySerGlnThrCysAspThr 369
 928 TGGGACACTGCCATCTCTTACAGCAGCAGACCTGTGTGGAGCCACCACTGTGACACC 987
 370 LeuGlyMetAlaAspValGlyThrValCysAspProSerArgSerCysSerValIleGlu 389
 988 CTGGGATGCTGATGTGGTACCATCTGTGACCCCAAGAGAGCTGCTCTGTCAATTGAG 1047
 390 AspAspGlyLeuGlnAlaAlaPheThrThrAlaHisGluLeuGlyHisValPheAsnMet 409
 1048 GACGATGGGCTTCCATCAGCCTTCCACCATCTGCCACGAGCTGGGGCCACGCTTCAACATG 1107
 410 ProHisAspAlaLysGlnCysAlaSerLeuAsnGlyValAsnGlnAspSerHisMet 429
 1108 CCCATGACAAATGGAAGTCTGTGAGGAGGTGTGGGAAGCTCCGAGCCACCAACATG 1167
 430 MetAlaSerMetLeuSerAsnLeuAspHisSerGlnProTrpSerProCysSerGlyTyr 449
 1168 ATGTCCCGACCTTCATCCAGATGACGCGTGCACACCCCTGGTGCAGCTGCTGCTGCC 1227
 450 MetIleThrSerPheLeuAspAsnGlyHisGlyCysLeuMetAspLysProGlnAsn 469
 1228 ATCATCACCGACTTCTCTGGACAGCGGGCACGGTGAATGCTCTCTGGACCAACCCAG 1287
 470 ProIleGlnLeuProGlyAspLeuProGlyThrSerTyrAspAlaAsnArgGlnCysGln 489
 1288 CCATCTCCCTGCGGAGATCTGCGGGGCGGACGCTACACCTGAGCCAGAGTGGCAG 1347
 490 PheThrPheGlyGluAspSerLysHisCysProAspAlaAlaSerThrCysSerThrLeu 509
 1348 CTGGCTTTGGGTGGCTTCAGCCCTGTCTCT---TACATGCGATGACTGACCAACAGCTG 1404
 510 TrpCysThrGlyThrSerGlyValLeuValCysGlnThrLysHisPheProTrpAla 529
 1405 TGGTGACCGGGAAGGCAAGGACAGATGTGTGCGACAGCCCGCCACTTCCCTGGGCC 1464
 530 AspGlyThrSerCysGlyGluGlyLysTrpCysIleAsnGlyLysCysValAsnLys--- 548
 1465 GATGGCACCAAGCTGTGGCGAGGCGCAAGCTCTGCTCAAGGGGGCTCGGTGGAGAGACAC 1524
 549 AsnHisArgLysHisPheAspThrProPheHisGlySerTrpGlyMetTrpGlyProTrp 568
 1525 AACTCAACAGCNC-----AGGGTGGATGGTTCTTGGGCAATGGGATCCCTAT 1575
 569 GlyAspCysSerArgThrCysGlyGlyValGlnTrpThrMetArgGluCysAspAsn 588
 1576 GGCCCTTGTCTCGGCACATGTGGTGGGGGGGTGCGAGCTGGCGAGAGCGAGTGCACCAAC 1635
 589 ProValProLysAsnGlyLysTrpCysGluGlyLysArgValArgTyrArgSerCys 608
 1636 CCACCCCTCCCAACCGGGGCAAGTACTGCGAGGAGTGAAGGTGAATAATCCGATCTGTC 1695
 609 AsnLeuGluAspCysProAspAsn---AsnGlyLysThrPheArgGluGluGlnCysGlu 627
 1696 AACTGGAGCCTGCCCTCCAGCTAGCTTCCGGAAGAGCTTCCGGAGGAGCAGTGTGAG 1755
 628 AlaHisAsnGluPheSerLysAlaSerPheGlySerGlyProAlaValGluTrpIlePro 647
 1756 GCTTTCAACGGCTACACCAACAGCAGCACCACCGGCTCACTCTCGCGTGGCATGGTGCC 1815
 648 LysTyrAlaGlyValSerProLysAspArgCysLysLeuIleCysGlnAlaLysGlyIle 667
 1816 AAGTACTCCGGCGTGTCTCCCGGAGCAAGTGAAGTCACTCTGCCGAGCAATGGGCACT 1875

668 GlyTyrPhePheValLeuGlnProLysValValAspGlyThrProCysSerProAspSer 687
 1876 GGCTACTTCTATGTGTGCGCACCCAAAGTGTGGAGCGGACGCTGTCTCTCTGACTCC 1935
 688 ThrSerValCysValGlnGlyGlnCysValLysAlaGlyCysAspArgIleIleAspSer 707
 1936 ACCTCGTCTGTGTCCAAAGCAAGTGCATCAAGCTGGCTGTGATGGGAACCTGGGCTCC 1995
 708 LysLysLysPheAspLysCysGlyValCysGlyLysGlySerThrCysLysLysIle 727
 1996 AAGAAGAGATTCCAGCAAGTGTGGGTGTGGGGGAGACAAATAGAGCTCAAGAAGAGTG 2055
 728 SerGlySerValThrSerAlaLysProGlyTyrHisAspIleIleThrIleProThrGly 747
 2056 ACTGAGCTCTTCCACCAAGCCATGTCATATTTCGTGGTGCCATCCCGCAGGC 2115
 748 AlaThrAsnIleGluValLysGlnArgAsnGlnArgGlySerArgAsnAsnGlySerPhe 767
 2116 GCCTCAAGCATCAGATCCGCCAGCGGTTTCAAGGGGTGATCGGGGATGACAACTAC 2175
 768 LeuAlaIleLysAlaAlaAspGlyThrTyrIleLeuAsnGlyAspTyrThrLeuSerThr 787
 2176 CTGGCTCTGAAGAACAGCCCAAGTACTGCTCAACGGCATTTTCGTGGTGTGCGCG 2235
 788 LeuGluGlnAspIleMetTyrLysGlyValValLeuArgTyrSerGlySerSerAlaAla 807
 2236 GTGGAGCGGACCTGTGTGTGAAGGCGAGTCTGTGCGGTACAGCGGCACGCGCAGCG 2295
 808 LeuGluArgIleArgSerPheSerProLeuLysGluProLeuThrIleGlnValLeuThr 827
 2296 GTGGAGAGCTGTGAGGCTTCCCGGCCATCTCGAGCGCTGACCGGTGGAGTCTCTCTCC 2355
 828 ValGlyAsnAlaLeuArgProLysIleLysTyrThrTyrPheValLysLysLys--- 845
 2356 GTGGGAGAGTACACCGCCCGGGTCCGCTACTCTCTTCTATCTGCCCAAGAGCCCTCG 2415
 846 -----LysGluSer-----PheAsnAlaIle 852
 2416 GAGGACAAAGTCTCTCATCCAAAGGACCCCGGGGACCTCTGTCTTGTGCACACAGCGTC 2475
 853 ProThrPheSer-----AlaTrpValIle 860
 2476 CTGAGCTCTTCCAAACAGGTGGAGCGAGCCGAGCGAGCCCTCGACCGCTGGTGGCT 2535
 861 GluGluTrpGlyGluCysSerLysSerCysGluLeuGlyTrpGlnArgArgLeuValGlu 880
 2536 GGAGCTGGGGGGCGTGTCTCCGCGAGTGTGGCGAGTGTGGCGAGCGGGCGTGGAC 2595
 881 CysArgAspIleAsnGlyGln-----ProAlaSerGluCysAlaLysGluValLys 897
 2596 TGGCGGGGCTCCCGCGGCGAGCGCAGCTGCTGCTGTGTGATGACGCCCAT------CGG 2649
 898 ProAlaSerThrArgProCysAlaAspHisProCysProGlnTrpGlnLeuGlyGluTrp 917
 2650 CCCTGGAGACACCAAGCTTCCGGGAG----CCCTGCCCCACCTGGAGCTCAGCGCTGG 2706
 918 SerSerCysSerLysThrCysGlyLysGlyTyrLysLysThrSerLeuLysCysLeuSer 937
 2707 TCACCTGTCTCAAGAGCTGCGCGGGGATTTTCAGAGCGCTCACTCAAGTGTGTGGC 2766
 938 HisAspGlyGlyValLeuSerHisAspSerCysAspProLeuLysLysProLysHisPhe 957
 2767 CACGAGCGCGGTGTGTGGCGCGGACCAAGTGAACCTTGACCCGACCGCCCGAGGAG- 2823
 958 IleAspPheCysThrMetAlaGluCys 966
 2824 CTGGACTTCTGCTGCTCGGCGCGGTGC 2850

RESULT 8
 US-09-369-364A-8
 ; Sequence 8, Application US/09369364A
 ; Patent No. 6391610
 ; GENERAL INFORMATION:

```

: APPLICANT: Apte, Suneel
: APPLICANT: Hurskainen, Tiina L.
: APPLICANT: Hirchata, Satoshi
: TITLE OF INVENTION: Nucleic Acids Encoding Zinc Metalloproteases
: FILE REFERENCE: 26473/4007/10-30-00
: CURRENT APPLICATION NUMBER: US/09/369,364A
: CURRENT FILING DATE: 1999-08-06
: NUMBER OF SEQ ID NOS: 31
: SOFTWARE: Patentin Ver. 2.1
:

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Alignment Scores:	9.27e-199	Length:	3338
Pred. NO.:	2271.50	Matches:	452
Score:	61.66%	Conservative:	151
Percent Similarity:	46.22%	Mismatches:	288
Best Local Similarity:	42.96%	Indels:	87
Query Match:		Gaps:	22
DB:	3		

US-09-373-658C-126 (1-967) x US-09-369-364A-8 (1-3638)

Qy	3	ArgAlaValProGluGlyPheGlyArgArgLysLeuGlySerAspMetGlyAsnAlaGlu	22
Db	203	CGCCTCGGGCCACCAGCACCTCGCCCGCGCGCGGATCTTCTCCCTCCCGCGCTCG	262
Qy	23	ArgAlaProGlySerArgSerPheGlyProVal	38
Db	263	CAGCACTCTGCCCCCCTGCTCGCGACCCACACACACCGGCTGGCGCCCTCTCTGCTG	322
Qy	39	LeuAlaAlaLeuLeuAlaValSerAspAlaLeuGlyArgProSer	54
Db	323	CTGTCTATTGCGAGCTCGCCCGCCGCGCACTGCTCTGCGGAGCCCGCGCGCGCGGAAC	382
Qy	55	---GluGluAspGluGluValValProGluLeuGluArgValProGlyHisGlyThr	73
Db	383	GGGGCGCAGGCTCGAGCTAGTGTGCCC-----ACGGCGTGTGCGCGCAGCGCAGC	436
Qy	74	---ThrArgLeuArgLeuHisAlaPheAspGlnLeuAspLeuAspValProProAsp	92
Db	437	GAGCTCGGCTCTCCACCTGCTCGCGCTTCGGCCAGAGGCTTCGTGTGCTGCGCTCGCGCGCTGAC	496
Qy	93	SerSerPheLeuAlaProGlyPheThrLeuGluAsnValGlyArgLysSerGlySerAsp	112
Db	497	GCCAGCTTCTTGGCCCGCGAATTTCAGATCAGCGCCTCGGGGGCTCGACCGCGCGCGCC	556
Qy	113	ThrProLeuProGluThrAspLeuAlaHisCysPheTyrSerGlyThrValAsnGlyAsp	132
Db	557	GGG-----GGCAGCCGGGACTCGTGGCTGCTTCTCTCTGCGCACAGTGAATCGAGAA	610
Qy	133	ProSerSerAlaAlaLeuSerLeuCysGluGlyValArgGlyAlaPheTyrLeuLeu	152
Db	611	CGGGAGTCGTGGCGGCGATGAGCTGTGTCGGGCTGGAGCGGCTGTTTCTGCTGGCA	670
Qy	153	GlyGluAlaTyrPheIleGlnProLeuProAlaAlaSer	167
Db	671	GGCGAGGAGTTTCAACCATCCAGCCACAGGGCGCTGGGGACTCCCTGGACACAGCCTCATCGC	730
Qy	168	LeuAlaThrAlaProGlyGluLysPro	177
Db	731	CTGCGAGCGTGGGGGCCGGGACAGCGCGCGAGACCCCGGGCTCGCTGCGCGCGAAGTT	790
Qy	178	-----ProAlaProLeuGlnPheHisLeuLeuArgArgAsnArgGlnGlyAspVal	194

QY 548 LysAsnHisArgLysHisPheAspThrProPheHisGlySerTyrGlyMetTyrGlyPro 567
Db 1868 AAGAGGATGTGGAGATCCCAAGGCTGTGTAGATGGAGACTGGGGTCCCTGGAGACC 1927
QY 568 TrpGlyAspCysSerArgThrCysGlyGlyValGlnTyrThrMetArgGluCysAsp 587
Db 1928 TGGGGACAATGTTCTCGACCTGTGGTGGAGGATACAAATCTCGAACCGTGAATGTAT 1987
QY 588 AsnProValProLysAsnGlyLysTyrCysGluGlyLysArgValArgTyrArgSer 607
Db 1988 AATCCCAATGCTCAGATGAGGAAGATTTTGGCTGGTGAAGAGTCAAGATCCCAATCA 2047
QY 608 CysAsnLeuGluAspCysProAspAsnAsnGlyLysThrPheArgGluGlnCysGlu 627
Db 2048 TGCACACACAGAGATGTCACCA--AACGGAAAGCTCCGGAGCAGAGTGTGAG 2104
QY 628 AlaHisAsnGluPheSerLysAlaSerPheGlySerGlyProAlaValGluTyrPhePro 647
Db 2105 AAATATAATGCTACACACACTGACCTG--GATGGAAATTCCTGACAGTGGTCCCC 2161
QY 648 LysTyrAlaGlyValSerProLysAspArgCysLysLeuLeuCysGlnAlaLysGlyLe 667
Db 2162 AAGTATTACAGAGTGTCCCGGAGACCGATGCAAGCTGTTTGCAGAGCCCGTGGGAGG 2221
QY 668 GlyTyrPhePheValLeuGlnProLysValValAspGlyThrProCysSerProAspSer 687
Db 2222 AGTGAGTTCAAAGTGTGAAGCTAAGTGAATGATGGCACTCTGTGTGACCGGATACT 2281
QY 688 ThrSerValCysValGlnGlyGlnCysValLysAlaGlyCysAspArgLysLeuAspSer 707
Db 2282 CTGTCCATCTCGCTCCGGGGCAATGTGTTAAGCTGGCTGTGACCATGTGGTGAATCA 2341
QY 708 LysLysLysPheAspLysCysGlyValCysGlyGlyAsnGlySerThrCysLysLysLe 727
Db 2342 CCTAAGAAGCTGGACAAATGTGGGTGTGTGGGGGCAAGGGCACTGCTGTAGGAAGATC 2401
QY 728 SerGlySerValThrSerAlaLysProGlyTyrHisAspLysLeuThrThrGly 747
Db 2402 TCGGTTCTTTTACCCCTTCAGTTATGGCTACATGACATTTGACCATCCAGCTGGT 2461
QY 748 AlaThrAsnLeuGluValLysGlnArgAsnGlnArgGlySerArgAsnAsnGlySerPhe 767
Db 2462 GCCACAAACATTTGATGTGAACAGCGAGTCACCCAGGGGTGAGGAACGACGCGAGTAC 2521
QY 768 LeuAlaLysAlaAlaAspGlyThrTyrLysLeuAsnGlyAspTyrThrLeuSerThr 787
Db 2522 CTGGCGTGAAGACAGCAATGGGCAGTACCTGCTCAATGGTAACTGGCCATCTCTGCC 2581
QY 788 LeuGluGlnAspLeuMetTyrLysGlyValValLeuArgTyrSerGlySerSerAlaAla 807
Db 2582 ATAGAGCAAGACATCTTGGTGAAGGGAGCCATCTGAAGTACAGTGGCTCATGGCTACC 2641
QY 808 LeuGluArgLysArgSerPheSerProLeuLysGluProLeuThrLysGlnValLeuThr 827
Db 2642 CTGGAGCGGCTGCAGAGCTTCCAGGCCCTGCTGAGCTCTTACAGTACAGTCTCTGACT 2701
QY 828 Val--GlyAsnAlaLeuArgProLysLysLysLysLysLysLysLysLysLysLysLys 842
Db 2702 GTGTCTGGTGGAGTCTTCCCTCCAAAGTCCAGATATACCTTCTTTGTGCCCAATGACATG 2761
QY 843 -----LysLysLysLysLysLysLysLysLysLysLysLysLysLysLysLysLys 855
Db 2762 GACTTCAGCTGAGATAGCAGGAAGAGCAACCAACCATCATTCAGTCACTGCC 2821
QY 856 ----SerAlaTrpValLeuGluGluTyrGlyLysSerLysSerCysGluLeuGlyTyr 874
Db 2822 TCTCGGAGTGGGTCTCGGAGACTGTGTCTGAATGTCCGAGCACTGTCAGAGGTAGCTGG 2881
QY 875 GlnArgArgLeuValGluCysArgAspLysLeuAsnGlyGlnProAlaSerGluCysAlaLys 894
Db 2882 CAGCGCGGAGCTGTGTGAATGACAGGAGCCCTCAGTCCAGGCTCTGACACCTGTGATGAG 2941

QY 895 GluValLysProAlaSerThrArgProCysAlaAspHisProCysPro-----Gln 911
Db 2942 GCTCTCAAAACCTGAGGATGCCAAGCCTGTGGAAAGCAGCGGTGCTCCCTCTGATCCCT 3001
QY 912 Trp-----GlnLeuGlyGluTyrSerSerCysSerLys 922
Db 3002 TGGTGGAAATCTCTTAGGCTTATGGATTTGGGGTACTGG-----TGTAACAGA 3049
RESULT 9
US-09-392-184-7/c
; Sequence 7, Application US/09392184
; Patent No. 6395889
; GENERAL INFORMATION:
; APPLICANT: Robison, Keith E.
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN
; TITLE OF INVENTION: PROTEASE HOMOLOGS
; FILE REFERENCE: 5800-55
; CURRENT APPLICATION NUMBER: US/09/392,184
; CURRENT FILING DATE: 1999-09-09
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 3126
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)-(3126)
; OTHER INFORMATION: reprotolysin (ADAM family of metalloprotease)
US-09-392-184-7
Alignment Scores:
Pred. No.: 4.8e-189 Length: 3126
Score: 2165.00 Matches: 443
Percent Similarity: 62.49% Conservative: 140
Best Local Similarity: 47.48% Mismatches: 246
Query Match: 40.95% Indels: 106
DB: 3 Gaps: 24
US-09-373-658c-126 (1-967) x US-09-392-184-7 (1-3126)
QY 76 LeuArgLeuHisAlaPheAspGlnGlnLeuAspLeuAspValProAspSerSerPhe 95
Db 3116 CTCACCTGTCCGCTTCGGCAAGGCTTCGTGCTGGCGTGGCGCCGACGACGAGCTTC 3057
QY 96 LeuAlaProGlyPheThrLeuGlnAsnVal-----GlyArgLysSerGlySerAsp 112
Db 3056 CTGGCGCCGACTTCAAGATCGAGCGCTCGGGGGCTCCGGCGCGGCGACCGGGGGC--- 3000
QY 113 ThrProLeuProGluThrAspLeuAlaHisCysPheTyrSerGlyThrValAsnGlyAsp 132
Db 2999 -----GAGCGGGGGCTCGCGGCTGTCTTCTTCTCCGCGCACCGTCCAGCGCTCC 2952
QY 133 ProSerSerAlaAlaLeuSerLeuCysGluGlyValArgGlyAlaPheTyrLeuLeu 152
Db 2951 GCCGAGTCTGTGGCGGGTTCAGCTGTGCGGGGGCTGAGCGGCTCTCTTCTCTGCGAC 2892
QY 153 GlyGluAlaTyrPheLeuGlnProLeuProAlaAlaSer-----GluArg 167
Db 2891 GGGAGAGAGTTTCACTTCCAGCGCGGCGGGGGGGCTCCCTGGGTTCAGCCGACCGC 2832
QY 168 LeuAlaThrAlaAlaProGlyGluLysProProAlaProLeuGlnPheHisLeuLeuArg 187
Db 2831 CTGACGCGCTGGGTCCCGC-CGGAGCCCGCCCTCC-----GCG 2791
QY 188 ArgAsnArgGlnGlyAspValGlyGlyThrCysGlyValValAspAspGluProArgPro 207
Db 2790 AGCACCCGAGTGGGAGGTGAGAGCGGAGAG---GGGTTCAGAGGAGGAGAGAGACCA 2734
QY 208 ThrGly-LysAlaGluThrGluAspGluAspGluGlyThrGluGlyGluAspGlyPyr 227
Db 2733 CCAGGAGGACAGCGAGGAGGAGGAGCCAAAGAGAGGAGGCGGAGGCGCTGACGAGCGGCC 2674

Db 624 CTGGACATCGCGT-----ACTGAGGTGCACAGGGCTCTCCACTGTGGT 580
Qy 935 -----CysLeuSerHisAspGlyGlyValLeuSerHisAspSerCysAspProLeuLy 952
Db 579 GACTGGGTCTCTGGCCATAT-CAAGGCACACGGCCCAAGGGCTC---CAATGGCC 524
Qy 952 sLysProLyHisPheIleAspPheCysThr 962
Db 523 GCAACCC-----CTCCAGTACTGCACA 502

RESULT 10
US-09-122-126B-1
; Sequence 1, Application US/09122126B
; Patent No. 6451575
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: AGGRECAN DEGRADING METALLO PROTEASES
; FILE REFERENCE: DM6909
; CURRENT APPLICATION NUMBER: US/09/122,126B
; CURRENT FILING DATE: 1998-07-24
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 4192
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (406)..(2916)
US-09-122-126B-1

Alignment Scores:
Pred. No.: 5,26e-188 Length: 4192
Score: 2156.00 Matches: 450
Percent Similarity: 60.55% Conservative: 144
Best Local Similarity: 45.87% Mismatches: 281
Query Match: 40.78% Indels: 109
DB: 3 Gaps: 26

US-09-373-658C-126 (1-967) x US-09-122-126B-1 (1-4192)

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Qy 27 SerArgSerPheGlyProValProThrLeuLeuLeuLeuAlaAlaLeuAlaVal 46
Db 491 TGGCGCTCTCTGGCTG-GTGTGGCTGCTTCTGCTACTGTGGCTCTCTCTGCCCC- 546
Qy 47 SerAspAlaLeuGlyArgProSerGluGluAspGluLeuValProGluLeu- 65
Db 547 TCAGCCCGGTGGCCAGCCCTCCCGGGGAGAGAGATCGTGTTCAGAGAGCTC 606
Qy 66 -----GluArgValProGlyHisGlyThr---ThrArgLeu-----ArgLeuHisAla 80
Db 607 AACGGCAGCTCTGCTGGCTGGCGGCCCTCCAGGCTGTGTGGCTGGAGGCC 666
Qy 81 PheAspGlnGlnLeuAspLeuAspValProAspSerSerPheLeuAlaProGlyPhe 100
Db 667 TTTGGGAGAGCGCTGCTACTAGAGCTGGAGCAGGACTCCCGTGTGCGAGGCGCTG 726
Qy 101 ThrLeuGlnAsnValGlyArgLys-----SerGlySerAspThrProLeuPro 116
Db 727 ACAGTGCAGTACCTTGGCCAGCGCCCTGAGTGTGCTGGTGGAGCAGAG-----CCT 777
Qy 117 GluThrAspLeuAlaHisCysPheTy-SerGlyThrValAsnGlyAspProSerAla 136
Db 778 GGCACC-----TACCTGACTGGCACCATCAATGAGATCCGAGTCCGCTG 822
Qy 137 AlaAlaLeuSerLeuCysGluGly---ValArgGlyAlaPheTyLeuLeuGlyGluAla 155
Db 823 GCATCTGTGACTGGGATGGGGAGCCCTGTGTAGGCGTGTGTACAAATATCGGGGGCTGAA 882

Qy 156 TyrPheIleGlnProLeuProAlaAlaSerGluArgLeuAlaThrAlaAlaProGlyGlu 175
Db 883 CTCCACCTCCAGCCCTGGAGGGAGGACCCCTAACTCTGCT---GGGGACCTGGGGCT 939
Qy 176 LysProProAlaProLeuGlnPheHisLeuLeuArgAsnArgGlnGlyAspValGly 195
Db 940 -----CACATCTACGCGCGAAG----- 957
Qy 196 GlyThrCysGlyValValAspAspGluProArgProThrGlyLysAlaGluThrGluAsp 215
Db 957 ----- 957
Qy 216 GluAspGluGlyThrGluGlyGluAspGluGlyProGlnTrpSerProGlnAspProAla 235
Db 958 -----AGTCTGCGCAGCGGTCAAGGTGCCATGTGCAACGTCAAGGCTCT- 1002
Qy 236 LeuGlnGlyValGlyGlnProThrGlyThrGlySerIleArgLysLysArgPheValSer 255
Db 1003 -----CTTGAAGCCCAAGCCAGCCAGACCCCGA---AGAGCCAGAGCCCTTGTTC 1050
Qy 256 SerHisArgTyValGluThrMetLeuValAlaAspGlnSerMetAlaGluPheHisGly 275
Db 1051 CTGAGTAGATTGTGGAGACACTGTGTGGCAGATGACAAGATGCCCGCATTCACCGT 1110
Qy 276 SerGlyLeuLysHisTyLeuLeuThrLeuPheSerValAlaAlaArgLeuTyLysHis 295
Db 1111 GCGGGGCTAAAGCGCTACTCTGCTAAACAGTGTGCGCAGCAGCAGCAGGCTTCAAGCAC 1170
Qy 296 ProSerIleArgAsnSerValSerLeuValValValLysIleLeuValIleHisAspGlu 315
Db 1171 CCAAGCATCCGCAATCTGTGCTGGTGGTCACTCGGCTAGTGATCTCTGGGGTCAAGGC 1230
Qy 316 GlnLysGlyProGluValThrSerAsnAlaAlaLeuThrLeuArgAsnPheCysAsnTrp 335
Db 1231 GAGGAGGGGCCCAAGTGGGGCCAGTGTCTGCCAGACCTCGCGCAGCTTCTGTGCTCG 1290
Qy 336 GlnLysGlnHisAsnProProSerAspArgAspAlaGluHisTyAspThrAlaIleLeu 355
Db 1291 CAGCGGGGCTCAACACCCCTGAGGACTCGGACCTCGACCATTTTGACACAGCCATTTCTG 1350
Qy 356 PheThrArgGlnAspLeuCysGlySerGlnThrCysAspThrLeuGlyMetAlaAspVal 375
Db 1351 TTTACCGCTCAGACCTGTGTGGTCTCCACTTGCACACGCTGGGTATGGCTGATGTG 1410
Qy 376 GlyThrValCysAspProSerArgSerCysSerValIleGluAspAspGlyLeuGlnAla 395
Db 1411 GGCACCGTCTGTACCCCGCTCGAGCTGTGCCATGTGTGGAGATGATGGGCTCCAGTCA 1470
Qy 396 AlaPheThrThrAlaHisGluLeuGlyHisValPheAsnMetProHisAspAspAlaLys 415
Db 1471 GCCTTCACTGCTGCTCATGAATGGGTCTATGTCTTCAACATGTCTCCATGATGACATCCCAAG 1530
Qy 416 GlnCysAlaSerLeuAsnGly---ValAsnGlnAspSerHisMetMetAlaSerMetLeu 434
Db 1531 CCATGATCATGTTGAATGGGCTTTGAGCAGCCCTCTCGCCATGTCTGAGGCGCTGTGATG 1590
Qy 435 SerAsnLeuAspHisSerGlnProTrpSerProCysSerGlyTyMetIleThrSerPhe 454
Db 1591 GCTCATGTGGATCTGTGGAGGCTCTGTCTCCCTGTGAGTGCCTTCATCAGTACTTC 1650
Qy 455 LeuAspAsnGlyHisGlyGluCysLeuMetAspLysProGlnAsnProIleGlnLeuPro 474
Db 1651 CTGGACATGGCTATGGGCTCTCTCTTAGACAAACACAGAGGCTCCATTCATCTGCT 1710
Qy 475 GlyAspLeuProGlyThrSerTyAspAlaAsnArgGlnCysGlnPheThrPheGlyGlu 494
Db 1711 GTGACTTTCTCCGCAAGGACTATGATGTGACCGCCAGTGCAGCTGACCTCTCGGGCCC 1770
Qy 495 AspSerLysHisCysProAspAlaAlaSerThrCysSerThrLeuTrpCysThrGlyThr 514
Db 1771 GACTCAGCCATTTGTCCACAGCTGCCCGCCCTGTGCTGCCCTCTGGTGTCTGGGCCAC 1830
Qy 515 SerGlyGlyValLeuValCysGlnThrLysPheProTrpAlaAspGlyThrSerCys 534

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Db      1831 CTCATGGCCATGCGCATGTGCCAGACCAAACTCGCCCTGGCGCATGGCACCCCTGC 1890
QY      535 GlyGluGlyLysTrpCysIleAsnGlyLysCysValAsnLysAsnHisArgIlyHisPhe 554
Db      1891 GGGCCCGCACAGCCCTGCATGGGTGCTGCTCCACATGACAGCAGCTCAGGACTTC 1950
QY      555 AspThrProPheHisGlySerTrpGlyMetTrpGlyProTrpGlyAspCysSerArgThr 574
Db      1951 AATATTCCACAGCGTGGTGGGTCTCTGGGACCACTGGGGTACTGCTCTCGGACC 2010
QY      575 CysGlyGlyGlyValGlnTrpThrMetArgGluCysAspAsnProValProLysAsnGly 594
Db      2011 TGTGGGGTGGTGTCCAGTTCCTCCCGAGCTGCACGAGGCTGTCCCGGATGAT 2070
QY      595 GlyLysTrpCysGluGlyLysArgValArgTrpArgSerCysAsnLeuGluAspCysPro 614
Db      2071 GGCAGAGTACTGTGAGGGCGCGGTACCCGCTTCGCTCCGCAACACTGAGGACTGCCCA 2130
QY      615 AspAsnAsnGlyLysThrPheArgGluGluGlnCysGluAlaHisAsnGluPheSerLys 634
Db      2131 ACTGGCTACGCCCTGACCTTCGCGAGGAGCAGTGTGCTTACAAACCCACCGCAC 2190
QY      635 AlaSerPheGlySerGlyProAla---ValGluTrpIleProLysTrpAlaGlyValSer 653
Db      2191 CTC---TTCAAGAGCTTCCAGGGCCCATGGACTGGTTCCTCGCTACACAGCGGTGGCC 2247
QY      654 ProLysAspArgCysLysLeuIleCysGlnAlaLysGlyIleGlyTrpPhePheValLeu 673
Db      2248 CCCCAGGACCAAGTGCATACTCACTCCAGGCGCCGGCAGCTGGGTCTACTATGTGTG 2307
QY      674 GlnProLysValValAspGlyThrProCysSerProAspSerThrSerValCysValGln 693
Db      2308 GAGCCACGGGTGATAGGAGCCCTGTTCCTCCGAGCAGCTCTCGGTCTGTGTCCAG 2367
QY      694 GlyGlnCysValLysAlaGlyCysAspArgIleIleAspSerLysLysLysPheAspLys 713
Db      2368 GGCCGATGATCATTCGCTGTGATCGATCATTCATGGCTCCACAGAAGAAGTTTGACAG 2427
QY      714 CysGlyValCysGlyLysAsnGlySerThrCysLysLysLysIleSerGlySerValThrSer 733
Db      2428 TGCATGCTGTGGCGAGGGACGGTCTGTGTTGCAGCAAGCAGTCAGGCTCTCTCAGGAA 2487
QY      734 AlaLysProGlyTrpHisAspIleIleThrIleProThrGlyValaThrAsnIleGlyVal 753
Db      2488 TTCAGGTACGGATACAACTGTTGGTACTATCCCGCGGGGCCACCCACCATTTCTGTTC 2547
QY      754 LysGlnArgAsnGlnArgGlySerArgAsnAsnGlySerPheLeuAlaIleLysAlaAla 773
Db      2548 CGGCAGCAGGAAACCTCGCCACCGAGC-----ATCTACTTGGCCCTGAAGCTGCCA 2601
QY      774 AspGlyThrTrpIleLeuAsnGlyAspTrpThrLeuSerThrLeuGluGlnAspIleMet 793
Db      2602 GATGGCTCTATCCCTCAATGTGTAATACACGCTGATCCCTCCCGCCACAGATGTGTA 2661
QY      794 TyrLysGlyValVal---LeuArgTrpSerGlySerSerAlaAlaLeuGluArgIleArg 812
Db      2662 CTGCTTGGGGCAGTCAAGTTGGCTACAGCGGGGCCACTGCAGCTTCAGACACACTGTCA 2721
QY      813 SerPheSerProLeuLysGluProLeuThrIleGlnValLeuThrValGlyAsnAlaLeu 832
Db      2722 GGCCATGGGCCCATGCGCCAGCCTTTGACACTGCAGTCTAGTGGCTGCGAACCCCGCAG 2781
QY      833 ArgProLysIleLysTrpThrPheValLysLysLysGluSerPheAsnAlaIle 852
Db      2782 GACACAGCGCTCGATACAGCTCTTCGTGCGCCCGCGCCAGCCCTTCA---ACGCCACGC 2838
QY      853 ProThrPheSerAlaTrpVal-IleGluGlu-----Trp----- 863
Db      2839 CCACATCCCGAGGACTGGCTGCGACCCGAGAGCAGATTCGTGGAGATCTCTCGGGGCGC 2898
QY      864 ----GlyGluCysSer-----LysSerCys 870
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Db      2899 CCCTGGCGGGCAGGAATAAACCCTCACTATCCCGGCTGCCCTTCTTGGGSCACCGGGGCCT 2958
QY      870 sGluLeuGlyTrpGlnArgArg-----LeuValGluCysArgAspIleAsnG 886
Db      2959 CGGACTTAGCTGGGAGAAAGAGAGAGCTTCTGTTGCTGCTCTCATGTAAGACTCAGTGGG 3018
QY      886 yGlnProAlaSerGluCysAlaLysValLysProAlaSerThrArgProCysAlaAs 906
Db      3019 GAGG-----GGCTGTGGCGTGAGACCTGCCCTCTCTGCCCCCTAATGCGCAGG 3069
QY      906 pHisProCysPro-----GlnTrpGln-----LeuGlyGluTrpSerSerCysSe 921
Db      3070 CTGGCCCTGCCCTGGTTCCTGCTCCCTGGGAGCAGTGTGGGTAGTGATGGAAG--CG 3127
QY      921 rlystThrCysGlyLysGlyTyrLysLysThrSerLeuLysCysLeuSerHisAspGlyG 941
Db      3128 GCTGACAGACAGCCCTCCATCTAAACTGCCCTCTGCCCTCGGGTCAACAGGAGGAGG 3187
QY      941 Y 941
Db      3188 G 3188

RESULT 11
US-09-634-286A-1
; Sequence 1, Application US/09634286A
; Patent No. 6521436
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: AGGREGAN DEGRADING METALLO PROTEASES
; FILE REFERENCE: DM6909A
; CURRENT APPLICATION NUMBER: US/09/634,286A
; CURRENT FILING DATE: 2000-08-09
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 1
; LENGTH: 4192
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (406)..(2916)
US-09-634-286A-1

Alignment Scores:
Pred. No.: 5,26e-188 Length: 4192
Score: 2156.00 Matches: 450
Percent Similarity: 60.53% Conservative: 144
Best Local Similarity: 45.87% Mismatches: 281
Query Match: 40.78% Indels: 109
DB: 4 Gaps: 26

US-09-373-658C-126 (1-967) x US-09-634-286A-1 (1-4192)
QY      7 GluGlyPheGlyArgArgLysLeuGlySerAspMetGlyAsnAlaGluArgAlaProGly 26
Db      432 GAGGGCTTGGCAGGCGCTGCTGT-GGGAGAGCCACCCCTGCTCTCTCCCATTTG 490
QY      27 SerArgSerPheGlyProValProThrLeuLeuLeuAlaAlaLeuAlaVal 46
Db      491 TGCCGCTCTCTCTGGGTG-GTGTGGGTGCTTCTGCTACTGCTGCGCTCTCTCTGCCCC 546
QY      47 SerAspAlaLeuGlyArgProSerGluGluAspGluGluLeuValProGluLeu 65
Db      547 TCAGCCCGCTGGCCAGCCCTCCCGGGAGGAGAGATCGTGTTCAGAGAGCTC 606
QY      66 -----GluArgValProGlyHisGlyThr---ThrArgLeu-----ArgLeuHisAla 80
Db      607 AACGGCAGCGTCTGCTGGCTCGGCGGCCCTGCCAGGCTGTGTGCGCTTGCAGGCG 666
QY      81 PheAspGlnGlnLeuAspLeuAspValProProAspSerSerPheLeuAlaProGlyPhe 100
Db      667 TTTGGGAGACGCTGCTACTAGCTGGAGAGGACTCCGGTGTGAGGCTCGAGGGGCTG 726
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Db 1471 GCCTTCACTGCTGCTCATGAACGGGTCAATGCTTCAACATGCTCCATGACAACTCCCAAG 1530
Qy 416 GlnCysAlaSerLeuAenGly---ValAenGlnAspSerHisMetMetAlaSerMetLeu 434
Db 1531 CCATGATCATGTTGAATGGCCCTTTCGAGCACTCTCGCCATGTCATGGCCCTCTGTATG 1590
Qy 435 SerAenLeuAspHisSerGlnProTTPSerProCysSerGlyTyrMetIleThrSerPhe 454
Db 1591 GCTCATGTGATCTGAGGAGCCCTGTCTCCCTCTGAGTGCCTGCTTCATCATGACTTC 1650
Qy 455 LeuAspAenGlyHisGlyGluCysLeuMetAspLysProGlnAenProIleGlnLeuPro 474
Db 1651 CTGACAAATGCTATGGCACTGTCTCTTAGACAAACACAGAGGCTCCATTTGCATCTGCCT 1710
Qy 475 GlyAspLeuProGlyThrSerTyrAspAlaAenArgGlnCysGlnPheThrPheGlyGlu 494
Db 1711 GTGATTTTCCCTGGCAAGGACTATGATGCTAGCGCCAGTGCAGCTTCCTGGGCC 1770
Qy 495 AspSerLysHisCysProAspAlaAenSerThrCysSerThrLeuTyrCysThrGlyThr 514
Db 1771 GACTCAGCCATTTGTCACAGCTGCCCGCCCTGTGCTGCCCTCTGGTCTCTGGCCAC 1830
Qy 515 SerGlyGlyValLeuValCysGlnThrLysHisPheProTyrAlaAspGlyThrSerCys 534
Db 1831 CTCAATGGCCATGTCATGTCACAGCTGCCCGCCCTGTGCTGCCCTCTGGTCTCTGGCC 1890
Qy 535 GlyGluGlyLysTyrCysIleAenGlyLysCysValAenLysAenHisA-GlyHisPhe 554
Db 1891 GGGCCCGCACAGGCGCTGCATGGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 1950
Qy 555 AspThrProPheHisGlySerTyrGlyMetTyrProTyrGlyAspCysSerArgThr 574
Db 1951 AATATTCCACAGGCTGTGCTGGGTGCTTGGGGACCATGGGTGCTGCTCTCGACC 2010
Qy 575 CysGlyGlyGlyValGlnTyrMetArgGluCysAspAenProValProLysAenGly 594
Db 2011 TGTGGGGTGTGTGTCAGTTCTCTCCGAGAGTGCACGAGGCTGTCCCGCGAATGGT 2070
Qy 595 GlyLysTyrCysGluGlyLysArgValArgTyrArgSerCysAenLeuGluAenCysPro 614
Db 2071 GGCAGTACTGTGAGGGCCCGTACCGGCTTCCGCTCTCCGCAACATCGAGGAGTGCCTCA 2130
Qy 615 AspAenAenGlyLysThrPheArgGluGlnCysGluAlaHisAenGluPheSerLys 634
Db 2131 ACTGGCTCAGCCCTGACTTCCGAGGAGGAGTGTGCTGCTTACCAACCCAGCCGAC 2190
Qy 635 AlaSerPheGlySerGlyProAla---ValGluTyrPheProLysTyrAlaGlyValSer 653
Db 2191 CTC---TTCAAGAGCTTCCAGGGCCCATGAGTGGGTTCCTCGCTACACAGGCGTGGCC 2247
Qy 654 ProLysAspArgCysLysLeuIleCysGlnAlaLysGlyIleGlyTyrPhePheValLeu 673
Db 2248 CCCAGGACCATGTCAACTCACCTGCGAGCCCGCCGCTACTGCTGCTGCTGCTGCTG 2307
Qy 674 GlnProLysValValAspGlyThrProCysSerProAspSerThrSerValCysValGln 693
Db 2308 GAGCCAGGGTGTGTAGTGGAGCCCTTGTTCCTCGGACAGCTCTCTGGTCTGTGTCTAG 2367
Qy 694 GlyCysValLysAlaGlyCysAspArgIleIleAspSerLysLysLysPheAspLys 713
Db 2368 GGCCGATGATCCATGCTGGCTGTGATGCTCATTTGCTCCAGAGAAAGTGTTCACAG 2427
Qy 714 CysGlyValCysGlyLysAenGlySerThrCysLysLysIleSerGlySerValThrSer 733
Db 2428 TGCAATGGTGTGCGAGGGGACGGTTCGTGTGTCAGCAAGCAGTCCCTCCAGGAAA 2487
Qy 734 AlaLysProGlyTyrHisAspIleIleThrProThrGlyAlaThrAenIleGluVal 753
Db 2488 TTCAGGTACGATACAAATGTGGTCACTATCCCGGGGGGACCCACATTTCTGTGTC 2547
Qy 754 LysGlnArgAenGlnArgGlySerArgAenAenGlySerPheLeuAlaIleLysAlaAla 773

Db 2548 CGCAGCAGGGAACCCCTGGCCACCGGAGC-----ATCTACTTGGCCCTCGAAGCTGCCA 2601
Qy 774 AspGlyThrTyrIleLeuAenGlyAspTyrThrLeuSerThrLeuGluGlnAspIleMet 793
Db 2602 GATGGCTCTTATGCTTCATGCTGATGTGAATACACGCTGATGCTCCCTCCCAACAGATGTGTA 2661
Qy 794 TyrLysGlyValVal---LeuArgTyrSerGlySerSerAlaLeuLeuGluArgIleArg 812
Db 2662 CTGCTGGGGCAGTCACTGCTGCGCTACAGCGGGGCCACTGCAGCTCAGAGACACTGTCA 2721
Qy 813 SerPheSerProLysGluProLeuThrIleGlnValLeuThrValGlyAenAlaLeu 832
Db 2722 GGCATGGGCCACTGGCCGCTTTGACACTCTCAAGTCTCTAGTGGTGGCAACCCCCAG 2781
Qy 833 ArgProLysIleLysTyrThrPheValLysLysLysGluSerPheAenAlaIle 852
Db 2782 GACACAGCCTCCGATACAGCTTCTGTCGCCCCCGCCGACCTTCA---ACGCCACGC 2838
Qy 853 ProThrPheSerAlaTyrVal-IleGluGlu-----Tyr----- 863
Db 2839 CCACTCCCGAGACTGGCTGCACCGAAGACACAGATCTTGGAGATCTTGGCGCGCGC 2898
Qy 864 ----GlyGluCysSer----- 870
Db 2899 CCTGGCGCGGAGAAATAACCTCACTATCCCGGCTGCCCTTCTGGGCACCGGGGCT 2958
Qy 870 sGluLeuGlyTyrPheArgArg-----LeuValGluCysArgAspIleAenGly 886
Db 2959 CGGACTTGTGGAGAAAGAGAGAGCTTCTGTGTGCTGCTCATGCTTAAGACTCAGTGGG 3018
Qy 886 yGlnProAlaSerGluCysAlaLysGluValLysProAlaSerThrArgProCysAlaAs 906
Db 3019 GAGG-----GGCTGTGGCGGTGAGACTGCGCCCTCTCTGCTGCTTAATGCGCAGG 3069
Qy 906 pHisProCysPro-----GlnTyrPheGln-----LeuGlyGluTyrSerSerCysSe 921
Db 3070 CTGGCCCTGCGCTGGTTCCTGCGCCGAGGAGTGTAGTGGTATGGAAG--GG 3127
Qy 921 xLysThrCysGlyLysGlyTyrLysLysThrSerLeuLysCysLeuSerHisAspGlyVgl 941
Db 3128 GCTGACAGACAGCCCTCCATCTAAACTGCCCTCTGCTGCGGTTCACAGAGGAGG 3187
Qy 941 Y 941
Db 3188 G 3188

RESULT 13

US-09-122-126B-14
; Sequence 14, Application US/09122126B
; Patent No. 6451575
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: AGGRECAN DEGRADING METALLO PROTEASES
; FILE REFERENCE: DM6909
; CURRENT APPLICATION NUMBER: US/09/122,126B
; CURRENT FILING DATE: 1998-07-24
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 14
; LENGTH: 3250
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (121)..(2910)
; US-09-122-126B-14
Alignment Scores:
Pred. No.: 5,09e-167 Length: 3250
Score: 1926.50 Matches: 400
Percent Similarity: 53.53% Conservative: 123
Best Local Similarity: 40.94% Mismatches: 325
Query Match: 36.44% Indels: 130

DB:	3	Gaps:	18	
US-09-373-658c-126 (1-967) x US-09-122-126B-14 (1-3250)				
QY	5	ValProGluGlyPheGlyArgArgGlySerAspMetGlyAsnAlaGluArg-Al 24		1010
DB	156	GTTCCGCTCCCTGGCCGC-----GGTCGGCCCGCCGCGAC 194		1069
QY	24	aProGlySerArgSerPheGlyProValProThrLeuLeuLeuAlaAlaLeuLeu 44		328
DB	195	ACCTCCAGGATAAGCGCGCAGCTCCGACT-----GCTGC 233		1129
QY	44	uAlaValSerAspAlaLeuGlyArgProSerGluGluAspGluGluValValProG1 64		348
DB	234	ACGACCGCCAGCCCCCGCGGAGAGGTGAGGTGAGGAGCGAGCGCGCCT-- 291		1189
QY	64	uLeuGluArgValProGlyHisGly-----ThrThrArgLeuArgLeuHisAlaPh 81		1249
DB	292	-----CCCGGCCACCCGACCCCTGGCGCAGCGCGCAGGCAAGGGGCT 338		1309
QY	81	eAspGlnGlnLeuAsp----- 86		408
DB	339	GGTGAGACATCCACCACTACTCCGCGCGCGCAAGGTGGGCTACTCTGTACGC 398		1369
QY	87	-----LeuAspValProProAspSerSerPheLeuAlaProGlyPh 100		428
DB	399	GGCGCGCGGAGTTCCTTGAGCTGGAGCGAGATGTTGCTGGGGCATTTGCTGGCTT 458		1429
QY	100	eThrLeuGlnAsnValGlyArgLysSerGlySerAspThrProLeuProGluThrAspLe 120		1489
DB	459	CGTG-----CCGCGAGCGCGGCGAGTGGCGCTGGCGCCCTGGCGCCACCG 500		1499
QY	120	uAlaHisCysPheTyrSerGlyThrValAsnGlyAspProSerSerAlaAlaLeuSe 140		468
DB	501	CAGCACTCTCTATCGGGGACACGTGACGCTAGTCCCGCTCTCTGGCTGTCTTTGA 560		1549
QY	140	rLeuCysGluGlyValArgGlyAlaPheTyrLeuLeuGlyGluAlaTyrPheileGlnPr 160		488
DB	561	CCTCTGTGGGGTCTGACGGCTTCTTCGGGTCAAGCAGCGCGCTACACCTAAAGCC 620		1609
QY	160	oLeu-----ProAlaAlaSerGlu----- 166		508
DB	621	ACTGTGCGCGACCCCTGGCGCGAGGAGAAAGGGCGCGGTGTCGGGGATGGTCCGC 680		1666
QY	167	-ArgLeu-AlaThrAla-----AlaP 173		528
DB	681	ACGGATCTCTGCACGTCTACACCCGCGAGGGCTTCAGCTTCGAGGCGCTGCCCGCGCGC 740		1726
QY	173	roGlyGluLysProProAlaProLeuGlnPheHisLeuLeuArgArgAsnArgGlnGlyA 193		548
DB	741	CAGCTGCGAANCCCGCGCTCCA----- 763		1786
QY	193	spValGlyGlyThrCysGlyValValAspGluProArgProThrGlyLysAlaGluT 213		568
DB	764	-----CACCGAGGCCACGACGATGCTCCGCG 791		1846
QY	213	hrGluAspGluaspGluGlyThrGluGlyGluAspGluGlyProGlnTrpSerProGlnA 233		588
DB	792	GC-----ACAGCAACCCGAGCGGACGCGCAGCAGCTGG-----CCTCGCA 830		1906
QY	233	spProAlaLeuGlnGlyValGlnProThrGlyThr-----GlySerI 248		608
DB	831	GCTCTGGACAGTCCGCTCTCCGCCCTCGGGGCTCAGGACCGACAGCTGGTGGCG 890		1966
QY	248	leArgLysLysArgPheValSerSerHisArgTyrValGluThrMetLeuAlaAlaAspG 268		628
DB	891	G-CGCGCGCGCTCCATCTCCGCGCGCGCCAGGTGGAGTGTCTGTGGTGGCTGAGC 949		2023
QY	268	lnSerMetAlaGluPheHisGlySerGlyLeuLysHisTyrLeuLeuThrLeuPheSerV 288		648
DB	950	CGTCCATGGCGGTTGTATGGCGGGGCTCGAGCATTAACCTGTGACCTGGCGCTCA 1009		2083
QY	288	aAlaAlaArgLeuTyrLysHisProSerIleArgAsnSerValSerLeuValValVal 308		668

2084 AATATGACGGTGTCTGCCAGCGGATGTGTGCAAGCTGACCTGCAGAGCCAGGGCACTG 2143
QY lyTyPhePheValLeuGlnProLysValValaspGlyThrProCysSerProAspSerT 688
2144 GCTACTATGTGTATTTCTTCCAAAGGTGACCGATGCACTGAATGTAGCCGTACAGTA 2203
QY hrSerValCysValGlnGlyGlnCysValLysAlaGlyCysAspArgLleIleAspSerL 708
2204 ATTCCGTCTGCGTCCGGGGAAGTGTGTGAACTGGCTGTGACCGCATATTGGCTCAA 2263
QY yslYslYslPheAspLysCysGlyValCysGlyGlyAsnGlySerThrCysLysLysLys 728
2264 AGCTGCAGTATGACAAAGTCGAGTATGTGAGGAGCACTCCAGCTGTACAAAGATTG 2323
QY erGlySerValThrSerAlaLysProGlyTyHisaspLleIleThrIleProThrGlyA 748
2324 TTGGAACTTTAATAAGAAAGTAAGGGTTTACACTGACGTGGTGGAGATTCTTGAAGGG 2383
QY laThrAsnIleGluValLysGlnArgAsnGlnArgGlySerArgAsnAsnGlySerPheL 768
2384 CAACCCACATAAAGTTCGACAGTTCAAAGCCAAAGACAGACTAGATTCTAGCTATT 2443
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2444 TAGCCCTGAAAGAAAGAAACGGTGAGTACCTTATCAATGAAAGTATCATGATCTCCACTT 2503
QY euGluGlnaspIleMetTyLysGlyValValLeuArgTyThrSerGlySerSerAlaAlaL 808
2504 CAGAGACTATCATTTGATCAATCAATGGAACAGTCACTGATGAGTGGAGCCACAGGG 2563
QY euGluArgIleArg-----SerPheSerProLeuLysGluProLeuThrIleGlnValL 826
2564 ATGACTTCCTGCATGGCTGGCTGCTCTGCTCCAGAGAAATCTTAATAGTCAGATTC 2623
QY euThrValGlyAsnAlaLeuArgProLysIleLysTyThrTyThrPheVal---LysLysL 845
2624 TTGCAACAGACCCCACTAAACCATTAGATGCTCGTTATAGCTTTTGTGTTCCCAAGA 2683
QY yslYslGluSerPheAsnAlaIleProThrPheSerAla----- 857
2684 CCACTCCAAAGTAACCTCTGCTACTAGTATGCGAGCAATAAGTGGGATCACACTT 2743
QY TrpValIleGluLutProGlyGluCysSerLysSerCysGluLeuGlyT 874
2744 CGCAGCGCAGTGGGTCAACGGGCCCATGGCTCGCTGCTCTGAGACCTGTGACACAGTT 2803
QY rpGlnArgArgLeuValGluCysArgAspIleAsnGlyGlnProAlaSerGluCysAlaL 894
2804 GGCACACCAACAGCGTGCAGTCCAGGATGMAACCGGAAGTTAGCAAAAGGATGTCTC 2863
QY ysGluValLysProAlaSerThrArgProCysAlaAspHisProCys 909
2864 TCTCCAAAGGCCTTCTCGCTTTAAGCAATGCTTTGTAAGAAATGT 2910

RESULT 14

US-09-634-286A-14
; Sequence 14, Application US/09634286A
; Patent No. 6521436
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: AGGREGAN DEGRADING METALLO PROTEASES
; FILE REFERENCE: DM6909A
; CURRENT APPLICATION NUMBER: US/09/634, 286A
; CURRENT FILING DATE: 2000-08-09
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 14
; LENGTH: 3250
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (121)..(2910)

US-09-634-286A-14
Alignment Scores:
Pred. No.: 5,09e-167 Length: 3250
Score: 1926.50 Matches: 400
Percent Similarity: 53.53% Conservative: 123
Best Local Similarity: 40.94% Mismatches: 325
Query Match: 36.44% Indels: 130
DB: 4 Gaps: 18
US-09-373-658C-126 (1-967) x US-09-634-286A-14 (1-3250)
QY 5 ValProGluGlyPheGlyArgArgLysLeuGlySerAspMetGlyAsnAlaGluArg-Al 24
Db 156 GTTCCGCTGCTCCCTGGCGC-----GGTCGGCCCCCGCGAC 194
QY 24 aProGlySerArgSerPheGlyProValProThrLeuLeuLeuAlaAlaLeuLe 44
Db 195 ACCTGCCCAAGGATAAAAGCCGGCGAGCTCCGACT-----GCTGC 233
QY 44 uAlaValSerAspAlaLeuGlyArgProSerGluGluAspGluGluLeuValValProGl 64
Db 234 AGCAGCCGCCAGCCCCCGCGCGGAGGAGGTGCAGAGCGAGCGAGCCT-- 291
QY 64 uLeuGluArgValProGlyHisGly-----ThrThrArgLeuArgLeuHisAlaPh 81
Db 292 -----CCCGGCCACCCGCGAGCCCTGGCGCAGCGCGCAGGAGCAAGGGGCT 338
QY 81 eAspGlnGlnLeuAsp----- 86
Db 339 GGTGCAGAACATCGACAACTCTACTCCGCGCGCGCAAGGTGGGTACTCTGCTTACGC 398
QY 87 -----LeuAspValProProAspSerSerPheLeuAlaProGlyPh 100
Db 399 GGCAGCGCGAGAGTCTCTTGACCTTGAGCGAGATGGTTCGTGGGCATTGCTGCTT 458
QY 100 eThrLeuGlnAsnValGlyArgLysSerGlySerAspThrProLeuProGluThrAspLe 120
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QY 120 uAlaHisCysPheTySerGlyThrValAsnGlyAspProSerSerAlaAlaLeuSe 140
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Db 561 CCTCTGTGGGGTCTCGACGGCTTCTTCGGCGGTCAACAGCGCGGCTACACCTTAAAGCC 620
QY 160 oLeu-----ProAlaAlaSerGlu----- 166
Db 621 ACTGCTCGCGGAGCCCTGGCGGAGGAAGAAAGGGCGCGTGTACGGGATGGGTCCGC 680
QY 167 -ArgLeu-AlaThrAla-----Alap 173
Db 681 ACGGATCTCGACGTCTACACCCCGAGGGCTTCAGCTTCGAGGCCCTGCGCGCGCGC 740
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Db 741 CAGCTCGGAAACCCCGCGGTCCA----- 763
QY 193 spValGlyGlyThrCysGlyValValAspAspGluProArgProThrGlyLysAlaGluT 213
Db 764 -----CACCGAGGAGCCCGCAGCATGCTCCGCG 791
QY 213 hrGluAspGluAspGluGlyThrGluGlyGluAspGluGlyProGlnTrpSerProGlnA 233
Db 792 GC-----ACAGCAACCGGAGCGGACGCGCAGCACTGG--CCTCGCA 830
QY 233 spProAlaLeuGlnGlyValGlyGlnProThrGlyThr-----GlySerI 248
Db 831 GCTCTTGGACAGTCGCGCTCTCGCGCGTGGGGCTCAGGACCGCAGAGCTGGCG 890
QY 248 leArgLysLysArgPheValSerSerHisArgTyValGluThrMetLeuValAlaAspG 268


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; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 14
; LENGTH: 3250
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (121)..(2910)
US-10-247-685-14

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Score: 1926.50 Matches: 400
Percent Similarity: 53.53% Conservative: 123
Best Local Similarity: 40.94% Mismatches: 325
Query Match: 36.44% Indels: 130
DB: 4 Gaps: 18

US-09-373-658C-126 (1-967) x US-10-247-685-14 (1-3250)
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DB 195 ACCTGCCAGGATAAAGCGGGCAGCCTCGACT-----GCTGC 233
QY 44 uAlaValSerAspAlaLeuGlyArgProSerGluGluAspGluGluLeuValProGl 64
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QY 64 uLeuGluArgValProGlyHisGly-----ThrThrArgLeuArgLeuHisAlaPh 81
DB 292 -----CCGGCCACCCGCCACCCCTTGGCGCAGCGCGGAGGAGGAGGAGGCT 338
QY 81 eAspGlnGlnLeuAsp----- 86
DB 339 GGTGCGAAGCATCGAACCACTTACTCGGGCGGGCAAGGTGGGCTTACCTGCTTACGC 398
QY 87 -----LeuAspValProProAspSerSerPheLeuAlaProGlyPh 100
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Job time : 502 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: May 23, 2005, 18:18:14 ; Search time 104 Seconds
(without alignments)
3110.277 Million cell updates/sec

Title: US-09-373-658c-126

Perfect score: 5287

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Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1434725 seqs, 334507595 residues

Total number of hits satisfying chosen parameters: 1434725

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	5232	99.0	967	13	US-10-105-929-2
3	5232	99.0	967	14	US-10-115-286-2
4	5232	99.0	967	16	US-10-757-450-2
5	5224	98.8	967	16	US-10-755-889-134
6	5224	98.8	967	17	US-10-741-600-1603
7	5224	98.8	967	17	US-10-741-600-1604
8	5221.5	98.8	968	10	US-09-373-658-125
9	5144	97.3	950	11	US-09-373-658-2
10	5144	97.3	950	11	US-09-989-687-2
11	5140	97.2	949	17	US-10-667-281-2
12	5136	97.1	950	17	US-10-741-600-1605
13	5036	95.3	931	9	US-09-741-151-4

14	4293.5	81.2	968	13	US-10-163-316-7	Sequence 7, Appli
15	4293.5	81.2	968	16	US-10-391-364-82	Sequence 82, Appli
16	4264.5	80.7	951	15	US-10-381-793-3	Sequence 3, Appli
17	4260.5	80.6	950	9	US-09-321-987B-4	Sequence 4, Appli
18	3922	74.2	727	9	US-09-445-023A-1	Sequence 1, Appli
19	3922	74.2	727	14	US-10-097-597-1	Sequence 1, Appli
20	3922	74.2	727	14	US-10-097-580-1	Sequence 1, Appli
21	3656	69.2	727	9	US-09-445-023A-12	Sequence 12, Appli
22	3656	69.2	727	14	US-10-097-597-12	Sequence 12, Appli
23	3656	69.2	727	14	US-10-097-580-12	Sequence 12, Appli
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25	3297	62.4	608	9	US-09-803-589-8	Sequence 8, Appli
26	3297	62.4	608	13	US-10-105-923-13	Sequence 13, Appli
27	2794	52.8	551	9	US-09-802-582-16	Sequence 16, Appli
28	2794	52.8	551	13	US-10-105-929-16	Sequence 16, Appli
29	2794	52.8	551	14	US-10-365-227-16	Sequence 16, Appli
30	2635	49.8	518	9	US-09-803-589-10	Sequence 10, Appli
31	2495.5	47.2	924	15	US-10-093-463-28	Sequence 28, Appli
32	2478	46.9	950	9	US-10-275-107-59	Sequence 59, Appli
33	2477.5	46.9	950	9	US-09-741-151-2	Sequence 2, Appli
34	2477.5	46.9	950	9	US-09-965-631-4	Sequence 77, Appli
35	2477.5	46.9	950	16	US-10-391-364-77	Sequence 56, Appli
36	2477.5	46.9	950	17	US-10-753-267-56	Sequence 4, Appli
37	2477.5	46.9	950	17	US-10-961-020-4	Sequence 1, Appli
38	2471.5	46.7	950	16	US-10-763-210-1	Sequence 1, Appli
39	2467	46.7	577	15	US-10-425-114-39241	Sequence 39241, A
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41	2323	43.9	924	15	US-10-425-114-39107	Sequence 39107, A
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43	2320.5	43.9	890	11	US-09-989-687-4	Sequence 4, Appli
44	2265.5	42.9	905	9	US-09-918-171A-9	Sequence 9, Appli
45	2190	41.4	823	13	US-10-163-316-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1

US-09-989-687-126
; Sequence 126, Application US/09989687
; Publication No. US20040002449A1
; GENERAL INFORMATION:
; APPLICANT: Hastings, Gregg A.
; APPLICANT: Ruben, Steven M.
; TITLE OF INVENTION: Meth1 and Meth2 Polynucleotides and Polypeptides
; FILE REFERENCE: 1488.107000D
; CURRENT APPLICATION NUMBER: US/09/989,687
; CURRENT FILING DATE: 2001-11-21
; NUMBER OF SEQ ID NOS: 126
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 126
; LENGTH: 967
; TYPE: PRT
; ORGANISM: ITGL-TSP
US-09-989-687-126

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Best Local Similarity 100.0%; Pred. No. 0;
Matches 967; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy	121	AHCFYSTGVNGDPSSAAALSICGVRCGFYLLGAYFIQPLPAASERLATAAPGKPPAP	180
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-105-929-2

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Best Local Similarity 99.0%; Pred. No. 0;
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; Publication No. US20030166065A1
; GENERAL INFORMATION:
; APPLICANT: Jonak, Zdenka
; Trulli, Stephen
; Fornwald, James
; Terrett, Jonathan
; Hastings, Gregg
; TITLE OF INVENTION: No. US20030166065A1el Integrin Ligand ITGL-TSP
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ratner & Prestia
; STREET: Box 980
; CITY: Valley Forge
; STATE: PA
; COUNTRY: USA
; ZIP: 19482
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/115,286
; FILING DATE: 04-Apr-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/845,496
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Prestia, Paul F
; REGISTRATION NUMBER: 23,031
; REFERENCE/DOCKET NUMBER: GH-70000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-407-0700
; TELEFAX: 610-407-0701
; TELEX: 846169
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 967 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-115-286-2
Query Match 99.0%; Score 5232; DB 14; Length 967;
Best Local Similarity 99.0%; Pred. No. 0;
Matches 957; Conservative 4; Mismatches 6; Indels 0; Gaps 0;
Qy 1 MQRAVPGGRRKLGSDMGNAERAPGSRFGPVTLLLLAAALLAVSDALGRPSDEEL 60
Db 1 MQRAVPGGRRKLGSDMGNAERAPGSRFGPVTLLLLAAALLAVSDALGRPSDEEL 60
Qy 61 VVPELEVPVGHGTRRLRHAFDQQLDLDVPPDSSFLAPGFTLQNVGRKSGSDTLPETDL 120
Db 61 VVPELEVPVGHGTRRLRHAFDQQLDLDVPPDSSFLAPGFTLQNVGRKSGSETLPETDL 120
Qy 121 AHCFYSGTVNGDPSSAAALSICEGVGAFYLLGAYFIQPLPAASERLATAAPGKPPAP 180
Db 121 AHCFYSGTVNGDPSSAAALSICEGVGAFYLLGAYFIQPLPAASERLATAAPGKPPAP 180

Qy 181 LQFHLLRRNRQGDVGTCGVVDDEPRPTGKAETEDDEGTEGDEGQWSPQDPALQGVG 240
Db 181 LQFHLLRRNRQGDVGTCGVVDDEPRPTGKAETEDDEGTEGDEGQWSPQDPALQGVG 240
Qy 241 OPTGTGSIIRKGRFVSSHRYVETMLVADQSMAPGSLGHYLLTLFSVAARLYKHSIRN 300
Db 241 OPTGTGSIIRKGRFVSSHRYVETMLVADQSMAPGSLGHYLLTLFSVAARLYKHSIRN 300
Qy 301 SVSLVVVKILVHDEQKPEVTSNAALTILRNFCNWKQHNPPSDRDAEHYDTAILTFTRQD 360
Db 301 SVSLVVVKILVHDEQKPEVTSNAALTILRNFCNWKQHNPPSDRDAEHYDTAILTFTRQD 360
Qy 361 LCGSQTCDTLGMADVCTVCDPSRSCSVIBDDGLQAAFTTAHELGHVFNMPHDDAKQCASL 420
Db 361 LCGSQTCDTLGMADVCTVCDPSRSCSVIBDDGLQAAFTTAHELGHVFNMPHDDAKQCASL 420
Qy 421 NGVNDQSHMWASMLNLDHSDQWSPCSGYMITSFLDNHGHGECIMDKPQNPQLPGDLPGT 480
Db 421 NGVNDQSHMWASMLNLDHSDQWSPCSGYMITSFLDNHGHGECIMDKPQNPQLPGDLPGT 480
Qy 481 SYDANRQCQFTFGEDSKHCPDAASTCTSLWCTCTSGGLVVCQTKHFPWADGTSCGEGKWC 540
Db 481 SYDANRQCQFTFGEDSKHCPDAASTCTSLWCTCTSGGLVVCQTKHFPWADGTSCGEGKWC 540
Qy 541 INKGVNKNHRKHFDPFHGSMGWGPGWDCSRTCGGVOYTWRECDNPVPKNGKTCYCEG 600
Db 541 INKGVNKNHRKHFDPFHGSMGWGPGWDCSRTCGGVOYTWRECDNPVPKNGKTCYCEG 600
Qy 601 KRVYRSCNLEDCPDNNGKTFREEQCEAHNEFSAKSGSPAVIEWIPKYAGVSPKDRCKL 660
Db 601 KRVYRSCNLEDCPDNNGKTFREEQCEAHNEFSAKSGSPAVIEWIPKYAGVSPKDRCKL 660
Qy 661 ICOAKGIGYFFVLQPKVVDGTPCSPDSTVCGVQCVKAGCDRIIDSKKFDFKCGVCGGN 720
Db 661 ICOAKGIGYFFVLQPKVVDGTPCSPDSTVCGVQCVKAGCDRIIDSKKFDFKCGVCGGN 720
Qy 721 GSTCKKISGVSATKPGYHDIITPTGATNIEVKQRNQRSGRNGSFLATKAADGTIYN 780
Db 721 GSTCKKISGVSATKPGYHDIITPTGATNIEVKQRNQRSGRNGSFLATKAADGTIYN 780
Qy 781 GDYTLSTLEQDINMYGVLYRSGSSAALRIRSFPLKEPLTIQVLTGVALRPKIKYTY 840
Db 781 GDYTLSTLEQDINMYGVLYRSGSSAALRIRSFPLKEPLTIQVLTGVALRPKIKYTY 840
Qy 841 FVKKKESFNAIPTFSAWVIEEWGECSSCELGWQRRLVECRDINGOPASECAKEVPAS 900
Db 841 FVKKKESFNAIPTFSAWVIEEWGECSSCELGWQRRLVECRDINGOPASECAKEVPAS 900
Qy 901 TRPCADHPCPQWLGWSSCKTCGKGYKTSKLKCLSHDGGVLSHSCDPLKKPKHIFD 960
Db 901 TRPCADHPCPQWLGWSSCKTCGKGYKTSKLKCLSHDGGVLSHSCDPLKKPKHIFD 960
Qy 961 CTWAECS 967
Db 961 CTWAECS 967
RESULT 4
US-10-757-450-2
; Sequence 2, Application US/10757450
; Publication No. US20040175794A1
; GENERAL INFORMATION:
; APPLICANT: Jonak, Zdenka
; Trulli, Stephen
; Fornwald, James
; Terrett, Jonathan
; Hastings, Gregg
; TITLE OF INVENTION: Novel Integrin Ligand ITGL-TSP
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ratner & Prestia
; STREET: Box 980
; CITY: Valley Forge

STATE: PA
 COUNTRY: USA
 ZIP: 19482
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FastSeq for Windows Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/10/757,450
 FILING DATE: 04-Apr-2002
 CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/10/115,286
 FILING DATE: 04-Apr-2002
 APPLICATION NUMBER: 08/845,496
 FILING DATE: <Unknown>
 ATTORNEY/AGENT INFORMATION:
 NAME: Prestia, Paul F.
 REGISTRATION NUMBER: 23,031
 REFERENCE/DOCKET NUMBER: GH-70000
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 610-407-0700
 TELEFAX: 610-407-0701
 TELEX: 846169
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 967 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 SEQUENCE DESCRIPTION: SEQ ID NO: 2:
 US-10-757-450-2

Query Match 99.0%; Score 5232; DB 16; Length 967;
 Best Local Similarity 99.0%; Pred. No. 0;
 Matches 957; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY	1	MORAVPEGGRKGLSDMGNAERAPGSRSGFVPPTLLLAALLAVSDALGRPSDEDEL	60
DB	1	MORAVPEGGRKGLSDMGNAERAPGSRSGFVPPTLLLAALLAVSDALGRPSDEDEL	60
QY	61	VYPELERVPGHGTTLRLHAFQDLDVPPDSSFLAPGFTLQNVGRKSGSTPLPETDL	120
DB	61	VYPELERVPGHGTTLRLHAFQDLDVPPDSSFLAPGFTLQNVGRKSGSTPLPETDL	120
QY	121	AHCFYSGTVNGDPSSAAALSLCEGVGAFYLLGEAYFIQPLPAASERLATAAPGKPPAP	180
DB	121	AHCFYSGTVNGDPSSAAALSLCEGVGAFYLLGEAYFIQPLPAASERLATAAPGKPPAP	180
QY	181	LQFHLLRRNQDVGTCGVVDDEPRPTCKAETDEDETEGEDEGPQSPDPALQGVG	240
DB	181	LQFHLLRRNQDVGTCGVVDDEPRPTCKAETDEDETEGEDEGPQSPDPALQGVG	240
QY	241	QPTGTSIRKKRFVSSHRYVETMLVADQSMAFHSGSLKHYLLTFSVAARLYKHSIN	300
DB	241	QPTGTSIRKKRFVSSHRYVETMLVADQSMAFHSGSLKHYLLTFSVAARLYKHSIN	300
QY	301	SVSLVVVKLVHDEQKGEVTSNAALTILRNFCNWKQHNPPSDRDAEHYDTAILFTROD	360
DB	301	SVSLVVVKLVHDEQKGEVTSNAALTILRNFCNWKQHNPPSDRDAEHYDTAILFTROD	360
QY	361	LCGSOTCDTLGMADVTCVDRSCSVIEDDGLQAAFTTAHELGHVFNMPHDDAKQACSL	420
DB	361	LCGSOTCDTLGMADVTCVDRSCSVIEDDGLQAAFTTAHELGHVFNMPHDDAKQACSL	420
QY	421	NGVNQDSHMAWMLSNLDHSQWPCSGYMTITSFLDNGHCECLMDKQPNPIQLPGDLPT	480
DB	421	NGVNQDSHMAWMLSNLDHSQWPCSGYMTITSFLDNGHCECLMDKQPNPIQLPGDLPT	480
QY	481	SYDANRQCQFTFGEDSKHCPDAAASTCTLWCTGTSGGVLVVCQTKHPFWADGTSCEGKWC	540

DB	481	SYDANRQCQFTFGEDSKHCPDAAASTCTLWCTGTSGGVLVVCQTKHPFWADGTSCEGKWC	540
QY	541	INGKCVNKHKKHFDTPPHGSGWGMGPGWDCSRTCGGVOYTMRECDNPVPNGGKYCSG	600
DB	541	INGKCVNKHKKHFDTPPHGSGWGMGPGWDCSRTCGGVOYTMRECDNPVPNGGKYCSG	600
QY	601	KVRYRSCNLEDCPDNNGKTFRFEOCEAHNBSKASFGSGPAVEWIPKYAGVSPKDRCKL	660
DB	601	KVRYRSCNLEDCPDNNGKTFRFEOCEAHNBSKASFGSGPAVEWIPKYAGVSPKDRCKL	660
QY	661	ICQAKGIGYFFVLQPKVVDGTPCSPDSTSVQGVQCVKAGCDRIIDSKKKFKDCKGCGGN	720
DB	661	ICQAKGIGYFFVLQPKVVDGTPCSPDSTSVQGVQCVKAGCDRIIDSKKKFKDCKGCGGN	720
QY	721	GSTCKKISGSVTSAPGPHDIITPTGATNIVKORNGSRNNGSFLAIAKADGTIYLN	780
DB	721	GSTCKKISGSVTSAPGPHDIITPTGATNIVKORNGSRNNGSFLAIAKADGTIYLN	780
QY	781	GDYTLSTLEODIMYKGVVLYSGSSAALERIRSFSPLEPLTIQVLTGVALRPKIKYTY	840
DB	781	GDYTLSTLEODIMYKGVVLYSGSSAALERIRSFSPLEPLTIQVLTGVALRPKIKYTY	840
QY	841	FVKKKESFNAPTFSAWVIEWEGSCSKCELGWQRLVECRDINGQPASECAKEVKPAS	900
DB	841	FVKKKESFNAPTFSAWVIEWEGSCSKCELGWQRLVECRDINGQPASECAKEVKPAS	900
QY	901	TRPCADHPCPQWLGWSSCSKTCGKYKTSKLSKLSHDGGVLSHSDCDPLKKPHFIDF	960
DB	901	TRPCADHPCPQWLGWSSCSKTCGKYKTSKLSKLSHDGGVLSHSDCDPLKKPHFIDF	960
QY	961	CTMAECS 967	
DB	961	CTMAECS 967	

RESULT 5
 US-10-755-889-134
 ; Sequence 134, Application US/10755889
 ; Publication No. US20040171823A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Bristol-Myers Squibb Company
 ; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES ASSOCIATED WITH THE NF- κ B
 ; TITLE OF INVENTION: PATHWAY
 ; FILE REFERENCE: D0284 NP
 ; CURRENT APPLICATION NUMBER: US/10/755,889
 ; CURRENT FILING DATE: 2004-01-13
 ; PRIOR APPLICATION NUMBER: U.S. 60/440,068
 ; PRIOR FILING DATE: 2003-01-14
 ; PRIOR APPLICATION NUMBER: U.S. 60/469,757
 ; PRIOR FILING DATE: 2003-05-12
 ; NUMBER OF SEQ ID NOS: 823
 ; SOFTWARE: Patent in version 3.2
 ; SEQ ID NO 134
 ; LENGTH: 967
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-10-755-889-134

Query Match 98.8%; Score 5224; DB 16; Length 967;
 Best Local Similarity 98.8%; Pred. No. 0;
 Matches 955; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

QY	1	MORAVPEGGRKGLSDMGNAERAPGSRSGFVPPTLLLAALLAVSDALGRPSDEDEL	60
DB	1	MORAVPEGGRKGLSDMGNAERAPGSRSGFVPPTLLLAALLAVSDALGRPSDEDEL	60
QY	61	VYPELERVPGHGTTLRLHAFQDLDVPPDSSFLAPGFTLQNVGRKSGSTPLPETDL	120
DB	61	VYPELERVPGHGTTLRLHAFQDLDVPPDSSFLAPGFTLQNVGRKSGSTPLPETDL	120
QY	121	AHCFYSGTVNGDPSSAAALSLCEGVGAFYLLGEAYFIQPLPAASERLATAAPGKPPAP	180
DB	121	AHCFYSGTVNGDPSSAAALSLCEGVGAFYLLGEAYFIQPLPAASERLATAAPGKPPAP	180

181 LQPHLLRRNRQDVGTCGVVDDEPRPTGKAETEDDEGTEDEGEDEGPQSPDPAALQGVG 240
181 LQPHLLRRNRQDVGTCGVVDDEPRPTGKAETEDDEGTEDEGEDEGPQSPDPAALQGVG 240
241 QPTGTGSIIRKGRFVSSHRVYETMLVADQSMABPHGSLGKHYLLTLFSVAARLYKHPISRN 300
241 QPTGTGSIIRKGRFVSSHRVYETMLVADQSMABPHGSLGKHYLLTLFSVAARLYKHPISRN 300
301 SVSLVVVKILVTHDEQKGPVTSNAALTLRNFNCWQKQHNPPSDRDAEHVDTAILFTROD 360
301 SVSLVVVKILVTHDEQKGPVTSNAALTLRNFNCWQKQHNPPSDRDAEHVDTAILFTROD 360
361 LCGSQTCDTLGMADVGTCDPSRSCSVIEDDGLQAAFTTAHELGHVFNPHDDAKQCSL 420
361 LCGSQTCDTLGMADVGTCDPSRSCSVIEDDGLQAAFTTAHELGHVFNPHDDAKQCSL 420
421 NGVNDQSHMWASMLNLDHSHQSPWPCSAAYMITSLFNGHGECLMDKPHNPQLPGDLPGT 480
421 NGVNDQSHMWASMLNLDHSHQSPWPCSAAYMITSLFNGHGECLMDKPHNPQLPGDLPGT 480
481 SYDANRQCQFTFGEDSKHCPDAASTCSTLWCTGSGVLVCOQKHPFADGTSCGEGKWC 540
481 SYDANRQCQFTFGEDSKHCPDAASTCSTLWCTGSGVLVCOQKHPFADGTSCGEGKWC 540
541 INKCVNKNRKHFDTPFHGSGWGMGPWGDCSRTCGGQVQYTMRECDNPVPKNGKCYCEG 600
541 INKCVNKNRKHFDTPFHGSGWGMGPWGDCSRTCGGQVQYTMRECDNPVPKNGKCYCEG 600
601 KRVRYSNCLEDCPDNNGKTFREEQCEAHNEFSGKASFGSGPAVEWIPKYAGVSPKDRCKL 660
601 KRVRYSNCLEDCPDNNGKTFREEQCEAHNEFSGKASFGSGPAVEWIPKYAGVSPKDRCKL 660
661 ICOAKGIGYFFVLQPKVVDGTPCSPDSTSVCOGQCVKAGCDRIIDSXKKFDCGVCN 720
661 ICOAKGIGYFFVLQPKVVDGTPCSPDSTSVCOGQCVKAGCDRIIDSXKKFDCGVCN 720
721 GSTCKKISGVTSAKPGYHDIITPTGATNIEVKQRNQRNNGSFLAIKAADGTYILN 780
721 GSTCKKISGVTSAKPGYHDIITPTGATNIEVKQRNQRNNGSFLAIKAADGTYILN 780
781 GDTLSTLEQDQIMYKGVLYRSGSSAALERIRSFPLKEPLTIQVLTGVNALRPKIKYTY 840
781 GDTLSTLEQDQIMYKGVLYRSGSSAALERIRSFPLKEPLTIQVLTGVNALRPKIKYTY 840
841 FVKKKESFNAIPTFSAWVIEEWGECSSKCELGWQRLVECRDINGOPASECAKEVPAS 900
841 FVKKKESFNAIPTFSAWVIEEWGECSSKCELGWQRLVECRDINGOPASECAKEVPAS 900
901 TRPCADHPCQWOLGEWSSCKTCGKGYKKTSLKCLSHDGGVLSHSDCDPLKPKHFIDF 960
901 TRPCADHPCQWOLGEWSSCKTCGKGYKKTSLKCLSHDGGVLSHSDCDPLKPKHFIDF 960
961 CTMAECS 967
961 CTMAECS 967

RESULT 6
US-10-741-600-1603
; Sequence 1603, Application US/10741600
; Publication No. US20050026169A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001499
; CURRENT APPLICATION NUMBER: US/10/741.600
; CURRENT FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 73997
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1603
; LENGTH: 967

; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-741-600-1603
Query Match 98.8%; Score 5224; DB 17; Length 967;
Best Local Similarity 98.9%; Pred. No. 0;
Matches 956; Conservative 4; Mismatches 7; Indels 0; Gaps 0;
QY 1 MORAYPEGFRGKLGSDMGNAERAPGSRSGFVPVPTLLLLAALLAVSDALGRPSEDEEL 60
DB 1 MORAYPEGFRGKLGSDMGNAERAPGSRSGFVPVPTLLLLAALLAVSDALGRPSEDEEL 60
QY 61 VVPELERVPHGHTTRRLHAFDQQLDLDVPPDSSFLAPGFTLQNVGRKSGSDTLPETDL 120
DB 61 VVPELERVPHGHTTRRLHAFDQQLDLDVPPDSSFLAPGFTLQNVGRKSGSDTLPETDL 120
QY 121 AHCFYSGTVNGDPSSAAALSCEGVGAFYLGEAYFIQPLPAASERLATAAPEGKPPAP 180
DB 121 AHCFYSGTVNGDPSSAAALSCEGVGAFYLGEAYFIQPLPAASERLATAAPEGKPPAP 180
QY 181 LQPHLLRRNRQDVGTCGVVDDEPRPTGKAETEDDEGTEDEGEDEGPQSPDPAALQGVG 240
DB 181 LQPHLLRRNRQDVGTCGVVDDEPRPTGKAETEDDEGTEDEGEDEGPQSPDPAALQGVG 240
QY 241 QPTGTGSIIRKGRFVSSHRVYETMLVADQSMABPHGSLGKHYLLTLFSVAARLYKHPISRN 300
DB 241 QPTGTGSIIRKGRFVSSHRVYETMLVADQSMABPHGSLGKHYLLTLFSVAARLYKHPISRN 300
QY 301 SVSLVVVKILVTHDEQKGPVTSNAALTLRNFNCWQKQHNPPSDRDAEHVDTAILFTROD 360
DB 301 SVSLVVVKILVTHDEQKGPVTSNAALTLRNFNCWQKQHNPPSDRDAEHVDTAILFTROD 360
QY 361 LCGSQTCDTLGMADVGTCDPSRSCSVIEDDGLQAAFTTAHELGHVFNPHDDAKQCSL 420
DB 361 LCGSQTCDTLGMADVGTCDPSRSCSVIEDDGLQAAFTTAHELGHVFNPHDDAKQCSL 420
QY 421 NGVNDQSHMWASMLNLDHSHQSPWPCSAAYMITSLFNGHGECLMDKPHNPQLPGDLPGT 480
DB 421 NGVNDQSHMWASMLNLDHSHQSPWPCSAAYMITSLFNGHGECLMDKPHNPQLPGDLPGT 480
QY 481 SYDANRQCQFTFGEDSKHCPDAASTCSTLWCTGSGVLVCOQKHPFADGTSCGEGKWC 540
DB 481 SYDANRQCQFTFGEDSKHCPDAASTCSTLWCTGSGVLVCOQKHPFADGTSCGEGKWC 540
QY 541 INKCVNKNRKHFDTPFHGSGWGMGPWGDCSRTCGGQVQYTMRECDNPVPKNGKCYCEG 600
DB 541 INKCVNKNRKHFDTPFHGSGWGMGPWGDCSRTCGGQVQYTMRECDNPVPKNGKCYCEG 600
QY 601 KRVRYSNCLEDCPDNNGKTFREEQCEAHNEFSGKASFGSGPAVEWIPKYAGVSPKDRCKL 660
DB 601 KRVRYSNCLEDCPDNNGKTFREEQCEAHNEFSGKASFGSGPAVEWIPKYAGVSPKDRCKL 660
QY 661 ICOAKGIGYFFVLQPKVVDGTPCSPDSTSVCOGQCVKAGCDRIIDSXKKFDCGVCN 720
DB 661 ICOAKGIGYFFVLQPKVVDGTPCSPDSTSVCOGQCVKAGCDRIIDSXKKFDCGVCN 720
QY 721 GSTCKKISGVTSAKPGYHDIITPTGATNIEVKQRNQRNNGSFLAIKAADGTYILN 780
DB 721 GSTCKKISGVTSAKPGYHDIITPTGATNIEVKQRNQRNNGSFLAIKAADGTYILN 780
QY 781 GDTLSTLEQDQIMYKGVLYRSGSSAALERIRSFPLKEPLTIQVLTGVNALRPKIKYTY 840
DB 781 GDTLSTLEQDQIMYKGVLYRSGSSAALERIRSFPLKEPLTIQVLTGVNALRPKIKYTY 840
QY 841 FVKKKESFNAIPTFSAWVIEEWGECSSKCELGWQRLVECRDINGOPASECAKEVPAS 900
DB 841 FVKKKESFNAIPTFSAWVIEEWGECSSKCELGWQRLVECRDINGOPASECAKEVPAS 900
QY 901 TRPCADHPCQWOLGEWSSCKTCGKGYKKTSLKCLSHDGGVLSHSDCDPLKPKHFIDF 960
DB 901 TRPCADHPCQWOLGEWSSCKTCGKGYKKTSLKCLSHDGGVLSHSDCDPLKPKHFIDF 960
QY 961 CTMAECS 967
961 CTMAECS 967

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Db          961 CTMAECS 967
|||||
RESULT 7
US-10-741-600-1604
; Sequence 1604, Application US/10741600
; Publication No. US20050026169A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; FILE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001499
; CURRENT APPLICATION NUMBER: US/10/741,600
; CURRENT FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 73997
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1604
; LENGTH: 967
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-741-600-1604

Query Match      98.8%; Score 5224; DB 17; Length 967;
Best Local Similarity 98.9%; Pred. No. 0;
Matches 956; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 1 MORAVPEGFGRKLGSDMGNARAPGSRSGFVPVPTLLLLAAALLAVSDALGRPSDEBEL 60
Db 1 MORAVPEGFGRKLGSDMGNARAPGSRSGFVPVPTLLLLAAALLAVSDALGRPSDEBEL 60
QY 61 VVPELERVPGHGTTRLRHAFQDQDLDPDSSFLAPGFTLQNVGRKSGDTPLEPDTL 120
Db 61 VVPELERAPGHGTTRLRHAFQDQDLDPDSSFLAPGFTLQNVGRKSGDTPLEPDTL 120
QY 121 AHCFSYGTGVNGDPSSAAALSCEGVGAFYLLGEAYFIQPLPAASERLATAAPGKPPAP 180
Db 121 AHCFSYGTGVNGDPSSAAALSCEGVGAFYLLGEAYFIQPLPAASERLATAAPGKPPAP 180
QY 181 LQFHLRRNRQDVGTCGVVDDEPRPTGKATEDEDEGEDEGGPQSPDPAALQGVG 240
Db 181 LQFHLRRNRQDVGTCGVVDDEPRPTGKATEDEDEGEDEGGPQSPDPAALQGVG 240
QY 241 OPTGTGSRIRKRFVSSHRYVETMLVADQSMAEFHGSLGKHYLLTLFVVAARLYKHPISR 300
Db 241 OPTGTGSRIRKRFVSSHRYVETMLVADQSMAEFHGSLGKHYLLTLFVVAARLYKHPISR 300
QY 301 SVSLVVVKILVIHDBQKGPVTSNAALTILRNFCNNKQHNPPSDRDAEHYDTAILFTTRQD 360
Db 301 SVSLVVVKILVIHDBQKGPVTSNAALTILRNFCNNKQHNPPSDRDAEHYDTAILFTTRQD 360
QY 361 LCGSQTCDTLGMADVGTCDPSRSCSVIEDDGLQAAFTTAHLGHVFNPHDPAKQACSL 420
Db 361 LCGSQTCDTLGMADVGTCDPSRSCSVIEDDGLQAAFTTAHLGHVFNPHDPAKQACSL 420
QY 421 NGVNQDSHMAWMLNLDHSPWPCSGYMTISFLDNGHGECLMDKQNPQIQLPGDLPT 480
Db 421 NGVNQDSHMAWMLNLDHSPWPCSGYMTISFLDNGHGECLMDKQNPQIQLPGDLPT 480
QY 481 SYDANRQCOFTFGEBSKHCPDAASTCSTLWCTGTSGGVLVCOTKHFPWADGTCGEGKWC 540
Db 481 SYDANRQCOFTFGEBSKHCPDAASTCSTLWCTGTSGGVLVCOTKHFPWADGTCGEGKWC 540
QY 541 INKCVKNRKHFDTPFHGSGMGMGPWGDGCSRTCGGQVYTMRECDNPVKNQKGYCEG 600
Db 541 INKCVKNRKHFDTPFHGSGMGMGPWGDGCSRTCGGQVYTMRECDNPVKNQKGYCEG 600
QY 601 KVRVRSNLEDCPNNGKTFREOCEAHNEFSKASFGSGPAVEWIPKYAGVSPKORCKL 660
Db 601 KVRVRSNLEDCPNNGKTFREOCEAHNEFSKASFGSGPAVEWIPKYAGVSPKORCKL 660
QY 661 ICAQKIGIGYFFVLQPKVVDGTPCSPDSTSVCVQGCVKAGCDRIIDSKKKPKDCGVCN 720
Db 661 ICAQKIGIGYFFVLQPKVVDGTPCSPDSTSVCVQGCVKAGCDRIIDSKKKPKDCGVCN 720
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Db          961 CTMAECS 967
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RESULT 8
US-09-373-658-125
; Sequence 125, Application US/09373658
; Publication No. US20030092900A1
; GENERAL INFORMATION:
; APPLICANT: Iruela-Arispe, Luisa
; APPLICANT: Hastings, Gregg A.
; APPLICANT: Ruben, Steven M.
; APPLICANT: Jonak, Zdenka L.
; APPLICANT: Trulli, Stephen H.
; APPLICANT: Fronwald, James A.
; APPLICANT: Terrett, Jonathan A.
; TITLE OF INVENTION: Meth1 and Meth2 Polynucleotides and Polypeptides
; FILE REFERENCE: 1488.1070006
; CURRENT APPLICATION NUMBER: US/09/373,658
; CURRENT FILING DATE: 1999-08-13
; NUMBER OF SEQ ID NOS: 125
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 125
; LENGTH: 968
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-373-658-125

Query Match      98.8%; Score 5221.5; DB 10; Length 968;
Best Local Similarity 98.9%; Pred. No. 0;
Matches 957; Conservative 4; Mismatches 6; Indels 1; Gaps 1;

QY 1 MORAVPEGFGRKLGSDMGNARAPGSRSGFVPVPTLLLLAAALLAVSDALGRPSDEBEL 59
Db 1 MORAVPEGFGRKLGSDMGNARAPGSRSGFVPVPTLLLLAAALLAVSDALGRPSDEBEL 60
QY 60 LVVPELEVPVPGHGTTRLRHAFDQDQDLDPDSSFLAPGFTLQNVGRKSGDTPLEPDT 119
Db 61 LVVPELERAPGHGTTRLRHAFDQDQDLDPDSSFLAPGFTLQNVGRKSGDTPLEPDT 120
QY 120 LAHCFYSYGTGVNGDPSSAAALSCEGVGAFYLLGEAYFIQPLPAASERLATAAPGKPPA 179
Db 121 LAHCFYSYGTGVNGDPSSAAALSCEGVGAFYLLGEAYFIQPLPAASERLATAAPGKPPA 180
QY 180 PLOFHLLBRNRQDVGTCGVVDDEPRPTGKATEDEDEGEDEGGPQSPDPAALQGV 239
Db 181 PLOFHLLBRNRQDVGTCGVVDDEPRPTGKATEDEDEGEDEGGPQSPDPAALQGV 240
QY 240 GQPTGTGSRIRKRFVSSHRYVETMLVADQSMAEFHGSLGKHYLLTLFVVAARLYKHPISR 299
Db 241 GQPTGTGSRIRKRFVSSHRYVETMLVADQSMAEFHGSLGKHYLLTLFVVAARLYKHPISR 300
QY 300 NSVSLVVVKILVIHDBQKGPVTSNAALTILRNFCNNKQHNPPSDRDAEHYDTAILFTTRQ 359
Db 300 NSVSLVVVKILVIHDBQKGPVTSNAALTILRNFCNNKQHNPPSDRDAEHYDTAILFTTRQ 359
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Db 301 NSVSLVVVKKILVIHDEQKPEVTSNAALTNRNFCNWQKQHNPPSDRDAEHYDTAILFTRQ 360
QY 360 DLCSGTCOTLGMADVGTWCDPRSCSVIEDDGLQAAFTTAHGLHGFVNPHDPAKQAS 419
Db 361 DLCSGTCOTLGMADVGTWCDPRSCSVIEDDGLQAAFTTAHGLHGFVNPHDPAKQAS 420
QY 420 LNVGVNDSHMMASMLNLDHSPQSPSCGYMITSFLDNGHGECLMDKPNPIQLPGDLFG 479
Db 421 LNVGVNDSHMMASMLNLDHSPQSPSCGYMITSFLDNGHGECLMDKPNPIQLPGDLFG 480
QY 480 TSYDANRQCOFTFGEDSKHCPDAASTCTLWCTGTSGVLVVCOTKPPPHADGTSCEGKW 539
Db 481 TSYDANRQCOFTFGEDSKHCPDAASTCTLWCTGTSGVLVVCOTKPPPHADGTSCEGKW 540
QY 540 CINGKCVNKHRRKHFTPPFHSGMGMGPWGDSCRTCGGVQYTMRECDNPPVKNKGKCYE 599
Db 541 CINGKCVNKHRRKHFTPPFHSGMGMGPWGDSCRTCGGVQYTMRECDNPPVKNKGKCYE 600
QY 600 GKRVYRSCNLEDCPDNNGKTFREEQCEAHNEFSKASFGSGPAVEWIPKYAGVSPKDRCK 659
Db 601 GKRVYRSCNLEDCPDNNGKTFREEQCEAHNEFSKASFGSGPAVEWIPKYAGVSPKDRCK 660
QY 660 LICOAKGIGYFFVLQPKVVDGTPCSPDSTSVCVQGCVKAGCDRIIDSKKPKCGVCGG 719
Db 661 LICOAKGIGYFFVLQPKVVDGTPCSPDSTSVCVQGCVKAGCDRIIDSKKPKCGVCGG 720
QY 720 NGSTCKKISGSVTSAPKGVHDIIITPTGATNIEVKQNRQSGRNGSFLAKAAGTYIL 779
Db 721 NGSTCKKISGSVTSAPKGVHDIIITPTGATNIEVKQNRQSGRNGSFLAKAAGTYIL 780
QY 780 NGDYTLSTLEQDLMYKGVLRYSGSSAALRIRSFSPKLEPLTIQVLTGVNLRPKIKYT 839
Db 781 NGDYTLSTLEQDLMYKGVLRYSGSSAALRIRSFSPKLEPLTIQVLTGVNLRPKIKYT 840
QY 840 YFVKKKESFNAIPTFSAWIEBWGECSSKSELGWQRLVECRDINGQPASECAKEVKA 899
Db 841 YFVKKKESFNAIPTFSAWIEBWGECSSKSELGWQRLVECRDINGQPASECAKEVKA 900
QY 900 STRPCADHPCPQWLGEWSSCKTCGKYKTSKCLSHDGVLSHDSCDPLKPKHFID 959
Db 901 STRPCADHPCPQWLGEWSSCKTCGKYKTSKCLSHDGVLSHDSCDPLKPKHFID 960
QY 960 FCTMAECS 967
Db 961 FCTMAECS 968

RESULT 9

US-09-373-658-2
; Sequence 2, Application US/09373658
; Publication No. US20030092900A1
; GENERAL INFORMATION:
; APPLICANT: Iruela-Arispe, Luisa
; APPLICANT: Hastings, Gregg A.
; APPLICANT: Ruben, Steven M.
; APPLICANT: Jonak, Zdenka L.
; APPLICANT: Trulli, Stephen H.
; APPLICANT: Fronwald, James A.
; APPLICANT: Terrett, Jonathan A.
; TITLE OF INVENTION: Meth1 and Meth2 Polynucleotides and Polypeptides
; FILE REFERENCE: 1488.1070006
; CURRENT APPLICATION NUMBER: US/09/373,658
; CURRENT FILING DATE: 1999-08-13
; NUMBER OF SEQ ID NOS: 125
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 950
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-373-658-2
Query Match 97.3%; Score 5144; DB 10; Length 950;
Best Local Similarity 98.9%; Pred. No. 0;

Matches 940; Conservative 4; Mismatches 6; Indels 0; Gaps 0;
QY 18 MGNAERAPGSRSGFPVPTLLLLAAALLAVSDALGRPSEDEELVPELERVPGHGTTLR 77
Db 1 MGNAERAPGSRSGFPVPTLLLLAAALLAVSDALGRPSEDEELVPELERVPGHGTTLR 60
QY 78 LHAFOOQLDLVPPDSSFLAPGFTLQNVGRKSGSDTLPETDLAHFYSGTVNGDPSAA 137
Db 61 LHAFOOQLDLVPPDSSFLAPGFTLQNVGRKSGSETPLPETDLAHFYSGTVNGDPSAA 120
QY 138 ALSLCGVRGAFVLLGEAYFIQPLPAASERLATAAPEKPPAPLQPHLLRRNRQGVGGT 197
Db 121 ALSLCGVRGAFVLLGEAYFIQPLPAASERLATAAPEKPPAPLQPHLLRRNRQGVGGT 180
QY 198 CGVVDDEPRTGKAETDEDETEGEDEGPQSPDPAALQGVQOQTGTGTSIRKRFVSSH 257
Db 181 CGVVDDEPRTGKAETDEDETEGEDEGPQSPDPAALQGVQOQTGTGTSIRKRFVSSH 240
QY 258 RYVETMLVADQSMABFHGSLKHYLLTLFSVAARLYKHPSIRNSVSLVVKILVIHDEQK 317
Db 241 RYVETMLVADQSMABFHGSLKHYLLTLFSVAARLYKHPSIRNSVSLVVKILVIHDEQK 300
QY 318 GPEVTSNAALTNRNFCNWQKQHNPPSDRDAEHYDTAILFTRQDLCSGTCOTLGMADVGT 377
Db 301 GPEVTSNAALTNRNFCNWQKQHNPPSDRDAEHYDTAILFTRQDLCSGTCOTLGMADVGT 360
QY 378 VCDPSRSCSVIEDDGLQAAFTTAHGLHGFVNPHDPAKQASLNGVNDSHMMASMLSNL 437
Db 361 VCDPSRSCSVIEDDGLQAAFTTAHGLHGFVNPHDPAKQASLNGVNDSHMMASMLSNL 420
QY 438 DHSQPSPCSGYMITSFLDNGHGECLMDKPNPIQLPGDLPGTSDYANRQCOFTFGEDSK 497
Db 421 DHSQPSPCSGYMITSFLDNGHGECLMDKPNPIQLPGDLPGTSDYANRQCOFTFGEDSK 480
QY 498 HCPDAASTCTLWCTGTSGVLVVCOTKPPHWDGTSCEGKWCINGKCVNKHRRKHFTDP 557
Db 481 HCPDAASTCTLWCTGTSGVLVVCOTKPPHWDGTSCEGKWCINGKCVNKHRRKHFTDP 540
QY 558 FHSGWGMWGPWGDSCRTCGGVQYTMRECDNPPVKNKGKTCGKRVYRSCNLEDCPDNN 617
Db 541 FHSGWGMWGPWGDSCRTCGGVQYTMRECDNPPVKNKGKTCGKRVYRSCNLEDCPDNN 600
QY 618 GKTFFREEQCEAHNEFSKASFGSGPAVEWIPKYAGVSPKDRCKLICQAKGIGYFFVLQPKV 677
Db 601 GKTFFREEQCEAHNEFSKASFGSGPAVEWIPKYAGVSPKDRCKLICQAKGIGYFFVLQPKV 660
QY 678 VDGTPCSPDSTSVCVQGCVKAGCDRIIDSKKPKDKCGVCGNGSTCKKISGSVTSAPG 737
Db 661 VDGTPCSPDSTSVCVQGCVKAGCDRIIDSKKPKDKCGVCGNGSTCKKISGSVTSAPG 720
QY 738 YHDIITPTGATNIEVKQNRQSGRNGSFLAKAAGTYILNGDYTLSTLEQDIMYKGV 797
Db 721 YHDIITPTGATNIEVKQNRQSGRNGSFLAKAAGTYILNGDYTLSTLEQDIMYKGV 780
QY 798 VLRYSGSSAALRIRSFSPKLEPLTIQVLTGVNLRPKIKYTYFVKKKSGSFNAIPTFSA 857
Db 781 VLRYSGSSAALRIRSFSPKLEPLTIQVLTGVNLRPKIKYTYFVKKKSGSFNAIPTFSA 840
QY 858 WVIIEWGECSSKSELGWQRLVECRDINGQPASECAKEVKASTRPCADHPCPQWLGEW 917
Db 841 WVIIEWGECSSKSELGWQRLVECRDINGQPASECAKEVKASTRPCADHPCPQWLGEW 900
QY 918 SSCSKTCGKYKTSKCLSHDGVLSHDSCDPLKPKHFIDFCTMAECS 967
Db 901 SSCSKTCGKYKTSKCLSHDGVLSHDSCDPLKPKHFIDFCTMAECS 950

RESULT 10

US-09-989-687-2
; Sequence 2, Application US/09989687
; Publication No. US20040002449A1
; GENERAL INFORMATION:
; APPLICANT: Hastings, Gregg A.

APPLICANT: Ruben, Steven M.
; TITLE OF INVENTION: Meth1 and Meth2 Polynucleotides and Polypeptides
; FILE REFERENCE: 1488.107000D
; CURRENT APPLICATION NUMBER: US/09/989,687
; CURRENT FILING DATE: 2001-11-21
; NUMBER OF SEQ ID NOS: 126
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 950
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-989-687-2

Query Match
Best Local Similarity 97.3%; Score 5144; DB 11; Length 950;
Matches 940; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 18 MGAERAPGSRSGFVPVPTLLLLAAALLAVSDALGRPSEDEELVPELERVFGHGTTRLR 77
Db 1 MGAERAPGSRSGFVPVPTLLLLAAALLAVSDALGRPSEDEELVPELERVFGHGTTRLR 60

QY 78 LHAFOQLDLVPPDSSFLAPGFTLQNVGRKSGSDTLPETDLAHCFTSGTVNGDPSSAA 137
Db 61 LHAFOQLDLVPPDSSFLAPGFTLQNVGRKSGSETPLPETDLAHCFTSGTVNGDPSSAA 120

QY 138 ALSLCGVRGAFYLLGEAFYIQLPAAASERLATAAPGKPPAPLOPHLLRRNRQDVGCT 197
Db 121 ALSLCGVRGAFYLLGEAFYIQLPAAASERLATAAPGKPPAPLOPHLLRRNRQDVGCT 180

QY 198 CGVDDPRPTGKAETDEDETEDEGEDEGPQSPDPAALQGVQPTGTGIRKRGFVSSH 257
Db 181 CGVDDPRPTGKAETDEDETEDEGEDEGPQSPDPAALQGVQPTGTGIRKRGFVSSH 240

QY 258 RIVETMLVADQSMABFPHSGSLKHYLLTLFSVAARLYKHPISIRNSVSLVVKILVHDEOK 317
Db 241 RIVETMLVADQSMABFPHSGSLKHYLLTLFSVAARLYKHPISIRNSVSLVVKILVHDEOK 300

QY 318 GPEVTSNAALTIRNFCNWKQHNPPSDRDAEHYDTAILFTRQDLCSQTCDTLGMADVGT 377
Db 301 GPEVTSNAALTIRNFCNWKQHNPPSDRDAEHYDTAILFTRQDLCSQTCDTLGMADVGT 360

QY 378 VCDPSRCSVIEDDDGLQAAFTTAHELGHVFNPHDDAKQACASLNGVNDQSHMWSMLSL 437
Db 361 VCDPSRCSVIEDDDGLQAAFTTAHELGHVFNPHDDAKQACASLNGVNDQSHMWSMLSL 420

QY 438 DHSQWSPSCGYMITSFLDNGHGECLMDKXPQNPQLPGDLPGTSYDANRQCQFTFGEDSK 497
Db 421 DHSQWSPSCGYMITSFLDNGHGECLMDKXPQNPQLPGDLPGTSYDANRQCQFTFGEDSK 480

QY 498 HCPDAASTCTLWCTGTSGGVLCVOTKHPFPAWADGTSCGEGKWCINGKCNKXNRKHFDP 557
Db 481 HCPDAASTCTLWCTGTSGGVLCVOTKHPFPAWADGTSCGEGKWCINGKCNKXNRKHFDP 540

QY 558 FHSGWGMGPWGDSCRTCGGVQYTMRECDNPVPKNGGKYCEGKRVYRSCNLEDCPDNN 617
Db 541 FHSGWGMGPWGDSCRTCGGVQYTMRECDNPVPKNGGKYCEGKRVYRSCNLEDCPDNN 600

QY 618 GHTFREQCEAHNEFSKASFGSGPAVEWIPKAGVSPKDRCKLIQAKGIGYFFVLQPKY 677
Db 601 GHTFREQCEAHNEFSKASFGSGPAVEWIPKAGVSPKDRCKLIQAKGIGYFFVLQPKY 660

QY 678 VDGTPCSPDSTSVCGQCVKAGCDRIIDSKKFKDKGCVGGNGSTCKKISGSVTSAXPG 737
Db 661 VDGTPCSPDSTSVCGQCVKAGCDRIIDSKKFKDKGCVGGNGSTCKKISGSVTSAXPG 720

QY 738 YHDIITPTGATNIEVKQRNQRSGRNGSFLAIKAADGTYYILNGDYTLSTLEQDIMYKGV 797
Db 721 YHDIITPTGATNIEVKQRNQRSGRNGSFLAIKAADGTYYILNGDYTLSTLEQDIMYKGV 780

QY 798 VLRYSGSSAALIRISFSLKEPLTIQVLTGVNALARPKIKYTFVKKKESFNALPTPSA 857
Db 781 VLRYSGSSAALIRISFSLKEPLTIQVLTGVNALARPKIKYTFVKKKESFNALPTPSA 840

QY 858 WVIBEWGCSKSCELGWORRLVECRDINGQPASECAKEVKPASTRPPCADHPCPQWOLGEM 917
Db 841 WVIBEWGCSKSCELGWORRLVECRDINGQPASECAKEVKPASTRPPCADHPCPQWOLGEM 900

QY 918 SSCSKTCGKGYKKTSLKCLSHDGGVLSHSDCDPLKPKPHFIDFCTMAECS 967
Db 901 SSCSKTCGKGYKKTSLKCLSHDGGVLSHSDCDPLKPKPHFIDFCTMAECS 950

RESULT 11
US-10-667-281-2
; Sequence 2, Application US/10667281
; Publication No. US20050100916A1
; GENERAL INFORMATION:
; APPLICANT: Klonowski, Paul
; APPLICANT: Allard, John
; APPLICANT: Heller, Renu
; APPLICANT: Van Wart, Harold
; TITLE OF INVENTION: Human Aggrecanase and Nucleic Acid
; TITLE OF INVENTION: Compositions Encoding the Same
; FILE REFERENCE: ROCH-002
; CURRENT APPLICATION NUMBER: US/10/667,281
; CURRENT FILING DATE: 2003-09-17
; PRIOR APPLICATION NUMBER: US/09/568,559
; PRIOR FILING DATE: 2000-05-09
; PRIOR APPLICATION NUMBER: 60/133,343
; PRIOR FILING DATE: 1999-05-10
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 949
; TYPE: PRT
; ORGANISM: human
US-10-667-281-2

Query Match
Best Local Similarity 97.2%; Score 5140; DB 17; Length 949;
Matches 939; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 19 GNAERAPGSRSGFVPVPTLLLLAAALLAVSDALGRPSEDEELVPELERVFGHGTTRLR 78
Db 1 GNAERAPGSRSGFVPVPTLLLLAAALLAVSDALGRPSEDEELVPELERVFGHGTTRLR 60

QY 79 HAFDQQLDLVPPDSSFLAPGFTLQNVGRKSGSDTLPETDLAHCFTSGTVNGDPSSAAA 138
Db 61 HAFDQQLDLVPPDSSFLAPGFTLQNVGRKSGSETPLPETDLAHCFTSGTVNGDPSSAAA 120

QY 139 LSLCEGVRGAFYLLGEAFYIQLPAAASERLATAAPGKPPAPLOPHLLRRNRQDVGCT 198
Db 121 LSLCEGVRGAFYLLGEAFYIQLPAAASERLATAAPGKPPAPLOPHLLRRNRQDVGCT 180

QY 139 GVVDDPRPTGKAETDEDETEDEGEDEGPQSPDPAALQGVQPTGTGIRKRGFVSSH 258
Db 181 GVVDDPRPTGKAETDEDETEDEGEDEGPQSPDPAALQGVQPTGTGIRKRGFVSSH 240

QY 259 YVETMLVADQSMABFPHSGSLKHYLLTLFSVAARLYKHPISIRNSVSLVVKILVHDEOK 318
Db 241 YVETMLVADQSMABFPHSGSLKHYLLTLFSVAARLYKHPISIRNSVSLVVKILVHDEOK 300

QY 319 PEVTSNAALTIRNFCNWKQHNPPSDRDAEHYDTAILFTRQDLCSQTCDTLGMADVGT 378
Db 301 PEVTSNAALTIRNFCNWKQHNPPSDRDAEHYDTAILFTRQDLCSQTCDTLGMADVGT 360

QY 379 CDPSPSCSVIEDDDGLQAAFTTAHELGHVFNPHDDAKQACASLNGVNDQSHMWSMLSL 438
Db 361 CDPSPSCSVIEDDDGLQAAFTTAHELGHVFNPHDDAKQACASLNGVNDQSHMWSMLSL 420

QY 439 HSQWSPSCGYMITSFLDNGHGECLMDKXPQNPQLPGDLPGTSYDANRQCQFTFGEDSK 498
Db 421 HSQWSPSCGYMITSFLDNGHGECLMDKXPQNPQLPGDLPGTSYDANRQCQFTFGEDSK 480

QY 499 CPDAASTCTLWCTGTSGGVLCVOTKHPFPAWADGTSCGEGKWCINGKCNKXNRKHFDP 558
Db 481 CPDAASTCTLWCTGTSGGVLCVOTKHPFPAWADGTSCGEGKWCINGKCNKXNRKHFDP 540

Db 481 CPDAASTCTLWCTGTGGVLVQCTKHFPWADGTSCEGKWCINGKCNKTHRKHFDTPF 540
Qy 559 HGSWGMWPGWDCSRFCGGVQVYTWRECDNVPKNGKYCEGKRVYRSCNLEDCPDNNG 618
Db 541 HGSWGMWPGWDCSRFCGGVQVYTWRECDNVPKNGKYCEGKRVYRSCNLEDCPDNNG 600
Qy 619 KTFREEQCEAHNEFSKASFGSPAVEWIPKYAGVSPKDRCKLICQAKGIGYFFVLQPKV 678
Db 601 KTFREEQCEAHNEFSKASFGSPAVEWIPKYAGVSPKDRCKLICQAKGIGYFFVLQPKV 660
Qy 679 DGTSPSPDSTSVQVQCCVQKAGCDRIIDSXKFPDKCGVCGNGSTCKKISGSVTSAPGY 738
Db 661 DGTSPSPDSTSVQVQCCVQKAGCDRIIDSXKFPDKCGVCGNGSTCKKISGSVTSAPGY 720
Qy 739 HDIITPTGATNIEVKQNRQSRNNGSFLAIKAADGTYILNGDYTLSTLEODIMYKGV 798
Db 721 HDIITPTGATNIEVKQNRQSRNNGSFLAIKAADGTYILNGDYTLSTLEODIMYKGV 780
Qy 799 LRYSGSSAALERIRSFSPLEPTIQVLTGNALRPKIYTYFVKKKESFNAIPTFSAM 858
Db 781 LRYSGSSAALERIRSFSPLEPTIQVLTGNALRPKIYTYFVKKKESFNAIPTFSAM 840
Qy 859 VIEWGECSKSELGWQRRLVECRDINGQPASECAKEVPASTRPCADHPCPQWOLGEWS 918
Db 841 VIEWGECSKSELGWQRRLVECRDINGQPASECAKEVPASTRPCADHPCPQWOLGEWS 900
Qy 919 SCSTKCGKYKTSKLCLSHDGVLSHSDCLPKPKHFDICTMAECS 967
Db 901 SCSTKCGKYKTSKLCLSHDGVLSHSDCLPKPKHFDICTMAECS 949

RESULT 12
US-10-741-600-1605
; Sequence 1605, Application US/10741600
; Publication No. US20050026169A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001499
; CURRENT APPLICATION NUMBER: US/10/741,600
; CURRENT FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 73997
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1605
; LENGTH: 950
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-741-600-1605

Query Match 97.1%; Score 5136; DB 17; Length 950;
Best Local Similarity 98.8%; Pred. No. 0;
Matches 939; Conservative 4; Mismatches 7; Indels 0; Gaps 0;
Qy 18 MGNARAPGSRGPGVPTLLALLAALVSDALGRPSEDEELVPELERVPGHGTTLR 77
Db 1 MGNARAPGSRGPGVPTLLALLAALVSDALGRPSEDEELVPELERVPGHGTTLR 60
Qy 78 LHAFDQQLDLVPPDSSFLAPGFTLQNVGRKSGSDTLPETDLAHCFYSCTVNGDPSSAA 137
Db 61 LHAFDQQLDLVPPDSSFLAPGFTLQNVGRKSGSETPLPETDLAHCFYSCTVNGDPSSAA 120
Qy 138 ALSICGVRGAFVLLGAYFIQPLPAASERLATAAPEKPPAPLOPHLLRNQGVGGT 197
Db 121 ALSICGVRGAFVLLGAYFIQPLPAASERLATAAPEKPPAPLOPHLLRNQGVGGT 180
Qy 198 CGVVDDPRPTGKAETDEDEGTEGEDEGQWPDQPALQGVQPTGTSIRKRVFSSH 257
Db 181 CGVVDDPRPTGKAETDEDEGTEGEDEGQWPDQPALQGVQPTGTSIRKRVFSSH 240
Qy 258 RYVETMLVADQSMAEFHGSLGHYLLTLFSAARLYKHPISIRNSVSLVVKILVIHDEQK 317
Db 241 RYVETMLVADQSMAEFHGSLGHYLLTLFSAARLYKHPISIRNSVSLVVKILVIHDEQK 300

Qy 318 GPEVTSNAALTILRNFCNWKQHNPPSDRDAEHYDTAILFTTRDLCGSCQDCTILGMADVGT 377
Db 301 GPEVTSNAALTILRNFCNWKQHNPPSDRDAEHYDTAILFTTRDLCGSCQDCTILGMADVGT 360
Qy 378 VCDPRSRSVIEDDGLQAAFTTAHELGHVFNPHDDAKOCASINGVNOQSHMMASLNL 437
Db 361 VCDPRSRSVIEDDGLQAAFTTAHELGHVFNPHDDAKOCASINGVNOQSHMMASLNL 420
Qy 438 DHSQWSPSCSGYMITSFLDNGHGECLMDKPNPIQLPGDLPGTSDYDANRQCQFTFGEDSK 497
Db 421 DHSQWSPSCSAYMITSFLDNGHGECLMDKPNPIQLPGDLPGTSDYDANRQCQFTFGEDSK 480
Qy 498 HCPDAASTCTLWCTGTGGVLVQCTKHFPWADGTSCEGKWCINGKCNKTHRKHFDTP 557
Db 481 HCPDAASTCTLWCTGTGGVLVQCTKHFPWADGTSCEGKWCINGKCNKTHRKHFDTP 540
Qy 558 FHSGWGMWPGWDCSRFCGGVQVYTWRECDNVPKNGKYCEGKRVYRSCNLEDCPDNN 617
Db 541 FHSGWGMWPGWDCSRFCGGVQVYTWRECDNVPKNGKYCEGKRVYRSCNLEDCPDNN 600
Qy 618 GKTFRREEQCEAHNEFSKASFGSPAVEWIPKYAGVSPKDRCKLICQAKGIGYFFVLQPKV 677
Db 601 GKTFRREEQCEAHNEFSKASFGSPAVEWIPKYAGVSPKDRCKLICQAKGIGYFFVLQPKV 660
Qy 678 VDGTPSPDSTSVQVQCCVQKAGCDRIIDSXKFPDKCGVCGNGSTCKKISGSVTSAPKG 737
Db 661 VDGTPSPDSTSVQVQCCVQKAGCDRIIDSXKFPDKCGVCGNGSTCKKISGSVTSAPKG 720
Qy 738 YHDIITPTGATNIEVKQNRQSRNNGSFLAIKAADGTYILNGDYTLSTLEODIMYKGV 797
Db 721 YHDIITPTGATNIEVKQNRQSRNNGSFLAIKAADGTYILNGDYTLSTLEODIMYKGV 780
Qy 798 VLRYSGSSAALERIRSFSPLEPTIQVLTGNALRPKIYTYFVKKKESFNAIPTFSA 857
Db 781 VLRYSGSSAALERIRSFSPLEPTIQVLTGNALRPKIYTYFVKKKESFNAIPTFSA 840
Qy 858 WIEWGECSKSELGWQRRLVECRDINGQPASECAKEVPASTRPCADHPCPQWOLGEW 917
Db 841 WIEWGECSKSELGWQRRLVECRDINGQPASECAKEVPASTRPCADHPCPQWOLGEW 900
Qy 918 SCSTKCGKYKTSKLCLSHDGVLSHSDCLPKPKHFDICTMAECS 967
Db 901 SCSTKCGKYKTSKLCLSHDGVLSHSDCLPKPKHFDICTMAECS 950

RESULT 13
US-09-741-151-4
; Sequence 4, Application US/09741151
; Publication No. US20020086400A1
; GENERAL INFORMATION:
; APPLICANT: ZHU, Shiaoqing et al
; TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND
; FILE REFERENCE: CL001005
; CURRENT APPLICATION NUMBER: US/09/741,151
; CURRENT FILING DATE: 2000-12-08
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 931
; TYPE: PRT
; ORGANISM: Human
US-09-741-151-4

Query Match 95.3%; Score 5036; DB 9; Length 931;
Best Local Similarity 98.8%; Pred. No. 0;
Matches 920; Conservative 4; Mismatches 7; Indels 0; Gaps 0;
Qy 36 LLLAALLAALVSDALGRPSEDEELVPELERVPGHGTTLRLHAFDQQLDLVPPDSSF 95
Db 1 LLLAALLAALVSDALGRPSEDEELVPELERVPGHGTTLRLHAFDQQLDLVPPDSSF 60

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DB 61 LAPGFTLQVGRKSGSETLPETDLAHCFYSGTVNGDPSSAAALSLCEGVGAFYLLGEA 120
QY 156 YFIQPLPAASERLATAAPEGKPPALQPHLLRRNQDVGCTGCVVDDDEPRPTGKAETED 215
DB 121 YFIQPLPAASERLATAAPEGKPPALQPHLLRRNQDVGCTGCVVDDDEPRPTGKAETED 180
QY 216 EDEGTEGEDEGPQWSPQDPALQGVGOPTGTGTSIRKRRFVSSHRYVETMLVADQSMAPFHG 275
DB 181 EDEGTEGEDEGAQWSPQDPALQGVGOPTGTGTSIRKRRFVSSHRYVETMLVADQSMAPFHG 240
QY 276 SGLKHYLLTLFSAARLYKHPSIRNSVSLVVKILVIHDEQKGPVTSNAALTILNFCNW 335
DB 241 SGLKHYLLTLFSAARLYKHPSIRNSVSLVVKILVIHDEQKGPVTSNAALTILNFCNW 300
QY 336 OKQHNPPSDRDAEHYDVTAILFTRQDLCSQTCDTLGMADVGTCDPSRSCSVIEDDGLQA 395
DB 301 OKQHNPPSDRDAEHYDVTAILFTRQDLCSQTCDTLGMADVGTCDPSRSCSVIEDDGLQA 360
QY 396 AFTTAHELGHVFNPHDDAKQACASLNGVNDQSHMMASMLSLNLDHSPWSPCSGYMITSLF 455
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QY 456 DNGHGECLMDKQPNFIQLPGDLPSTSYDANROCOFTFGEDSKHCPDAASTCTLWCTGTS 515
DB 421 DNGHGECLMDKQPNFIQLPGDLPSTSYDANROCOFTFGEDSKHCPDAASTCTLWCTGTS 480
QY 516 GGVLVCOQTHFPWADGTSCEGKWCINGKCNVKNRKHFDTPFHGSGWGMWPGWDCSRTC 575
DB 481 GGVLVCOQTHFPWADGTSCEGKWCINGKCNVKNRKHFDTPFHGSGWGMWPGWDCSRTC 540
QY 576 GGGVOYTMRECDNPPVKGKGYCEGKRVYRSCNLEDCPDNNGKTFREBEQCEAHNEFSKA 635
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DB 841 RRLVRCRDINGOPASECAKEVPASTPCADHPQWOLGEMSSCKTCGKGYKKTSLKC 900
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RESULT 14
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; Sequence 7, Application US/10163316
; Publication No. US20020197703A1
; GENERAL INFORMATION:
; APPLICANT: Kapeller-Libermann, Rosana
; TITLE OF INVENTION: 6552, A Human Matrix Metalloproteinase and Uses
; FILE OF INVENTION: Therefor
; FILE REFERENCE: MPI01-025FIRNM
; CURRENT APPLICATION NUMBER: US/10/163,316
; CURRENT FILING DATE: 2002-06-05

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; PRIOR APPLICATION NUMBER: 60/297,863  
; PRIOR FILING DATE: 2001-06-13  
; NUMBER OF SEQ ID NOS: 10  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 7  
; LENGTH: 968  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-10-163-316-7
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Query Match 81.2%; Score 4293.5; DB 13; Length 968;
Best Local Similarity 81.0%; Pred. No. 0;
Matches 790; Conservative 58; Mismatches 112; Indels 15; Gaps 5;

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QY 58 EELVPELERVPGHG--TTRLRLHAFDOQLDLDVPPDSFLAPGFTLQNVGRKSGSDTPL 115
DB 61 EELVPLSERAPGHDSTTTRLRLDAFCQQLHLKLPDSGFLAPGFTLQTVGRSPGEA 120
QY 116 --PETDLAHCYFSGTVNGDPSSAAALSLCEGVGAFYLLGEAYFIQPLP-AASERLATAA 172
DB 121 LDPTGDLAHCYFSGTVNGDPSSAAALSLCEGVGAFYLLQGEFFIQPAPGVATERLAPAV 180
QY 173 PGEKPPALQPHLLRRNQDVGCTGCVVDDDEPRPTGKAETEDDEGEDEGEQWSPQ 232
DB 181 PEESASRPPQHLRRRRRGGGAKCGVMDDELFT-----SDSRPESQNTNRQWMPVR 233
QY 233 DPALQGVGOPTGTGTSIRKRRFVSSHRYVETMLVADQSMAPFHGSLKHYLLTLFSAARL 292
DB 234 DPTPDACKPGSPGIRKRRFVSSPRYVETMLVADQSMADFHGSLKHYLLTLFSAARF 293
QY 293 YKHPISIRNSVSLVVKILVIHDEQKGPVTSNAALTILNFCNWQKHNPSPSDRDAEHYDT 352
DB 294 YKHPISIRNSVSLVVKILVIHDEQKGPVTSNAALTILNFCNWQKHNPSPSDRDAEHYDT 353
QY 353 AILFTRQDLCSQTCDTLGMADVGTCDPSRSCSVIEDDGLQAAFTTAHELGHVFNMPHD 412
DB 354 AILFTRQDLCSQTCDTLGMADVGTCDPSRSCSVIEDDGLQAAFTTAHELGHVFNMPHD 413
QY 413 DAKQACASLNGVNDQSHMMASMLSLNLDHSPWSPCSGYMITSLFDNGHGECLMDKQPNIK 472
DB 414 DAKHCKASLNGVTDGSHLMSMLSLDHSQPHSPCSAYVWVTSFLDNGHGECLMDKQPNIK 473
QY 473 LPDLPSTSYDANROCOFTFGEDSKHCPDAASTCTLWCTGTSGGVLVCOQTHFPWADGT 532
DB 474 LPDLPSTSYDANROCOFTFGEDSKHCPDAASTCTLWCTGTSGGVLVCOQTHFPWADGT 533
QY 533 SCGEKWCINGKCNVKNRKHFDTPFHGSGWGMWPGWDCSRTC CGGVGYTMRECDNVPK 592
DB 534 SCGEKWCINGKCNVKNRKHFDTPFHGSGWGMWPGWDCSRTC CGGVGYTMRECDNVPK 593
QY 593 NGGKTCGKRVYRSCNLEDCPDNNGKTFREBEQCEAHNEFSKASFGSGPAVEWIPKYAGV 652
DB 594 NGGKTCGKRVYRSCNLEDCPDNNGKTFREBEQCEAHNEFSKASFGNEFTVWTPKYAGV 653
QY 653 SPKDRCKLICQAKGIGYFVLQPKVVDGTPCSPDSTSVCVQGOQKAGCDRIIDSKKFD 712
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DB 714 KCGVCGNGSTCKKISGVSATSAKPGYHDIITPTGATNIEVKORNGSRNNGSFLAIIKA 773
QY 773 ADGTYILNGDYTLSTLEQDIMYKGVVLYRSGSSAALERIRSPSPLEKEPLTIQVLTVGNAL 832
DB 774 ADGTYILNGDYTLSTLEQDIMYKGVVLYRSGSSAALERIRSPSPLEKEPLTIQVLTVGNAL 833
QY 833 RPKIKYTVFKKKESFNAIPTFSAWVIEEWGECSKSCELGHQRLVECRDINGOPASEC 892
DB 834 RPKIKYTVFKKKESFNAIPTFSAWVIEEWGECSKSCELGHQRLVECRDINGOPASEC 893
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OM protein - protein search, using sw model

Run on: May 23, 2005, 14:10:02 ; Search time 46 Seconds
(without alignments)
1569.253 Million cell updates/sec

Title: US-09-373-658c-126
Perfect score: 5287
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues
Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	5232	99.0	967	4	US-09-130-491-2
2	5140	97.2	949	4	US-09-568-559-2
3	4260.5	80.6	950	4	US-09-321-987B-4
4	3922	74.2	727	4	US-09-445-023A-1
5	3655	69.2	727	4	US-09-445-023A-12
6	3297	62.4	608	4	US-09-130-491-13
7	2794	52.8	551	4	US-09-130-491-16
8	2471.5	46.7	950	4	US-10-009-332-1
9	2265.5	42.9	905	3	US-09-369-364A-9
10	2124	40.2	837	4	US-09-122-126B-2
11	2124	40.2	837	4	US-09-634-286A-2
12	2124	40.2	837	4	US-10-247-685-2
13	1924	36.4	930	4	US-09-122-126B-15
14	1924	36.4	930	4	US-09-634-286A-15
15	1924	36.4	930	4	US-10-247-685-15
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17	1731.5	32.8	1882	3	US-09-369-364A-13
18	1608.5	30.4	2150	4	US-09-321-987B-2
19	1605.5	30.4	874	3	US-09-369-364A-15
20	1598	30.2	2165	4	US-09-800-729-155
21	1390.5	26.3	481	4	US-09-130-491-8
22	1293	24.5	518	3	US-09-369-364A-22
23	1287	24.3	1104	4	US-09-981-953A-4
24	1278.5	24.2	1224	4	US-09-930-872-4
25	1278.5	24.2	1224	4	US-10-217-774-4
26	1214.5	23.0	908	4	US-09-963-791-2
27	1207.5	22.8	997	3	US-09-369-364A-7

28	1176	22.2	1081	3	US-09-369-364A-17	Sequence 17, Appl
29	1151.5	21.8	757	4	US-09-963-791-24	Sequence 24, Appl
30	1100.5	20.8	1211	4	US-09-949-016-11401	Sequence 11401, A
31	1096	20.7	969	4	US-09-321-987B-5	Sequence 5, Appl
32	1083.5	20.5	1211	4	US-09-491-522-5	Sequence 5, Appl
33	1059	20.0	1205	4	US-09-491-522-11	Sequence 11, Appl
34	1029.5	19.5	859	3	US-09-369-364A-5	Sequence 5, Appl
35	1017	19.2	770	4	US-09-981-953A-2	Sequence 2, Appl
36	1001	18.9	1039	4	US-09-949-016-7859	Sequence 7859, Ap
37	781	14.8	589	4	US-09-963-791-12	Sequence 12, Appl
38	718	13.6	438	4	US-09-963-791-22	Sequence 22, Appl
39	712.5	13.5	245	3	US-09-369-364A-11	Sequence 11, Appl
40	595	11.3	1745	4	US-09-800-729-89	Sequence 89, Appl
41	593.5	11.2	507	4	US-09-963-791-10	Sequence 10, Appl
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45	566.5	10.7	1691	4	US-09-784-358-2	Sequence 2, Appl

ALIGNMENTS

RESULT 1

US-09-130-491-2
; Sequence 2, Application US/09130491
; Patent No. 6416974
; GENERAL INFORMATION:
; APPLICANT: Holtzman, Douglas A.
; APPLICANT: Goodearl, Andrew D.J.
; TITLE OF INVENTION: TANGO-71, TANGO-73, TANGO-74, TANGO-76, AND TANGO-83
; FILE REFERENCE: 09404/041001
; CURRENT APPLICATION NUMBER: US/09/130,491
; CURRENT FILING DATE: 1998-08-07
; EARLIER APPLICATION NUMBER: US 60/058,108
; EARLIER FILING DATE: 1997-09-05
; EARLIER APPLICATION NUMBER: US 60/054,961
; EARLIER FILING DATE: 1997-08-06
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 967
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-130-491-2

Query Match	99.0%	Score 5232	DB 4	Length 967
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				Gaps 0
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Qy	121	AHCFYSGTVNGDSSAAALSLCEGVRCGAFYLLGEAYFIQPLPAASERLATAAPGKPPAP	180	
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Qy	181	LQFHLLRRNQDVGVTGCGVVDDEPRPTGKAETDEDEGTGEGDEGQWSPQDPALQGVG	240	
Db	181	LQFHLLRRNQDVGVTGCGVVDDEPRPTGKAETDEDEGTGEGDEGQWSPQDPALQGVG	240	
Qy	241	QPTGTGSIKKRPFVSHRYVETMLVADQSMAEFHGSLGHYLLTFLFSVAARLYKHPISRN	300	
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Qy	301	SVSLVWVKILVIHDEQKGPVTSNAALTFLNFCNWKQHNPPSDRDAEHYDTAILFTROD	360	
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Db 361 LCGSOTCDTLGMADYCTVCDPSRSCSVIEDDGLQAAFTTAHELGHVFNPHDDAKQACSL 420
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QY 481 SYDANRQCFTTGBSCHKPCDAASTLWCTGTSGVLVCTQKHPFPAWADGTSCEGKWC 540
Db 481 SYDANRQCFTTGBSCHKPCDAASTLWCTGTSGVLVCTQKHPFPAWADGTSCEGKWC 540
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Db 541 INKCKVNKHREFTPHGSGWMPGDCSRTCGGVQYTMRECDNPVPKNGKCYCBG 600
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QY 841 FVKKKESFNAIPTSAWVIEBWGECSSCELGWQRRLVECRDINGQPASECAKEVKPAS 900
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QY 901 TPCADHPCQWOLGEWSSCSKTCGKYKTSIKCLSHDGGVLSHDSCDPLKKPKHFIDF 960
Db 901 TPCADHPCQWOLGEWSSCSKTCGKYKTSIKCLSHDGGVLSHDSCDPLKKPKHFIDF 960
QY 961 CTMAECS 967
Db 961 CTMAECS 967

RESULT 2

US-09-568-559-2
; Sequence 2, Application US/09568559
; Patent No. 6649377
; GENERAL INFORMATION:
; APPLICANT: Klonowski, Paul
; APPLICANT: Allard, John
; APPLICANT: Heller, Remu
; APPLICANT: Van Wart, Harold
; TITLE OF INVENTION: Human Aggreganase and Nucleic Acid
; TITLE OF INVENTION: Compositions Encoding the Same
; FILE REFERENCE: ROCH-002
; CURRENT APPLICATION NUMBER: US/09/568,559
; PRIOR FILING DATE: 2000-05-09
; PRIOR APPLICATION NUMBER: 60/133,343
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 949
; TYPE: PRT
; ORGANISM: human
US-09-568-559-2

Query Match 97.2%; Score 5140; DB 4; Length 949;
Best Local Similarity 98.9%; Pred. No. 0;
Matches 939; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

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QY 79 HAFDOQLDLVPPDSSFLAPGFTLQNVGRKSGSDTLPETDLAHCFYSGTVNGDPSSAAA 138
Db 61 HAFDOQLDLVPPDSSFLAPGFTLQNVGRKSGSETPLPETDLAHCFYSGTVNGDPSSAAA 120
QY 139 LSLCEGVRGAFYLLGEAYFIQPLPAASERLATAAPGKPPAPLQPHLLRRNRQGVGTC 198
Db 121 LSLCEGVRGAFYLLGEAYFIQPLPAASERLATAAPGKPPAPLQPHLLRRNRQGVGTC 180
QY 199 GVVDDEPRTKAEFTEDDECTEGEGPOKSPQDPAQGVGQPTGTSIRKKRVSSHR 258
Db 181 GVVDDEPRTKAEFTEDDECTEGEGPOKSPQDPAQGVGQPTGTSIRKKRVSSHR 240
QY 259 YVETMLVADQSMABPHGSLGHYLLTLFSAARLYKHPISIRNSVSLVVKILVHDEQKG 318
Db 241 YVETMLVADQSMABPHGSLGHYLLTLFSAARLYKHPISIRNSVSLVVKILVHDEQKG 300
QY 319 PEVTSNAALTUNFCNWOKQHNPPSDRDAEHYDTAILPTRQDLCSQTCDTLGMADVGT 378
Db 301 PEVTSNAALTUNFCNWOKQHNPPSDRDAEHYDTAILPTRQDLCSQTCDTLGMADVGT 360
QY 379 CDPSRSCSVIEDDGLQAAFTTAHELGHVFNPHDDAKQACASLNGVNDSHMAWMLSLNLD 438
Db 361 CDPSRSCSVIEDDGLQAAFTTAHELGHVFNPHDDAKQACASLNGVNDSHMAWMLSLNLD 420
QY 439 HSQWSPSCGYMITSLDNGHGECLMDKPQNPQIQLPGDLPGTSYDANRQCFTFGEDSKH 498
Db 421 HSQWSPSCGYMITSLDNGHGECLMDKPQNPQIQLPGDLPGTSYDANRQCFTFGEDSKH 480
QY 499 CPDAASTSTLWCTGTSGVIVCQKHPFPAWADGTSCEGKWCINGKCNVKNHKKHFDTPF 558
Db 481 CPDAASTSTLWCTGTSGVIVCQKHPFPAWADGTSCEGKWCINGKCNVKNHKKHFDTPF 540
QY 559 HGSWGMGPMGDCSRTCGGVQYTMRECDNPVPKNGKCYCBGKRVYRSCNLEDCPDNNG 618
Db 541 HGSWGMGPMGDCSRTCGGVQYTMRECDNPVPKNGKCYCBGKRVYRSCNLEDCPDNNG 600
QY 619 KTFREEQCEAHNEFSKASFGSGPAVEWIPKYAGVSPKDRCKLICOAKGIGYFFVLQPKV 678
Db 601 KTFREEQCEAHNEFSKASFGSGPAVEWIPKYAGVSPKDRCKLICOAKGIGYFFVLQPKV 660
QY 679 DGTCPSPDSTSVQVQCVKAGCDRIIDSKKKFKDCKGVCNGSTCKKISGVTSAKPGY 738
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QY 919 SCSTCKGKYKTSIKCLSHDGGVLSHDSCDPLKKPKHFIDFCTMAECS 967
Db 901 SCSTCKGKYKTSIKCLSHDGGVLSHDSCDPLKKPKHFIDFCTMAECS 949

RESULT 3

US-09-321-987B-4
; Sequence 4, Application US/09321987B
; Patent No. 6730820
; GENERAL INFORMATION:
; APPLICANT: Kimble, Judith E
; APPLICANT: Bleiloch, Robert H

TITLE OF INVENTION: Agent and Method for Modulating Cell Migration
FILE REFERENCE: 960296.95386
CURRENT APPLICATION NUMBER: US/09/321,987B
CURRENT FILING DATE: 1999-05-28
PRIOR APPLICATION NUMBER: 60/087,170
PRIOR FILING DATE: 1998-05-29
PRIOR APPLICATION NUMBER: 60/129,023
PRIOR FILING DATE: 1999-04-13
NUMBER OF SEQ ID NOS: 5
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 4
LENGTH: 950
TYPE: PRT
ORGANISM: Murine
US-09-321-987B-4

Query Match 80.6%; Score 4260.5; DB 4; Length 950;
Best Local Similarity 81.6%; Pred. No. 0;
Matches 781; Conservative 56; Mismatches 105; Indels 15; Gaps 5;

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QY 73 TTRLRHLAFDQQLDLVPPDSFLAPCFTLQNVGRKSGSDTPL--PETDLAHCFYSGTVN 130
DB 61 TTRLRDLDAFQQLHLKLPDPSGLAPGFTLTQVGRSPGSEAOHLDPGDLAHCFYSGTVN 120
QY 131 GDPSSAAALSLCGRVGAFVLLGEAFVIOPLP-AASERLATAPEKGPAPLQFHLIRN 189
DB 121 GDPGSAALSLCGRVGAFYLOGEFFIOPAPGATERLAPVPEESSARPOFHILRR 180
QY 190 RQGDVGTCGVVDEPRPTCKAETDEDECTEGEPOWSPDPAALQGVQPTGTGSR 249
DB 181 RRGSGAKCCGVMDDETLPT-----SDRPSQNTQNPVRDPTPDAGKSGFGSIR 233
QY 250 KKEFVSSHRVYETMLVADQSMABFHGSLKHYLLTLFVSAARLYKHPISIRNSVSLVVKI 309
DB 234 KKEFVSSPRVYETMLVADQSMADFHGSLKHYLLTLFVSAARLYKHPISIRNSVSLVVKI 293
QY 310 LVTHDQKGPVTSNAALTTLRNFQWQKQHPNPSDRDAEHYDTAILFTRODLCSQTCDT 369
DB 294 LVTYEKGKGPVTSNAALTTLRNFQWQKQHPNPSDRDAEHYDTAILFTRODLCSQTCDT 353
QY 370 LGMADVGTCDPSRSCSVIEDDGLQAAFTTAHELGHVFNPMHDDAKQACASLNGVNDQSH 429
DB 354 LGMADVGTCDPSRSCSVIEDDGLQAAFTTAHELGHVFNPMHDDAKQACASLNGVNDQSH 413
QY 430 MASMLSLNLDHSPWSPCSGYMITSFLDNGHGECLMDKPNPIQLPGDLPGTSDANRQC 489
DB 414 MASMLSLNLDHSPWSPCSGYMITSFLDNGHGECLMDKPNPIQLPGDLPGTSDANRQC 473
QY 490 FTFGEBSKHCPCDAASTCTLWCTGTSGGLVLCQTKHFPWADGTSCGEGKWCINGKVCN 549
DB 474 FTFGEBSKHCPCDAASTCTLWCTGTSGGLVLCQTKHFPWADGTSCGEGKWCINGKVCN 533
QY 550 HRKHFTDPPFHSGWGMWGPWGDSCRTCGGQVQYTMRECDNPVKNQKGYCEGKRVYRSCN 609
DB 534 DMKHFTDPPFHSGWGMWGPWGDSCRTCGGQVQYTMRECDNPVKNQKGYCEGKRVYRSCN 593
QY 610 LEDCPDNNKGTFRBQCEAHNEFSKASFGSGPAVEWIPKYAGVSPKDRCKLIQAKGI 669
DB 594 LEDCPDNNKGTFRBQCEAHNEFSKASFGSGPAVEWIPKYAGVSPKDRCKLIQAKGI 653
QY 670 FFVLQPKVVDGTPCSPDSTSVQVQGVQACGDRIDSKKKFKDQKCGVCGGNGSTCKKIS 729
DB 654 FFVLQPKVVDGTPCSPDSTSVQVQGVQACGDRIDSKKKFKDQKCGVCGGNGSTCKKIS 713
QY 730 SVTSAPGYHDIITIPGATNIEVKORNSRNGSFLAKADGYIILNGDITLSTLE 789
DB 714 IVTSTREGYHDIITIPGATNIEVKORNSRNGSFLAKADGYIILNGDITLSTLE 773
QY 790 QDIWYKGVWLYRSGSSAALERIRSFPLKEPLTIQVLTGVNLRPKIKYTYFVKKKESF 849

DB 774 QDLTYKGTVLYRSGSSAALERIRSFPLKEPLTIQVLTGVNLRPKIKYTYFVKKKTESP 833
QY 850 NAIPFSAWVIBEWGECSCSCELGWORRLVECRDINGQPASECACEKVKPASTRCPADHPC 909
DB 834 NAIPFSEWVIBEWGECSCSKTCSGWORRVVQCRDINGHPASECAKEVKPASTRCPADLPC 893
QY 910 PQWLGEWSSCKTCGKYKTKSLKCLSHDGGVLSHSDCDPLKKPKHFIDFTMAEC 966
DB 894 PHWQGDWSPCKTCGKYKTKSLKCVSHDGGVLSNESCDPLKKPKHYIDFCTLTQC 950

RESULT 4
US-09-445-023A-1
Sequence 1, Application US/09445023A
Patent No. 6565858
GENERAL INFORMATION:
APPLICANT: Hirose, Kunitaka
APPLICANT: Inoguchi, Eiichi
APPLICANT: Hakozaaki, Michinori
APPLICANT: Ishioka, Keiko
APPLICANT: Ishida, Yukako
APPLICANT: Matsushima, Kouji
APPLICANT: Kuno, Kouji
TITLE OF INVENTION: Human ADAMTS-1 protein, gene encoding the same, pharmaceutical
composition and method of immunologically analyzing human ADAMTS-1
FILE REFERENCE: Q57092
CURRENT APPLICATION NUMBER: US/09/445,023A
CURRENT FILING DATE: 1999-12-03
PRIOR APPLICATION NUMBER: JP 9-160422
PRIOR FILING DATE: 1997-06-03
NUMBER OF SEQ ID NOS: 14
SOFTWARE: PatentIn version 3.0
SEQ ID NO 1
LENGTH: 727
TYPE: PRT
ORGANISM: Homo sapiens
US-09-445-023A-1

Query Match 74.2%; Score 3922; DB 4; Length 727;
Best Local Similarity 98.2%; Pred. No. 0;
Matches 707; Conservative 5; Mismatches 8; Indels 0; Gaps 0;

QY 248 IRKRFVSSHRVYETMLVADQSMABFHGSLKHYLLTLFVSAARLYKHPISIRNSVSLVV 307
DB 8 LRKRFVSSPRVYETMLVADQSMABFHGSLKHYLLTLFVSAARLYKHPISIRNSVSLVV 67
QY 308 KILVHDEQKGPVTSNAALTTLRNFQWQKQHPNPSDRDAEHYDTAILFTRODLCSQTC 367
DB 68 KILVHDEQKGPVTSNAALTTLRNFQWQKQHPNPSDRDAEHYDTAILFTRODLCSQTC 127
QY 368 DTLMADVGTCDPSRSCSVIEDDGLQAAFTTAHELGHVFNPMHDDAKQACASLNGVNDQ 427
DB 128 DTLMADVGTCDPSRSCSVIEDDGLQAAFTTAHELGHVFNPMHDDAKQACASLNGVNDQ 187
QY 428 HMASMLSLNLDHSPWSPCSGYMITSFLDNGHGECLMDKPNPIQLPGDLPGTSDANRQ 487
DB 188 HMASMLSLNLDHSPWSPCSGYMITSFLDNGHGECLMDKPNPIQLPGDLPGTSDANRQ 247
QY 488 CQTFGEBSKHCPCDAASTCTLWCTGTSGGLVLCQTKHFPWADGTSCGEGKWCINGKVCN 547
DB 248 CQTFGEBSKHCPCDAASTCTLWCTGTSGGLVLCQTKHFPWADGTSCGEGKWCINGKVCN 307
QY 548 KNRKHFTDPPFHSGWGMWGPWGDSCRTCGGQVQYTMRECDNPVKNQKGYCEGKRVYRSCN 607
DB 308 KTDKHFDPFHSGWGMWGPWGDSCRTCGGQVQYTMRECDNPVKNQKGYCEGKRVYRSCN 367
QY 608 CNLEDCPDNNKGTFRBQCEAHNEFSKASFGSGPAVEWIPKYAGVSPKDRCKLIQAKGI 667
DB 368 CNLEDCPDNNKGTFRBQCEAHNEFSKASFGSGPAVEWIPKYAGVSPKDRCKLIQAKGI 427
QY 668 GYFVLQPKVVDGTPCSPDSTSVQVQGVQACGDRIDSKKKFKDQKCGVCGGNGSTCKKI 727

Db 428 GYFFVLQPKVVDGTPCSPDSTSVQVQCVKAGCDRIIDSKKKFKDCGVCNGSGTCKKI 487
QY 728 SGSVTSKPGYHDIITPTGATNIEVKORNGSRNNGSFLAIKAADGTIILNGDYTLST 787
Db 488 SGSVTSKPGYHDIITPTGATNIEVKORNGSRNNGSFLAIKAADGTIILNGDYTLST 547
QY 788 LQDQIMYKGVILRYSGSSAALIRISFSPKLEPLITQVLTGNALRPKIKYTYFVKKKKE 847
Db 548 LQDQIMYKGVILRYSGSSAALIRISFSPKLEPLITQVLTGNALRPKIKYTYFVKKKKE 607
QY 848 SFNAIPTSAWIEBWGECSSKCELGWQRLVECRDINGQPASECAKEVKPASTRPCADH 907
Db 608 SFNAIPTSAWIEBWGECSSKCELGWQRLVECRDINGQPASECAKEVKPASTRPCADH 667
QY 908 PCPQWLGEWSSCKTCGKYKTSIKLCLSHDGGVLSHSDCDPLKKPKHFIDPCTMAECS 967
Db 668 PCPQWLGEWSSCKTCGKYKTSIKLCLSHDGGVLSHSDCDPLKKPKHFIDPCTMAECS 727

RESULT 5
US-09-445-023A-12
; Sequence 12, Application US/09445023A
; Patent No. 6565858
; GENERAL INFORMATION:
; APPLICANT: Hirose, Kunitaka
; APPLICANT: Inoguchi, Biiji
; APPLICANT: Hakezaki, Michinori
; APPLICANT: Ishioka, Keiko
; APPLICANT: Ishida, Yukako
; APPLICANT: Matsushima, Kouji
; APPLICANT: Kuno, Kouji
; TITLE OF INVENTION: Human ADAMTS-1 protein, gene encoding the same, pharmaceutical
; TITLE OF INVENTION: composition and method of immunologically analyzing human ADAMTS
; FILE REFERENCE: Q57092
; CURRENT APPLICATION NUMBER: US/09/445,023A
; PRIOR FILING DATE: 1999-12-03
; PRIOR APPLICATION NUMBER: JP 9-160422
; PRIOR FILING DATE: 1997-06-03
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 12
; LENGTH: 727
; TYPE: PRT
; ORGANISM: Mus sp.
US-09-445-023A-12

Query Match 69.2%; Score 3656; DB 4; Length 727;
Best Local Similarity 89.0%; Pred. No. 1.9e-311;
Matches 647; Conservative 42; Mismatches 38; Indels 0; Gaps 0;

QY 241 QPTGTGSTRKKKPVSSHRVETMLVADQSMAEFHGSLGKHYLLTLFSAARLYKHPSTRN 300
Db 1 EPGSPGSRKKRFVSSPRVETMLVADQSMDFHSGSLGKHYLLTLFSAARLYKHPSTRN 60
QY 301 SVSLVVKVILVIHDEQKPEVTSNAALTLRNFCNWKQHNPPSDRDAEHYDTAILFTROD 360
Db 61 SISLVVKVILVIHDEQKPEVTSNAALTLRNFCNWKQHNPPSDRDAEHYDTAILFTROD 120
QY 361 LCGSOTCDTLGMADVGTVCDSRSCSVIEDDGLQAAFTTAHGLGHVFNMPHDDAKQCSAL 420
Db 121 LCGSOTCDTLGMADVGTVCDSRSCSVIEDDGLQAAFTTAHGLGHVFNMPHDDAKQCSAL 180
QY 421 NGVNODSHMAMSLNLDHSPWSPCSGYMITSFLDNGHGECLMDKPNQPIQLPGDLPGT 480
Db 181 NGVSGDHLMAASLSDHSPWSPCSGYMITSFLDNGHGECLMDKPNQPIQLPGDLPGT 240
QY 481 SYDANRCQFTFGEESKHCPCDAASTCTLTWCTGTSGGLVLCQTKHFPWADGTSCGEGKWC 540
Db 241 LYDANRCQFTFGEESKHCPCDAASTCTLTWCTGTSGGLVLCQTKHFPWADGTSCGEGKWC 300
QY 541 INGKCVNKNRKHFDTPFHGSGWGMGPWGDGCSRTCGGVQYVTRCNDPVPKNGGKYCBG 600
Db 301 VSGKCVNKTDMKHFAFPVHSGSGWGMGPWGDGCSRTCGGVQYVTRCNDPVPKNGGKYCBG 360

QY 601 KRVYRSNLEDCPDNNGKTFREEOCEAHNEPFSKASFGSGPAVEWIPKYAGVSPKDRCKL 660
Db 361 KRVYRSNLEDCPDNNGKTFREEOCEAHNEPFSKASFGNEPTVETPKYAGVSPKDRCKL 420
QY 661 IQOAKIGYFFVLQPKVVDGTPCSPDSTSVQVQCVKAGCDRIIDSKKKFKDCGVCNG 720
Db 421 TCEAKIGYFFVLQPKVVDGTPCSPDSTSVQVQCVKAGCDRIIDSKKKFKDCGVCNG 480
QY 721 GSTCKKISGVSITSAKPGYHDIITPTGATNIEVKORNGSRNNGSFLAIKAADGTIILN 780
Db 481 GSTCKKMSGIVTSTRPGYHDIITPTGATNIEVKORNGSRNNGSFLAIKAADGTIILN 540
QY 781 GDTLTSTLEQDQIMYKGVILRYSGSSAALIRISFSPKLEPLITQVLTGNALRPKIKYTY 840
Db 541 NGFTLTSTLEQDQIMYKGVILRYSGSSAALIRISFSPKLEPLITQVLTGNALRPKIKYTY 600
QY 841 FVKKKESFNAIPTFSAWVIEBWGECSSKCELGWQRLVECRDINGQPASECAKEVKPAS 900
Db 601 FMKKKTESFNAIPTFSAWVIEBWGECSSKCELGWQRLVECRDINGQPASECAKEVKPAS 660
QY 901 TRPCADHPCPQWLGEWSSCKTCGKYKTSIKLCLSHDGGVLSHSDCDPLKKPKHFIDF 960
Db 661 TRPCADHPCPQWLGEWSSCKTCGKYKTSIKLCLSHDGGVLSHSDCDPLKKPKHFIDF 720
QY 961 CTMAECS 967
Db 721 CTLTQCS 727

RESULT 6
US-09-130-491-13
; Sequence 13, Application US/09130491
; Patent No. 6416974
; GENERAL INFORMATION:
; APPLICANT: Holtzman, Douglas A.
; APPLICANT: Goodearl, Andrew D.J.
; TITLE OF INVENTION: TANGO-71, TANGO-73, TANGO-74, TANGO-76, AND TANGO-83
; FILE REFERENCE: 09404/041001
; CURRENT APPLICATION NUMBER: US/09/130,491
; CURRENT FILING DATE: 1998-08-07
; EARLIER APPLICATION NUMBER: US 60/058,108
; EARLIER FILING DATE: 1997-09-05
; EARLIER APPLICATION NUMBER: US 60/054,961
; EARLIER FILING DATE: 1997-08-06
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 13
; LENGTH: 608
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-130-491-13

Query Match 62.4%; Score 3297; DB 4; Length 608;
Best Local Similarity 90.9%; Pred. No. 4.3e-280;
Matches 599; Conservative 1; Mismatches 5; Indels 54; Gaps 1;

QY 309 ILVIHDEQKPEVTSNAALTLRNFCNWKQHNPPSDRDAEHYDTAILFTRODLCGSOTCD 368
Db 4 ILVIHDEQKPEVTSNAALTLRNFCNWKQHNPPSDRDAEHYDTAILFTRODLCGSOTCD 63
QY 369 TLGMADVGTVCDSRSCSVIEDDGLQAAFTTAHGLGHVFNMPHDDAKQCSALNGVNDQSH 428
Db 64 TLGMADVGTVCDSRSCSVIEDDGLQAAFTTAHGLGHVFNMPHDDAKQCSALNGVNDQSH 123
QY 429 WNASMLNLDHSPWSPCSGYMITSFLDNGHGECLMDKPNQPIQLPGDLPGTGYDANRC 488
Db 124 WNASMLNLDHSPWSPCSGYMITSFLDNGHGECLMDKPNQPIQLPGDLPGTGYDANRC 183
QY 489 OPTFGEDESKHCPCDAASTCTLTWCTGTSGGLVLCQTKHFPWADGTSCGEGKWCINGKCVNK 548
Db 184 OPTFGEDESKHCPCDAASTCTLTWCTGTSGGLVLCQTKHFPWADGTSCGEGKWCINGKCVNK 243

549 NHRKHFDTPPHGSMGMPGDCSRTCGGVQVYTMRECDNVPKNGGKYCEGRVYRSC 608
549 NHRKHFDTPPHGSMGMPGDCSRTCGGVQVYTMRECDNVPKNGGKYCEGRVYRSC 608
244 TDRKHFDTPPHGSMGMPGDCSRTCGGVQVYTMRECDNVPKNGGKYCEGRVYRSC 303
244 TDRKHFDTPPHGSMGMPGDCSRTCGGVQVYTMRECDNVPKNGGKYCEGRVYRSC 303
609 NLEDCPDNNGKTFRBQCEAHNEFSAKSPGSPAVEMPKYAGVSPKORCKLIQAKGIG 668
609 NLEDCPDNNGKTFRBQCEAHNEFSAKSPGSPAVEMPKYAGVSPKORCKLIQAKGIG 668
304 NLEDCPDNNGKTFRBQCEAHNEFSAKSPGSPAVEMPKYAGVSPKORCKLIQAKGIG 363
304 NLEDCPDNNGKTFRBQCEAHNEFSAKSPGSPAVEMPKYAGVSPKORCKLIQAKGIG 363
669 YFVLQPKVVDGTPCSPDSTSVCQGVQVYTMRECDNVPKNGGKYCEGRVYRSC 728
669 YFVLQPKVVDGTPCSPDSTSVCQGVQVYTMRECDNVPKNGGKYCEGRVYRSC 728
364 YFVLQPKVVDGTPCSPDSTSVCQGVQVYTMRECDNVPKNGGKYCEGRVYRSC 423
364 YFVLQPKVVDGTPCSPDSTSVCQGVQVYTMRECDNVPKNGGKYCEGRVYRSC 423
729 GSVTSAKPGYHDIITPTGATNIEVKORNGSRNNGSFLAIKAADGTIILNGDYTLSTL 788
729 GSVTSAKPGYHDIITPTGATNIEVKORNGSRNNGSFLAIKAADGTIILNGDYTLSTL 788
424 GSVTSAKPGYHDIITPTGATNIEVKORNGSRNNGSFLAIKAADGTIILNGDYTLSTL 483
424 GSVTSAKPGYHDIITPTGATNIEVKORNGSRNNGSFLAIKAADGTIILNGDYTLSTL 483
789 EQDIMYKGVVLYRSGSAAALERIRSFPLKEPTIQLTVGNALRPKIYTFVKKKES 848
789 EQDIMYKGVVLYRSGSAAALERIRSFPLKEPTIQLTVGNALRPKIYTFVKKKES 848
484 EQDIMYKGVVLYRSGSAAALERIRSFPLKEPTIQLTVGNALRPKIYTFVKKKES 543
484 EQDIMYKGVVLYRSGSAAALERIRSFPLKEPTIQLTVGNALRPKIYTFVKKKES 543
849 FNAIFSAWVIEBWGECSSKCELGWQRRLVECRDINGQPASECAKEVTPCADHP 908
849 FNAIFSAWVIEBWGECSSKCELGWQRRLVECRDINGQPASECAKEVTPCADHP 908
544 FNAIFSAWVIEBWGECSSKCELGWQRRLVECRDINGQPASECAKEVTPCADHP 560
544 FNAIFSAWVIEBWGECSSKCELGWQRRLVECRDINGQPASECAKEVTPCADHP 560
909 CPQWLGWSSCKTCGKYKTSKCLSHDGGVLSHSDCDPLKPKHFDICTMAECS 967
909 CPQWLGWSSCKTCGKYKTSKCLSHDGGVLSHSDCDPLKPKHFDICTMAECS 967
561 -----CSKTCGKYKTSKCLSHDGGVLSHSDCDPLKPKHFDICTMAECS 608
561 -----CSKTCGKYKTSKCLSHDGGVLSHSDCDPLKPKHFDICTMAECS 608

RESULT 7
US-09-130-491-16
; Sequence 16, Application US/09130491
; Patent No. 6416974
; GENERAL INFORMATION:
; APPLICANT: Holtzman, Douglas A.
; APPLICANT: Gooddeal, Andrew D.J.
; TITLE OF INVENTION: TANGO-71, TANGO-73, TANGO-74, TANGO-76, AND TANGO-83
; FILE REFERENCE: 09404/041001
; CURRENT APPLICATION NUMBER: US/09/130,491
; PRIOR FILING DATE: 1998-08-07
; EARLIER APPLICATION NUMBER: US 60/058,108
; EARLIER FILING DATE: 1997-09-05
; EARLIER APPLICATION NUMBER: US 60/054,961
; EARLIER FILING DATE: 1997-08-06
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 16
; TYPE: PRT
; LENGTH: 551
; ORGANISM: Rattus rattus

US-09-130-491-16
Query Match 52.8%; Score 2794; DB 4; Length 551;
Best Local Similarity 88.0%; Pred. No. 4,7e-236;
Matches 485; Conservative 35; Mismatches 31; Indels 0; Gaps 0;
417 CASLNGVNDSHMWSMLSLDHSQSPSCGYMITSFLDNGHCECLMDKXPQNPQLPGD 476
1 CASLNGVNDSHMWSMLSLDHSQSPSCGYMITSFLDNGHCECLMDKXPQNPQLPGD 60
477 LPGTSYDANRQCQFTFGEDSKHCPDAASTCTLWCTGTSGGLVLCQTKHPFWADGTS 536
61 LPGLYDANRQCQFTFGEDSKHCPDAASTCTLWCTGTSGGLVLCQTKHPFWADGTS 120
537 GKWCINGKCVKNHRKHFDTPPHGSMGMPGDCSRTCGGVQVYTMRECDNVPKNGGK 596
121 GKWCINGKCVKNHRKHFDTPPHGSMGMPGDCSRTCGGVQVYTMRECDNVPKNGGK 180
597 YCEGRVYRSCNLEDCPDNNGKTFRBQCEAHNEFSAKSPGSPAVEMPKYAGVSPKD 656
181 YCEGRVYRSCNLEDCPDNNGKTFRBQCEAHNEFSAKSPGSPAVEMPKYAGVSPKD 240
657 RCKLIQAKGIGYFVLQPKVVDGTPCSPDSTSVCQGVQVYTMRECDNVPKNGGK 716
657 RCKLIQAKGIGYFVLQPKVVDGTPCSPDSTSVCQGVQVYTMRECDNVPKNGGK 716

241 RCKLIQAKGIGYFVLQPKVVDGTPCSPDSTSVCQGVQVYTMRECDNVPKNGGK 300
241 RCKLIQAKGIGYFVLQPKVVDGTPCSPDSTSVCQGVQVYTMRECDNVPKNGGK 300
717 CGNGSTCKKISGVSSTSAKPGYHDIITPTGATNIEVKORNGSRNNGSFLAIKAADGT 776
717 CGNGSTCKKISGVSSTSAKPGYHDIITPTGATNIEVKORNGSRNNGSFLAIKAADGT 776
301 CGNGSTCKKISGVSSTSAKPGYHDIITPTGATNIEVKORNGSRNNGSFLAIKAADGT 360
301 CGNGSTCKKISGVSSTSAKPGYHDIITPTGATNIEVKORNGSRNNGSFLAIKAADGT 360
777 YILNGDYTLSTLQDIMYKGVVLYRSGSAAALERIRSFPLKEPTIQLTVGNALRPKI 836
777 YILNGDYTLSTLQDIMYKGVVLYRSGSAAALERIRSFPLKEPTIQLTVGNALRPKI 836
361 YILNGDYTLSTLQDIMYKGVVLYRSGSAAALERIRSFPLKEPTIQLTVGNALRPKI 420
361 YILNGDYTLSTLQDIMYKGVVLYRSGSAAALERIRSFPLKEPTIQLTVGNALRPKI 420
837 KYTFYVKKKESFNAIFSAWVIEBWGECSSKCELGWQRRLVECRDINGQPASECAKEV 896
837 KYTFYVKKKESFNAIFSAWVIEBWGECSSKCELGWQRRLVECRDINGQPASECAKEV 896
421 KYTFYVKKKESFNAIFSAWVIEBWGECSSKCELGWQRRLVECRDINGQPASECAKEV 480
421 KYTFYVKKKESFNAIFSAWVIEBWGECSSKCELGWQRRLVECRDINGQPASECAKEV 480
897 KPASTRTPCADHPCPQWLGWSSCKTCGKYKTSKCLSHDGGVLSHSDCDPLKPKH 956
897 KPASTRTPCADHPCPQWLGWSSCKTCGKYKTSKCLSHDGGVLSHSDCDPLKPKH 956
481 KPASTRTPCADHPCPQWLGWSSCKTCGKYKTSKCLSHDGGVLSHSDCDPLKPKH 540
481 KPASTRTPCADHPCPQWLGWSSCKTCGKYKTSKCLSHDGGVLSHSDCDPLKPKH 540
957 FIDFCTMAECS 967
957 FIDFCTMAECS 967
541 YIDFCTMAECS 551
541 YIDFCTMAECS 551

RESULT 8
US-10-009-332-1
; Sequence 1, Application US/10009332
; Patent No. 6716613
; GENERAL INFORMATION:
; APPLICANT: Yamanouchi Pharmaceutical Co., Ltd.
; APPLICANT: Kazusa DNA Research Institute
; TITLE OF INVENTION: NOVEL METALLOPROTEASE HAVING AGGRECANASE ACTIVITY
; FILE REFERENCE: 067541
; CURRENT APPLICATION NUMBER: US/10/009,332
; CURRENT FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: JPA Hei 11-321740
; PRIOR FILING DATE: 1999-11-11
; PRIOR APPLICATION NUMBER: JPA 2000-144020
; PRIOR FILING DATE: 2000-05-16
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 1
; TYPE: PRT
; LENGTH: 950
; ORGANISM: Homo sapiens

US-10-009-332-1
Query Match 46.7%; Score 2471.5; DB 4; Length 950;
Best Local Similarity 48.0%; Pred. No. 2.1e-207;
Matches 484; Conservative 153; Mismatches 253; Indels 101; Gaps 24;
36 LILALALLAVSDALGFPSEDELVVP-ELE-----RVP---GHGTTLRRLHAF 81
1 MLLGLILTLTAFAGRTAGGFEPREVVPVIRLDPDINGRRYRWGPEPESGQGLIFITAP 60
82 DQQLDLVDPDSFLAPGFTLQNVGRKSGSDTLP-----ETDLAHCFYSTGVNDPSSA 136
61 QEDFYHLTLTDAQFLAPAFSTEHLG-----VPLQGLTGGSSDLRRCFYSDVNAEPDSF 114
137 AALSCEGVKGFAYLLGEAYFIQPLPAASERLATAPEKPPAPLQFHLLRNQGVGG 196
115 AAVSLCGGLRGAFGYGAHYVISPPLNAS---APAAQRNSQGA---HLLQ---RRGVPGG 165
197 TCGVDDDEPPTKAEETDEDEGEDEGPQS-----PQDPALQGVGP-TGTGS 247
166 PSG-----DPTSRC-----GVASG---WNPAILRALDPYKPRRAGESRRRS 207
248 IRKRKFVSSHRYVETMLVADQSMAEFGSLKHYLLTLFSAARLYKHPSTRNSVSLVVV 307
208 GRKRKFVSIIRYVETMLVADQSMAEFGSLKHYLLTLFSAARLYKHPSTRNSVSLVVV 267
308 KILVHDEQKGPVTSNAALTLRNFCNWKQHNPPSDRDAHYDTAILFTQDLCGSGTCC 367
308 KILVHDEQKGPVTSNAALTLRNFCNWKQHNPPSDRDAHYDTAILFTQDLCGSGTCC 367

us-09-373-658c-126.ra1

```

; GENERAL INFORMATION:
; APPLICANT: Brisco-Myers Squibb Company
; TITLE OF INVENTION: AGGREGAN DEGRADING METALLO PROTEASES
; FILE REFERENCE: DM6909A
; CURRENT APPLICATION NUMBER: US/09/634, 286A
; CURRENT FILING DATE: 2000-08-09
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 837
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-634-286A-2

```

SEQ ID NO 2
LENGTH: 837
TYPE: PRT
ORGANISM: Homo sapiens
-09-634-286A-2

[illegible][illegible]

RESULT 12

US-10-247-685-2

; Sequence 2, Application US/10247685

; Patent No. 6753176

; GENERAL INFORMATION:

; APPLICANT: Bristol-Myers Squibb Company

; TITLE OF INVENTION: AGGRECAN DEGRADING METALLO PROTEASES

; FILE REFERENCE: DM6909D

; CURRENT APPLICATION NUMBER: US/10/247,685

; CURRENT FILING DATE: 2002-09-19

; NUMBER OF SEQ ID NOS: 21

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 2

; LENGTH: 837

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-247-685-2

Query Match 40.2%; Score 2124; DB 4; Length 837;

Best Local Similarity 49.0%; Pred. No. 5e-177; Indels 70; Gaps 18;

Matches 411; Conservative 132; Mismatches 225; Indels 70; Gaps 18;

QY 36 LILLAAALLAVSDALGRPSEDEELVPEL---ERVPGHGT--TRL--RLHAFDQQLDLV 89

DB 37 LLLLLLASLLPSARLASPLPREEEIVFPEKLGSLVPGSGAPARLLCRLQAFGETLLLEL 96

QY 90 PPDSSFLAPGFTLQNVGRK----SGSDTLPBTDLAHCFYSGTVNGDPSSAAALSLCBG- 144

DB 97 EQDSGVQVEGLTVQLGAPELLGAE---PGT-----YLTGTINGDPESVASLHWDCGA 148

QY 145 VRGAYLLGEAYFIOPAPASERLATAAPGKPPAPLOPHLLRRNRQGDVGTCGCVVDE 204

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QY 265 VADQSMARFHSGLKHVLLTLFVSVAARLYKHPISIRNSVSLVVKLVTHDQKGBEVTSN 324

DB 225 VADDRVAAAFHAGLXRYLLTVMAAAAKAFKHPISIRNPVSLVTVRLVILGSGEGPQGVPS 284

QY 325 AALTLRNFCKNQKQNPSPDRDAEYDTAILFTRDLCGSGTCDTLGMADVGVTCVCDPSRS 384

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QY 385 CSVIEDDGLQAFHTTAHELGHVFNPHDDAKQASLNG--VNQDSHMASMLNLDHSPQW 443

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QY 444 SPCSGYMITSLFDNGHGBCLMDKPNPQIQLPGDLPGTSDANRQCGFTFGEDSKHCPDAA 503

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DB 465 PPCAALWCSHNLHNGAMCTKHSPPWADGTPCPAQACMGGRCLHMDQLQDFNIPAGGWG 524

QY 564 MWGPWGDCSRTCGGVQVQYTMRECDNFPVKNQKGYCEGKRVYRSCNLEDCPDNNKGTRE 623

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QY 624 EOCENHNEFSKASFGSGA--VEWIPKYAGVSPKDRCKLIQAKGIGYFFVLQPKVVDGTP 682

DB 585 EQCAAYNHRDIL--FKSFFPGMDVVPRTYGVAPDQCKLTQARALGYTVVLEPRVVDGTP 643

QY 683 CSPDSTVCVQCVKAGCDRIIDSKKXFDKGVCGGNGSTCKKLSGVSWSAKPGYHDI 742

DB 644 CSPDSSSVQVQRCIHAGCDRIIGSKKXFDKCMWCGGSGGSGKSGSFRKFRYGINNVV 703

QY 743 TIPTGATNIEVKQRNQRNNGNSFLAIKAADGTVILNGDYTLSTLEQDIMYKGVV--LRY 801

Db 704 TIPAGATHILVRQGNPCGHR--IYIALKLPDGSYALNGEVTLMPSPTDVLPGAVSLRY 761
QY 802 SGSSAALERIRSFPLKEPLIQLVTCGNALRPKITYFYVKKKKESFNAPTFSAWV 859
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RESULT 13

US-09-122-126B-15

; Sequence 15, Application US/09122126B

; Patent No. 6451575

; GENERAL INFORMATION:

; APPLICANT: Bristol-Myers Squibb Company

; TITLE OF INVENTION: AGGRECAN DEGRADING METALLO PROTEASES

; FILE REFERENCE: DM6909

; CURRENT APPLICATION NUMBER: US/09/122,126B

; CURRENT FILING DATE: 1998-07-24

; NUMBER OF SEQ ID NOS: 21

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 15

; LENGTH: 930

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-122-126B-15

Query Match 36.4%; Score 1924; DB 4; Length 930;

Best Local Similarity 40.7%; Pred. No. 2e-159;

Matches 391; Conservative 125; Mismatches 314; Indels 130; Gaps 17;

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QY 168 -----LATAAPEKXPAPLOPHLLRRNRQGDVGTCGVVDDEP---RPTG 209

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DB 572 SWGWSGQSRSCGGGVQVQYTMRECDNFPVKNQKGYCEGKRVYRSCNLEDCPDNNKGTRE 630

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OM protein - nucleic search, using frame_plus_p2n model

Run on: May 23, 2005, 19:02:38 ; Search time 1179 Seconds
(without alignments)

5029.648 Million cell updates/sec

Title: US-09-373-658C-126

Perfect score: 5287

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Searched: 5695437 seqs, 3066160638 residues

Total number of hits satisfying chosen parameters: 11390874

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Published Applications NA:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	5287	100.0	4014	11	US-09-989-687-125	Sequence 125, Appl
2	5232	99.0	3430	18	US-10-473-974-98	Sequence 98, Appl
3	5232	99.0	4014	16	US-10-115-286-1	Sequence 1, Appl
4	5232	99.0	4014	18	US-10-757-450-1	Sequence 1, Appl
5	5232	99.0	4676	13	US-10-105-929-1	Sequence 1, Appl
6	5230	98.9	3889	19	US-10-667-281-1	Sequence 1, Appl
7	5224	98.8	4309	16	US-10-210-120-57	Sequence 57, Appl
8	5224	98.8	4447	18	US-10-753-889-133	Sequence 133, Appl
9	5224	98.8	4459	17	US-10-159-563-152	Sequence 192, Appl
10	5224	98.8	4459	17	US-10-159-563-308	Sequence 308, Appl
11	5224	98.8	4760	10	US-09-971-4298-17	Sequence 17, Appl
12	5202	98.4	4352	19	US-10-741-600-776	Sequence 776, Appl
13	5202	98.4	4459	19	US-10-741-600-777	Sequence 777, Appl
14	5202	98.4	4658	19	US-10-741-600-775	Sequence 775, Appl
15	5144	97.3	3261	10	US-09-373-658-1	Sequence 1, Appl
16	5144	97.3	3261	11	US-09-989-687-1	Sequence 1, Appl
17	5140.5	97.2	4848	17	US-10-425-114-26851	Sequence 26851, A
18	4302.5	81.4	21130	19	US-10-741-600-17789	Sequence 17789, A
19	4293.5	81.2	4858	19	US-10-764-420-37	Sequence 37, Appl
20	4287	81.1	4878	17	US-10-191-803-170	Sequence 170, Appl
21	4287	81.1	4878	17	US-10-152-319A-1840	Sequence 1840, Appl
22	4277.5	80.9	4180	10	US-09-373-658-20	Sequence 20, Appl
23	4277.5	80.9	4180	11	US-09-989-687-20	Sequence 20, Appl
24	4270.5	80.8	2871	18	US-10-473-974-23	Sequence 23, Appl
25	3922	74.2	2184	9	US-09-445-023A-2	Sequence 2, Appl
26	3922	74.2	2184	14	US-10-097-597-2	Sequence 2, Appl
27	3922	74.2	2184	14	US-10-097-580-2	Sequence 2, Appl
28	3652	69.1	2184	9	US-09-445-023A-13	Sequence 13, Appl
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31	3411	64.5	9248	10	US-09-373-658-21	Sequence 21, Appl
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33	3303	62.5	3147	18	US-10-718-332-1	Sequence 1, Appl
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38	2496	47.2	3446	9	US-09-965-631-7	Sequence 7, Appl
39	2496	47.2	3446	19	US-10-961-020-7	Sequence 24, Appl
40	2478.5	46.9	2937	17	US-10-275-107-24	Sequence 24, Appl
41	2478	46.9	2853	9	US-09-965-631-3	Sequence 3, Appl
42	2478	46.9	2853	18	US-10-391-364-76	Sequence 76, Appl
43	2478	46.9	2853	18	US-10-391-364-78	Sequence 78, Appl
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45	2478	46.9	2853	19	US-10-961-020-3	Sequence 3, Appl

ALIGNMENTS

RESULT 1

US-09-989-687-125
; Sequence 125, Application US/09989687
; Publication No. US20040002449A1
; GENERAL INFORMATION:
; APPLICANT: Hastings, Gregg A.
; APPLICANT: Ruben, Steven M.
; TITLE OF INVENTION: Meth1 and Meth2 Polynucleotides and Polypeptides
; FILE REFERENCE: 1488.107000D
; CURRENT APPLICATION NUMBER: US/09/989,687
; CURRENT FILING DATE: 2001-11-21
; NUMBER OF SEQ ID NOS: 126
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 125
; LENGTH: 4014
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (466)..(3366)

OTHER INFORMATION: US-09-989-687-125

Alignment Scores:

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Score: 5287.00 Matches: 967
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 11 Gaps: 0

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Qy 41 AlaAlaLeuAlaValSerAspAlaLeuGlyArgProSerGluGluAspGluLeu 60
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Qy PheValLysLysLysLysGluSerPheAsnAlaIleProThrPheSerAlaTrpValIle 860
Db 2986 TTCGTAAGAAAGAAAGGAATCTTTCAATGCTATCCCACTTTTTCAGCATGGGTCAAT 3045
Qy GluGluTrpGlyGluCysSerLysSerCysGluLeuGlyTrpGlnArgArgLeuValGlu 880
Db 3046 GAAGAGTGGGGCGAAATGTTCTAAGTCATGTGAATTTGGTTGGCAGAGAAGCTGGTAGAA 3105
Qy CysArgAspIleAsnGlyGlnProAlaSerGluCysAlaLysGluValLysProAlaSer 900
Db 3106 TGCAGAGACATTAATGGACAGCTGCTTCCAGTGTGCAAGAGTGAAGCCAGCCAGC 3165
Qy ThrArgProCysAlaAspHisProCysProGlnTrpGlnLeuGlyLysTrpSerSerCys 920
Db 3166 ACCAGACCTTGTGCAGACCATCCCTGCCCCAGTGGCAGCTGGGGAGTGGTCATCATGT 3225
Qy SerLysThrCysGlyLysGlyTyrLysLysThrSerLeuLysCysLeuSerHisAspGly 940
Db 3226 TCTAAGACCTGTGGAGGTTTCAAAAAACAAGCTTGAAGTGTCTGTCCCAATGATGGA 3285
Qy GlyValLeuSerHisAspSerCysAspProLeuLysLysProLysHisPheIleAspPhe 960
Db 3286 GGGGTGTATCTCATGACACTGTGATCTCTTAAAGAAACCTTAAACATTTTCATAGACTTT 3345
Qy CysThrMetAlaGluCysSer 967
Db 3346 TGCACAAATGGCAGAAATGCAT 3366

RESULT 2

US-10-473-974-98
; Sequence 98, Application US/10473974
; Publication No. US2004026580A1
; GENERAL INFORMATION:
; APPLICANT: GARCIA, TERESA
; APPLICANT: ROMAN ROMAN, SERGIO
; APPLICANT: BARON, ROLAND
; APPLICANT: CALL, KATHERINE
; APPLICANT: THEILLHABER, JOACHIM

; APPLICANT: CONNOLLY, TIMOTHY
; APPLICANT: JACKSON, AMANDA
; APPLICANT: BUSHNELL, STEVEN
; APPLICANT: RAWADI, GEORGES
; TITLE OF INVENTION: GENES INVOLVED IN OSTEOGENESIS, AND METHODS OF USE
; FILE REFERENCE: 37991-0023
; CURRENT APPLICATION NUMBER: US/10/473,974
; PRIOR FILING DATE: 2003-10-03
; PRIOR APPLICATION NUMBER: PCT/IB02/02211
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: 60/281,400
; PRIOR FILING DATE: 2001-04-05
; NUMBER OF SEQ ID NOS: 246
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 98
; LENGTH: 3430
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (3332)
; OTHER INFORMATION: a, c, g, t, other or unknown
US-10-473-974-98

Alignment Scores:
Pred. No.: 0 Length: 3430
Score: 5232.00 Matches: 957
Percent Similarity: 99.38% Conservative: 4
Best Local Similarity: 98.97% Mismatches: 6
Query Match: 98.96% Indels: 0
DB: 18 Gaps: 0

US-09-373-658c-126 (1-967) x US-10-473-974-98 (1-3430)

Qy 1 MetGlnArgAlaValProGluGlyPheGlyArgArgLysLeuGlySerPheMetGlyAsn 20
Db 187 ATGCAGCAGCTGTGCCCCGAGGGGTTCGGAAGCGCAGCTGGGACGACATCGGGAAC 246
Qy 21 AlaGluArgAlaProGlySerArgSerPheGlyProValProThrLeuLeuLeuAla 40
Db 247 GCGAGCGGGCTCCGGGGTCTCGAGCTTTGGCCCGTACCCACGCTGCTGCTGCC 306
Qy 41 AlaAlaLeuLeuAlaValSerAspAlaLeuGlyArgProSerGluGluAspGluLeu 60
Db 307 GCGGCGCTACTGGCCGTGTCCGACGCACCTCGGGCGCCCTCCGAGGAGGACGAGGACTA 366
Qy 61 ValValProGluLeuGluArgValProGlyHisGlyThrArgLeuArgLeuHisAla 80
Db 367 GTGGTCCGGAGCTGGAGCGCGCCCGGGACACGGGACACGCGCTTCCGCTGCACGCC 426
Qy 81 PheAspGlnGlnLeuAspLeuAspValProProAspSerSerPheLeuAlaProGlyPhe 100
Db 427 TTTGACACGACGCTGATCTGGAGCTGCGGCCCGACAGCAGCTTTTGGCGCCGCTTC 486
Qy 101 ThrLeuGlnAsnValGlyArgLysSerGlySerAspThrProLeuProGluThrAspLeu 120
Db 487 ACCTCCAGAACCTGGGGCGCAATCCGGTCCGAGACGCGCTTCCGGAACCGACCTG 546
Qy 121 AlaHisCysPheTyrSerGlyThrValAsnGlyAspProSerSerAlaAlaLeuSer 140
Db 547 GCGCACTGCTTCTACTCCGGCACCCGTGAATGGCGATCCCAAGCTCGGCTCGCCCTCAGC 606
Qy 141 LeuCysGluGlyValArgGlyAlaPheTyrLeuLeuGlyGluAlaTyrPheIleGlnPro 160
Db 607 CTCTGAGGGCGTGGCGCGCTTCTTACTGCTGGGGAGGCGGTATTTTCATCCAGCG 666
Qy 161 LeuProAlaAlaSerGluArgLeuAlaThrAlaAlaProGlyLysProProAlaPro 180
Db 667 CTGCCCCCGCCAGCGAGCGCTTCGCCACCGCGCCCGCCAGGGAGAAGCGCCGCGACCA 726
Qy 181 LeuGlnPheHisLeuLeuArgArgAsnArgGlnGlyAspValGlyThrCysGlyVal 200
Db 727 CTACAGTTCCACCTCTCTGGCGGGAATTCGACAGGCGACGTTAGCGCGCACGTGCGGGGTC 786

QY	201	ValAspAspGluProArgProThrGlyValAlaGluThrGluAspGluAspGluGlyThr	220
DB	787	GTGGACGACGAGCCCGCGGACTGGGAAGCGGAGACCGAAGACGAGGAGGACT	846
QY	221	GluGlyGluAspGluGlyProGlnTrpSerProGlnAspProAlaLeuGlnGlyValGly	240
DB	847	GAGGCGAGGACGAGGCGCTCAGTGGTCGCCGACGACCCGCGCATGCAAGCGTAGGA	906
QY	241	GlnProThrGlyThrGlySerIleArgLysLysArgPheValSerSerHisArgTyrVal	260
DB	907	CAGCCACACAGGAACGTGAAGACATAAGAAAGAACGATTTGTGTCCAGTCACCGCTATGTG	966
QY	261	GluThrMetLeuValAlaAspGlnSerMetAlaGluPheHisGlySerGlyLeuLysHis	280
DB	967	GAACCATGCTTGTGGCAGACCATCGATGGCAGAAATCCACGGCAGTGGTCTAAGACAT	1026
QY	281	TyrLeuLeuThrLeuPheSerValAlaAlaArgLeuTyrLysHisProSerIleArgAsn	300
DB	1027	TACCTTCTCAGTGTGTTTCGGTGGCAGCCAGATTTGTACAAACACCCACAGCATTCGTAT	1086
QY	301	SerValSerLeuValValLysIleLeuValIleHisAspGluGlnLysGlyProGlu	320
DB	1087	TCAGTTAGCTGTGTGTGTGAAGATCTTGTGTCATCCAGCATGAACAGGAGCGCGAA	1146
QY	321	ValThrSerAsnAlaAlaLeuThrLeuArgAsnPheCysAsnTrpGlnLysGlnHisAsn	340
DB	1147	GTGACCTCAATGCTGCCCTCACTGCGGAATTTTGGCACTGGCAGAGCAGACAAC	1206
QY	341	ProProSerAspArgAspAlaGluHisTyrAspThrAlaIleLeuPheThrArgGlnAsp	360
DB	1207	CAACCCAGTGACCGGGATGCAGAGCACTATGACACAGCAATTTCTTCCACGACAGGAC	1266
QY	361	LeuCysGlySerGlnThrCysAspThrLeuGlyMetAlaAspValGlyThrValCysAsp	380
DB	1267	TTGTGTGGGTCCACAGATGTGATCTCTTGGGATGGCTGATGTTGGAATCTGTGTGAT	1326
QY	381	ProSerArgSerCysSerValIleGluAspAspGlyLeuGlnAlaAlaPheThrThrAla	400
DB	1327	CCGAGCAGAAGCTGCTCCGTCATAGAAAGATGATGTTTCAAGCTGCCCTTCCACAGCC	1386
QY	401	HisGluLeuGlyHisValPheAsnMetProHisAspAspAlaLysGlnCysAlaSerLeu	420
DB	1387	CATGAATTAGGCCACGCTGTTAAACATGCCACATGATGATGCAAGCAGTGTGCCAGCCTT	1446
QY	421	AsnGlyValAsnGlnAspSerHisMetMetAlaSerMetLeuSerAsnLeuAspHisSer	440
DB	1447	AATGGTGTGAACGAGGATTTCCACATGATGGCGTCAATGCTTTCCAACCTGGACCAAGC	1506
QY	441	GlnProTrpSerProCysSerGlyTyrMetIleThrSerPheLeuAspAsnGlyHisGly	460
DB	1507	CAGCCTTGCTCTCTTGCAGTGCCTACATGATTACATCATTTCTGGATTAATGTCATGGG	1566
QY	461	GluCysLeuMetAspLysProGlnAsnProIleGlnLeuProGlyAspLeuProGlyThr	480
DB	1567	GAATGTTTGTGACAAAGCTCAGATCCAGATCCATACAGCTCCCGGCGATCTCCCTGGCACC	1626
QY	481	SerTyrAspAlaAsnArgGlnCysGlnPheThrPheGlyGluAspSerLysHisCysPro	500
DB	1627	TGCTAGCATGCCAACCGGAGTGCCAGTTTACATTTTGGGGAGGACTCCAAACACATGCCCT	1686
QY	501	AspAlaAlaSerThrCysSerThrLeuTrpCysThrGlyThrSerGlyGlyValLeuVal	520
DB	1687	GATGCAGCCAGACATGTAGACACTTGTGTGTACCGGACCTCTCGTGGGGTGTGTGGT	1746
QY	521	CysGlnThrLysHisPheProTrpAlaAspGlyThrSerCysGlyGluGlyLysTrpCys	540
DB	1747	TGTCAAAACCAACACTTCCCGTGGGCGGATGGCACCAGCTGTGGAGAGGAGAAATGTTGT	1806
QY	541	IleAsnGlyLysCysValAsnLysAsnHisArgLysHisPheAspThrProPheHisGly	560
DB	1807	ATCAACGGCAAGTGTGTGAACAAACCGACAGAAAGCATTTTGTATACGCTTTTTCATGGA	1866
QY	561	SerTyrGlyMetTrpGlyProTrpGlyAspCysSerArgThrCysGlyGlyValGln	580
DB	1867	AGCTGGGAGATGTGGGGCTTGGGAGACTGTTGAGAACCTGCGGTGGAGGATCCAG	1926
QY	581	TyrThrMetArgGluCysAspAsnProValProLysAsnGlyGlyLysTyrCysGluGly	600
DB	1927	TACACGATGAGGGAATGTGACAAACCCAGTCCCAAAGAAATGAGGGAAGTACTGTGAAGGC	1986
QY	601	LysArgValArgTyrArgSerCysAsnLeuGluAspCysProAspAsnAsnGlyLysThr	620
DB	1987	AAACCGAGTGGCTACAGATCTCTGTAACTTGAAGACTGTCCAGACAATTAATGAAAAACC	2046
QY	621	PheArgGluGluGlnCysGluAlaHisAsnGluPheSerLysAlaSerPheGlySerGly	640
DB	2047	TTTAGAGGAACATGTGAAGCACACACGAGTTTCAAAGCTTCTCTTGGGAGTGGG	2106
QY	641	ProAlaValGluTrpIleProLysTyrAlaGlyValSerProLysAspArgCysLysLeu	660
DB	2107	CCTGCGGTGGAATGGATTCCCAAGTACGCTGCGCTCTCAACCAAGACAGGTGCAAGCTC	2166
QY	661	IleCysGlnAlaLysGlyIleGlyTyrPhePheValLeuGlnProLysValValAspGly	680
DB	2167	ATCTCCCAAGCCAAAGGCATTTGGCTACTTCTTCTTTCAGCCCCAAGTTGTAGATGT	2226
QY	681	ThrProCysSerProAspSerThrSerValCysValGlnGlyGlnCysValLysAlaGly	700
DB	2227	ACTCCATGTAGCCAGATTCACCTCTGCTGTGTGCAAGGACAGTGTGTAAAAGCTGT	2286
QY	701	CysAspArgIleIleAspSerLysLysPheAspLysCysGlyValCysGlyGlyAsn	720
DB	2287	TGTGATCGCATCATAGACTCCAAAAAGAGTTTGTATAATGTGTGTTGCGGGGAAAT	2346
QY	721	GlySerThrCysLysLysIleSerGlySerValThrSerAlaLysProGlyTyrHisAsp	740
DB	2347	CGATCTACTTGTAAAAAATATACGATCAGTTACTAGTGCAAAAACCTCGATATCATAT	2406
QY	741	IleIleThrIleProThrGlyAlaThrAsnIleGluValLysGlnArgAsnGlnArgGly	760
DB	2407	ATCATCACATTTCCAACTGGAGCCACCAACATCGAAGTGAACAGCGGACACAGAGGGA	2466
QY	761	SerArgAsnAsnGlySerPheLeuAlaIleLysAlaAlaAspGlyThrTyrIleLeuAsn	780
DB	2467	TCACAGAAACAATGGCAGCTTCTTGCCATCAAAGCTGCTGATGGCACATATATTTCTAAT	2526
QY	781	GlyAspTyrThrLeuSerThrLeuGlnAspIleMetTyrLysGlyValValLeuArg	800
DB	2527	GGTGACTACCTTTGTCCACCTTAGACGAAGACATATATGACAAGGTGTTGTCTTGAGG	2586
QY	801	TyrSerGlySerSerAlaAlaLeuGluArgIleArgSerPheSerProLeuLysGluPro	820
DB	2587	TACAGGGCTCTCTGCGGCATTTGGAAGAAATTCGACGCTTTAGCCCTCTCAAGAGGCC	2646
QY	821	LeuThrIleGlnValLeuThrValGlyAsnAlaLeuArgProLysIleLysTyrThrTyr	840
DB	2647	TTGACCATCCAGGTCTTACTGTGGGCAATGCCCTTCGACCTAAAAATTAATACACCTAC	2706
QY	841	PheValLysLysLysGluSerPheAsnAlaIleProThrPheSerAlaTrpValIle	860
DB	2707	TTTCGTAAGAAAGAAGGAATCTTTCAATGCTATCCCCACCTTTTTCAGCATGGGTCAT	2766
QY	861	GluGluTrpGlyGluCysSerLysSerCysGluLeuGlyTrpGlnArgArgLeuValGlu	880
DB	2767	GAAGAGTGGGCGAATGTTCTAAGTCATGTGAATTTGGGTGGCAGAGAAGACTGGTAGAA	2826
QY	881	CysArgAspIleAsnGlyGlnProAlaSerGluCysAlaLysGluValLysProAlaSer	900
DB	2827	TGCCGAGACATTAATGGAAGCCTGCTTCCGAGTGTGCAAGGAAAGTGAAGCCAGCAGC	2886
QY	901	ThrArgProCysAlaAspHisProCysProGlnTrpGlnLeuGlyLysTrpSerSerCys	920
DB	2887	ACCAGACCTTGTGCAGACCATCCCTGCCCCAGTGCAGCTGGGGAGTGTTCATCATGT	2946
QY	921	SerLysThrCysGlyLysGlyTyrLysLysThrSerLeuLysCysLeuSerHisAspGly	940

Db 2947 TCTAAGACCTGTGGGAGGCTTACAAAAAGAGCTTGAAGTGTCTGTCCCATGATGGA 3006
Qy 941 GlyValLeuSerHisAspSerCysAspProLeuIlySProLysHisPheIleAspPhe 960
Db 3007 GGGGTGTATCTCATGAGAGCTGTGATCTCTTAAGAAACCTAAACATTTTCATAGACTTT 3066
Qy 961 CysThrMetAlaGluCysSer 967
Db 3067 TGCACATGGCAGATGCAGT 3087

RESULT 3

US-10-115-286-1
; Sequence 1, Application US/10115286
; Publication No. US20030166065A1
; GENERAL INFORMATION:
; APPLICANT: Jonak, Zdenka
; Trulli, Stephen
; Fornwald, James
; Terrett, Jonathan
; Hasting, Gregg
; TITLE OF INVENTION: No. US20030166065A1el Integrin Ligand ITGL-TSP
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ratner & Prestia
; STREET: Box 980
; CITY: Valley Forge
; STATE: PA
; COUNTRY: USA
; ZIP: 19482
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/115,286
; FILING DATE: 04-Apr-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/845,496
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Prestia, Paul F
; REGISTRATION NUMBER: 23,031
; REFERENCE/DOCKET NUMBER: GH-70000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-407-0700
; TELEFAX: 610-407-0701
; TELEX: 846169
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4014 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:

US-10-115-286-1
Alignment Scores:
Pred. No.: 0 Length: 4014
Score: 5232.00 Matches: 957
Percent Similarity: 99.38% Conservative: 4
Best Local Similarity: 98.97% Mismatches: 6
Query Match: 98.96% Indels: 0
DB: 16 Gaps: 0

US-09-373-658C-126 (1-967) x US-10-115-286-1 (1-4014)
Qy 1 MetGlnArgAlaValProGluGlyPheGlyArgArgLysLeuGlySerAspMetGlyAsn 20
Db 466 ATGCAGCGAGCTGTGCCCGAGGGTTTCGAAGGCGCAAGCTGGGCGAGCGCATGGGGAAC 525

Qy 21 AlaGluArgAlaProGlySerArgSerPheGlyProValProThrLeuLeuLeuLeuAla 40
Db 526 GCGGAGCGGGCTCCCGGGTCTCGAGCTTTGGGCCCGGTATCCACAGCTGTGTCTGCTCGCC 585
Qy 41 AlaAlaLeuLeuAlaValSerAspAlaLeuGlyArgProSerGluGluAspGluGluLeu 60
Db 586 GCGGCGCTACTGGCGCTGTGGACGCACTCGGGCGCCCTCCGAGGAGGACGAGGAGCTA 645
Qy 61 ValValProGluLeuGluArgValProGlyHisGlyThrThrArgLeuArgLeuHisAla 80
Db 646 GTGGTGGCGGAGCTGGAGCGCGCCCGGGACACGGGACCAACGCGCTTCCGCTTGCAGGCC 705
Qy 81 PheAspGlnGlnLeuAspValProProAspSerSerPheLeuAlaProGlyPhe 100
Db 706 TTTGACCAGCAGCTGGATCTGGAGCTGGCGCCCGACAGCAGCTTTTGGCGCGCGCTTC 765
Qy 101 ThrLeuGlnAsnValGlyArgLysSerGlySerAspThrProLeuProGluThrAspLeu 120
Db 766 ACCTCCAGAACCTGGGGCGCAATCCGGTCCGAGACGCGCTTCCGGAAACCGACCTG 825
Qy 121 AlaHisCysPheThrSerGlyThrValAsnGlyAspProSerSerAlaAlaLeuSer 140
Db 826 GCGACTGCTTCTACTCCGSCACCGTGATGGGATCCAGCTCGGCTGCGCGCTCAGC 885
Qy 141 LeuCysGluGlyValArgGlyAlaPheThrLeuLeuGlyGluAlaThrPheIleGlnPro 160
Db 886 CTCTGCGAGCGCTGCGCGCGCTTCTACTGCTGGGGAGGCGTATTTTCATCCAGCG 945
Qy 161 LeuProAlaAlaSerGluArgLeuAlaThrAlaAlaProGlyGluLysProProAlaPro 180
Db 946 CTGCGCGCGCCAGCGAGCGCTCGCCACCGCGCCCGCGGAGAGCGCGCGCACCA 1005
Qy 181 LeuGlnPheHisLeuLeuArgArgAsnArgGlnGlyAspValGlyGlyThrCysGlyVal 200
Db 1006 CTACAGTTCCACTCTCTGCGCGCGAATCGCAGGGCGACGTAGGGCGCACGTCGGGGTC 1065
Qy 201 ValAspAspGluProArgProThrGlyLysAlaGluThrGluAspGluAspGluGlyThr 220
Db 1066 GTGGACGAGCGAGCGCGCGCTGCGGAAAGCGAGACCGAAGACGAGGAGGACT 1125
Qy 221 GluGlyGluAspGluGlyProGlnThrSerProGlnAspProAlaLeuGlnGlyValGly 240
Db 1126 GAGGGCGAGGACGAGGGCGCTCAGTGGTCCCGCAGACCGCGCACGTCGAAGGCGTAGGA 1185
Qy 241 GlnProThrGlyThrGlySerIleArgLysArgPheValSerSerHisArgThrVal 260
Db 1186 CAGCCACAGAACTGGAGCATAAAGAAAGCGGATTTGTTCAGTCCCGCTATGTG 1245
Qy 261 GluThrMetLeuValAlaAspGlnSerMetAlaGluPheHisGlySerGlyLeuLysHis 280
Db 1246 GAAACCATGCTTGTGGCAGACCATCGATGGCAGATTCACGCGCAGTGGTCTAAAGCAT 1305
Qy 281 TyrLeuLeuThrLeuPheSerValAlaAlaArgLeuTyrLysHisProSerIleArgAsn 300
Db 1306 TACCTTCTCAGTTGTTTTCGGTGGCAGCCAGATTGTACAAACACCCCGAGCATTCGTAAT 1365
Qy 301 SerValSerLeuValValValLysIleLeuValIleHisAspGluGlnLysGlyProGlu 320
Db 1366 TCAGTTAGCCTGGTGGTGGTGAAGATCTTGGTCATCCAGATGAACAGAGGGGCGCGAA 1425
Qy 321 ValThrSerAsnAlaAlaLeuThrLeuArgAsnPheCysAsnTrpGlnLysGlnHisAsn 340
Db 1426 GTGACCTCCAAATGCTGCCCTCACTCTCGGGAACCTTTTGGCAACTGGCAGAGCAGCAAC 1485
Qy 341 ProProSerAspArgAspAlaGluHisTyrAspThrAlaIleLeuPheThrArgGlnAsp 360
Db 1486 CCACCCAGTACCGGGATGCAGAGCACTATGACACAGCAATTTCTTTCCACAGACAGGAC 1545
Qy 361 LeuCysGlySerGlnThrCysAspThrLeuGlyMetAlaAspValGlyThrValCysAsp 380
Db 1546 TTGTGTGGGTCCCAAGCATGTGATACTCTTGGGATGGCTGATGTGTGAACTGTGTGTGAT 1605

381 ProSerArgSerCysSerValIleGluAspAspGlyLeuGlnAlaAlaPheThrAla 400
1606 CCGAGCAGAGAGCTGCTCCGTCATAGAGAGATGATGGTTTACAAGCTGCCCTTCCACAGCC 1665
401 HisGluLeuGlyHisValPheAsnMetProHisAspAspAlaLysGlnCysAlaSerLeu 420
1666 CATGAATTAGGCCACCGTGTAAATGATGCAATGATGATGCAAGAGCAGTGTGCCAGCCTT 1725
421 AsnGlyValAsnGlnAspSerHisMetMetAlaSerMetLeuSerAsnLeuAspHisSer 440
1726 AATGGTGTGAACAGGATTTCCACATGATGGGGTCAATGCTTTTCCAACTGGACACACAGC 1785
441 GlnProTrpSerProCysSerGlyTyrMetIleThrSerPheLeuAspAsnGlyHisGly 460
1786 CAGCCTTGCTTCTCTTGCAGTGCCTACATGATTAATCATCTTTCTGGATTAATGGTCATGGG 1845
461 GluCysLeuMetAspLysProGlnAsnProIleGlnLeuProGlyAspLeuProGlyThr 480
1846 GAATGTTTGATGGACAAGCCTCAGAATCCATACAGTCCCAAGGCGATCTCCCTGGCACC 1905
481 SerTyrAspAlaAsnArgGlnCysGlnPheThrPheGlyGluAspSerLysHisCysPro 500
1906 TCGTACGATGCCAACCGGAGTCCAGATTTTACATTTGGGGAGGAGCTCCAAACACATGCCCT 1965
501 AspAlaAlaSerThrCysSerThrLeuTyrCysThrGlyThrSerGlyGlyValLeuVal 520
1966 GATGACGACGACATGATGACCTTGTGTGTATCCGACACCTCTGTGTGGGTGTGTGTG 2025
521 CysGlnThrLysHisPheProTrpAlaAspGlyThrSerCysGlyGluGlyLysTrpCys 540
2026 TGTCAAAACCAACACTTCCCGTGGCGGATGCCAGCTGTGGAGAGGGAATGGTGT 2085
541 IleAsnGlyLysCysValAsnLysAsnHisArgLysHisPheAspThrProPheHisGly 560
2086 ATCAACGGCAAGTGTGTGAACAAAACCCGACAGAAAGCAATTTTGATACGCTTTTTCATGGA 2145
561 SerTrpGlyMetTrpGlyProTrpGlyAspCysSerArgThrCysGlyGlyValGln 580
2146 AGCTGGGGAATGTGGGGCTTGGGAGACTGTTCGAGAACGTGCGGTGGAGAGTCCAG 2205
581 TyrThrMetArgGluCysAspAsnProValProLysAsnGlyGlyLysTyrCysGluGly 600
2206 TACACGATGAGGGAATGTGCAACACCGTCCCAAGATGGAGGAAGTACTGTGAAGGC 2265
601 LysArgValArgTyrArgSerCysAsnLeuGluAspCysProAspAsnAsnGlyLysThr 620
2266 AAACGAGTCCGCTACAGATCCTGTAACTTGAAGGACTGTCCAGACAAATATGGAAGAACCC 2325
621 PheArgGluGlnCysGluAlaHisAsnGluPheSerLysAlaSerPheGlySerGly 640
2326 TTTAGAGAGACAAATGTGAGACACACACAGAGTTTTCAAAGCTTCCCTTGGAGTGGG 2385
641 ProAlaValGluTrpIleProLysTyrAlaGlyValSerProLysAspArgCysLysLeu 660
2386 CTTGGGTGGATGGATTTCCCAAGTACGCTGCGCTCTCAACAAAGACAGGTGCAAGCTC 2445
661 IleCysGlnAlaLysGlyIleGlyTyrPhePheValLeuGlnProLysValValAspGly 680
2446 ATCTGCCAAGCAAGGCAATGGCTACTCTTCTGTTTTTCAGCCCCAAGTTTGTAGATGT 2505
681 ThrProCysSerProAspSerThrSerValCysValGlnGlnCysValLysAlaGly 700
2506 ATCCCATGTAGCCAGATTTCCACCTCTGTCTGTGTGCAAGGACAGTGTGTAAGCTGTGT 2565
701 CysAspArgIleIleAspSerLysLysLysPheAspLysCysGlyValCysGlyGlyAsn 720
2566 TGTGATCGCATCATAGACTCCAAAAAGAGTTTGATAAATGTGTGTGTGGGGGGAAT 2625
721 GlySerThrCysLysLysLysIleSerGlySerValThrSerAlaLysProGlyTyrHisAsp 740
2626 GGATCTACTTGTAAAAAATATACAGATCAGTTACTAGTAGTGAACAACTGGATATCATGAT 2685
741 IleIleThrIleProThrGlyAlaThrAsnIleGluValLysGlnArgAsnGlnArgGly 760

2686 ATCATCACAAATTTCCAACTGGAGCCACCAACATCGAAGTGAAACAGCGGAACAGAGGGA 2745
761 SerArgAsnAsnGlySerPheLeuAlaLysAlaLysAlaAspGlyThrTyrIleLeuAsn 780
2746 TCCAGGAAACAATGGCAGCTTTCTTGCCATCAAGCTGTGTGATGGCACAATATATCTTAAT 2805
781 GlyAspTyrThrLeuSerThrLeuGlnAspIleMetTyrLysGlyValValLeuArg 800
2806 GGTGACTACATTTGTCCACCTTAGAGCAAGACATTAATGTACAAAGGTGTGTCTTGAGG 2865
801 TyrSerGlySerSerAlaAlaLeuGluArgIleArgSerPheSerProLeuLysGluPro 820
2866 TACAGGGCTCTCTCGGCGCATTTGGAAGAAATTCGACGCTTTAGCCCTCTCAAGAGCCC 2925
821 LeuThrIleGlnValLeuThrValGlyAsnAlaLeuArgProLysLysLysTyrThrTyr 840
2926 TTAGCCATCCAGGTTCTTACTGTGGGCAATGCCCTTCGACCTTAAAAATTAATACACCTAC 2985
841 PheValLysLysLysGluSerPheAsnAlaIleProThrPheSerAlaTrpValIle 860
2986 TTCGTAAGAGAGAGAGAAATCTTTCAATGCTATCCCCACCTTTTTCAGCATGGGTCAIT 3045
861 GluGluTrpGlyGluCysSerLysSerCysGluLeuGlyTrpGlnArgArgLeuValGlu 880
3046 GAAGAGTGGGCGAATGTTCTAAGTCATGTGAATGGGTGGCAGAGAAGTGAAGCCAGCCAGC 3105
881 CysArgAspIleAsnGlyGlnProAlaSerGluCysAlaLysGluValLysProAlaSer 900
3106 TGCCGAGACATTAATGGAGCAGCTGCTTCCGAGTGTGCAAGGAAAGTGAAGCCAGCCAGC 3165
901 ThrArgProCysAlaAspHisProCysProGlnTrpGlnLeuGlyGluTrpSerSerCys 920
3166 ACCAGACCTTGTGACAGACCATCCCTGCCCCAGTGGCAGCTGGGGAGTGGTCAATGT 3225
921 SerLysThrCysGlyLysGlyTyrLysLysThrSerLeuLysCysLeuSerHisAspGly 940
3226 TCTAAGACCTGTGGGAAGGTTTACAAAAAGAAAGCTTGAAGTGTCTGTCCTCATGTGGA 3285
941 GlyValLeuSerHisAspSerCysAspProLeuLysLysProLysHisPheIleAspPhe 960
3286 GGGGTGTATCTCATGAGAGCTGTGATCCTTTAAAGAAACCTTAAACATTTTCATAGACTTT 3345
961 CysThrMetAlaGluCysSer 967
3346 TGCACATGGCAGATGCACT 3366

RESULT 4

US-10-757-450-1
; Sequence 1, Application US/10757450
; Publication No. US20040175794A1
; GENERAL INFORMATION:
; APPLICANT: Jonak, Zdenka
; Trulli, Stephen
; Fornwald, James
; Terrett, Jonathan
; Hastings, Gregg
; TITLE OF INVENTION: Novel Integrin Ligand ITGL-TSP
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESS: Ratner & Prestia
; STREET: Box 980
; CITY: Valley Forge
; STATE: PA
; COUNTRY: USA
; ZIP: 19482
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10757,450

FILING DATE: 15-Jan-2004
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/10/115,286
FILING DATE: 04-Apr-2002
APPLICATION NUMBER: 08/845,496
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Prestia, Paul F
REGISTRATION NUMBER: 23,031
REFERENCE/DOCKET NUMBER: GH-70000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-407-0700
TELEFAX: 610-407-0701
TELEX: 846169
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4014 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-757-450-1

Alignment Scores:
Pred. No.: 0 Length: 4014
Score: 5232.00 Matches: 957
Percent Similarity: 99.38% Conservations: 4
Best Local Similarity: 98.97% Mismatches: 6
Query Match: 98.96% Indels: 0
DB: 18 Gaps: 0

US-09-373-658c-126 (1-967) x US-10-757-450-1 (1-4014)

Qy	1	MetGlnArgAlaValProGluGlyPheGlyArgArgLysLeuGlySerAspMetGlyAsn	20
Db	466	ATGCAGCGAGCTGTGCCCGAGGGGTTCCGAAGGCGCAAGCTGGCGAGCGAGCATGGGGAAC	525
Qy	21	AlaGluArgAlaProGlySerArgSerPheGlyProValProThrLeuLeuLeuAla	40
Db	526	CGCGAGCGGGCTCCGGGGTCTCGAGCTTTGGGCGCCGTACCCACGCTGTGCTCGCC	585
Qy	41	AlaAlaLeuLeuAlaValSerAspAlaLeuGlyArgProSerGluGluAspGluLeu	60
Db	586	CGCGCGCTACTGGCCGTGTGGACGCACTCGGGCGCCCTCCGAGGAGGAGCGAGGCTA	645
Qy	61	ValValProGluLeuGluArgValProGlyHisGlyThrArgLeuArgLeuHisAla	80
Db	646	GTGGTCCCGAGCTGGAGCGCGCCCGGACACGGGACCGCGCTCCGCTGCACGCC	705
Qy	81	PheAspGlnGlnLeuAspLeuAspValProProAspSerSerPheLeuAlaProGlyPhe	100
Db	706	TTTGACGAGCTGGATCTGGAGCTCGGGCCCGACAGCAGCTTTTGGGCGCGGGCTTC	765
Qy	101	ThrLeuGlnAsnValGlyArgLysSerGlySerAspThrProLeuProGluThrAspLeu	120
Db	766	ACGCTCCAGAACGTGGGGCGCAATCCGGGTCCGAGACCGCGCTTCGGAAACCGCCTG	825
Qy	121	AlaHisCysPheTyrSerGlyThrValAsnGlyAspProSerSerAlaAlaLeuSer	140
Db	826	CGGCACCTGCTTACTCCGGCACCGCTGAATGGCGATCCACGCTCGGCTCGCGCTCAGC	885
Qy	141	LeuCysGluGlyValArgGlyAlaPheTyrLeuLeuGlyGluAlaTyrPheLeuGlnPro	160
Db	886	CTCTGCGAGCGGTGCGCGCGCTTCTACCTGTGGGGAGGGGTATTTTCATCCAGCGG	945
Qy	161	LeuProAlaAlaSerGluArgLeuAlaThrAlaAlaProGlyGluLysProProAlaPro	180
Db	946	CTGCCCCCGCCAGCAGCGCTCGCCACCGCCCGCCAGGGAGAGCGCGCGCACCA	1005
Qy	181	LeuGlnPheHisLeuLeuArgArgAsnArgGlnGlyValGlyThrCysGlyVal	200

Db	1006	CTACAGTTCACCTCTCGCGCGGAATCGCAGGGCGACGCTAGCGGCACGTCGGGGTC	1065
Qy	201	ValAspAspGluProArgProThrGlyLysAlaGluThrGluAspGluAspGluGlyThr	220
Db	1066	GTGGACGACGAGCCCGCGCGCTGGGAAAGCGAGACCGAAGCAGGAGGAGGACT	1125
Qy	221	GluGlyGluAspGluGlyProGlnTyrSerProGlnAspProAlaLeuGlnGlyValGly	240
Db	1126	GAGGGCGAGGACGAAGGGCTCAGTGGTCCGCCAGGACCCCGCAGCTGCAAGGCGTAGGA	1185
Qy	241	GlnProThrGlyThrGlySerIleArgLysLysArgPheValSerSerHisArgTyrVal	260
Db	1186	CAGCCACAGGAACCTCGAAGCATAGAAGAGCGATTGTGTCCAGTCAACCGCTATGTG	1245
Qy	261	GluThrMetLeuValAlaAspGlnSerMetAlaGluPheHisGlySerGlyLeuLysHis	280
Db	1246	GAAACCATGCTTGTGGCAGACCATCGATGGCAGAAATTCACGGCAGTGGTCTAAAGCAT	1305
Qy	281	TyrLeuLeuThrLeuPheSerValAlaAlaArgLeuTyrLysHisProSerIleArgAsn	300
Db	1306	TACCTTCTCACGTTGTTTTCGGTGGCAGCCAGATTGTACAAACACCCACGATTCGTAAT	1365
Qy	301	SerValSerLeuValValLysLysLeuValLysLeuValLysLeuValLysLeuValLys	320
Db	1366	TCAGTTAGCTGTGGTGGTGAAGATCTTGTTCATCCACGATGAACAGAGGGGCCGAA	1425
Qy	321	ValThrSerAsnAlaAlaLeuThrLeuArgAsnPheCysAsnTyrGlnLysGlnHisAsn	340
Db	1426	GTGACCTCCATGCTGCTCCCTCACTCTGGCGAATTTTGGCACTGGCAGAGCAGCAAC	1485
Qy	341	ProProSerAspArgAspAlaGluHisTyrAspThrAlaIleLeuPheThrArgGlnAsp	360
Db	1486	CCACCAGTGCACGGGATGCAGAGCACTATGACACAGCAATTTCTTTCCACGACAGGAC	1545
Qy	361	LeuCysGlySerGlnThrCysAspThrLeuGlyMetAlaAspValGlyThrValCysAsp	380
Db	1546	TTGTGTGGTGGTCCAGACATGTGATCTTTGGGATGGCTGATGTGGAACTGTGTGTAT	1605
Qy	381	ProSerArgSerCysSerValIleGluAspAspGlyLeuGlnAlaAlaPheThrAla	400
Db	1606	CCGAGCAGAGCTGCTCCGTCATAGAGATGATGTTTACAGCTGCTTCCACACAGCC	1665
Qy	401	HisGluLeuGlyHisValPheAsnMetProHisAspAspAlaLysGlnCysAlaSerIleu	420
Db	1666	CATGAATTAGCCACGCTGTTTAAACATGCCACATGATGATGCAAGCAGTGTGCGAGCTT	1725
Qy	421	AsnGlyValAsnGlnAspSerHisMetMetAlaSerMetLeuSerAsnLeuAspHisSer	440
Db	1726	AATGGTGTGAACAGGATTCACATGATGGCGTCAATGCTTTTCCAACTGGACACAGC	1785
Qy	441	GlnProTyrSerProCysSerGlyTyrMetIleThrSerPheLeuAspAsnGlyHisGly	460
Db	1786	CAGCTTGGTCTCTTCCAGTGGCTACATGATTTACATCATTTCTGGATATGTCATGGG	1845
Qy	461	GluCysLeuMetAspLysProGlnAsnProIleGlnLeuProGlyAspLeuProGlyThr	480
Db	1846	GAATGTTTGTGACAAAGCTCCAGATCCCATACAGCTCCAGCGCATCTCCCTGGCACC	1905
Qy	481	SerTyrAspAlaAsnArgGlnCysGlnPheThrPheGlyGluAspSerLysHisCysPro	500
Db	1906	TCGTACGATCCAAACCGCAGTGCAGTTTACATTTTGGGGAGGACTCCAAACATGCGCT	1965
Qy	501	AspAlaAlaSerThrCysSerThrLeuTyrCysThrGlyThrSerGlyGlyValLeuVal	520
Db	1966	GATGACGACGACATAGACATCTGTGTGTATCCGGCACCTCTGTGTGGGTCTGTGTG	2025
Qy	521	CysGlnThrLysHisPheProTyrAlaAspGlyThrSerCysGlyGluGlyLysTrpCys	540
Db	2026	TGTCAACCAACACATTTCCCGTGGCGGATGGCACCGCTGTGGAGAAGGAAATGGTGT	2085
Qy	541	IleAsnGlyLysCysValAsnLysAsnHisArgLysHisPheAspThrProPheHisGly	560
Db	2086	ATCAACGGCAAGTGTGTGAACAAACCCGACAGAAAGCATTTTGTATACGCTTTTTCATGA	2145

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QY 561 SerTTPGlyMetTTPGlyProTTPGlyAspCysSerArgThrCysGlyGlyValGln 580
Db 2146 AGCTGGGGAATGTGGGGGCTTGGGGAGACTGTTCGAGAACGTGCGGTGGAGAGTCCAG 2205
QY 581 TyrThrMetArgGluCysAspAsnProValProLysAsnGlyGlyTyrCysGluGly 600
Db 2206 TACACGATGAGGGAATGTGACAACTCCAGTCCCAAGAAATGGAGGAAGTACTGTGAAGC 2265
QY 601 LysArgValArgTyrArgSerCysAsnLeuGluAspCysProAspAsnGlyTyrThr 620
Db 2266 AAACGAGTGGCTACAGATCCTGTATACCTTGAGGACTGTCCAGACAAATATGAAAAACC 2325
QY 621 PheArgGluGluGlnCysGluAlaHisAsnGluPheSerLysAlaSerPheGlySerGly 640
Db 2326 TTTAGAGAGAACATGTGAGACACACACGAGTTTTCAAAAGCTTCTTTGGAGTGGG 2385
QY 641 ProAlaValGluTrpIleProLysTyrAlaGlyValSerProLysAspArgCysLysLeu 660
Db 2386 CTTGGGTGGATGGATTTCCCAAGTAGCTGCGCTCTCACAAAGACAGGTGCAAGCTC 2445
QY 661 IleCysGlnAlaIysGlyIleGlyTyrPhePheValLeuGlnProLysValValAspGly 680
Db 2446 ATCTGCCAAGCCAAAGGCATTTGGTACTTCTTCGTTTTGCAGCCCAAGGTTGTAGATGT 2505
QY 681 ThrProCysSerProAspSerThrSerValCysValGlnGlyClnCysValLysAlaGly 700
Db 2506 ACTCCATGTAGCCAGATTCACCTCTGTGTGTGCAAGGACAGTGTGTAAGAGCTGT 2565
QY 701 CysAspArgIleIleAspSerLysLysLysPheAspLysCysGlyValCysGlyGlyAsn 720
Db 2566 TGTGATCGCATCATAGACTCCAAAAAGAAAGTTTGATAAATGTGTGTTTGGCGGGAAAT 2625
QY 721 GlySerThrCysLysLysLysIleSerGlySerValThrSerAlaIysProGlyTyrHisAsp 740
Db 2626 GGATCTACTTGTAAAAAATATCAGGATCAGTTACTAGTGCAAAACCTGGATATCATGAT 2685
QY 741 IleIleThrIleProThrGlyAlaThrAsnIleGluValLysGlnArgAsnGlnArgGly 760
Db 2686 ATCATCACAAATTCCAACTGGAGCCCAACATCGAAGTGAACAGCGGAACACAGAGGGA 2745
QY 761 SerArgAsnAsnGlySerPheLeuAlaIleLysAlaAlaAspGlyThrTyrIleLeuAsn 780
Db 2746 TCCAGGAACAATGGCAGCTTTCTTGCCATCAAAAGCTGTGTGATGGCACATATATCTTAAT 2805
QY 781 GlyAspTyrThrIleuSerThrLeuGluGlnAspIleMetTyrLysGlyValValLeuArg 800
Db 2806 GGTGACTACACTTTGTCCACTTAGAGCAAGACATTTATGTACAAAGGTGTGTCTTGAGG 2865
QY 801 TyrSerGlySerSerAlaAlaLeuGluArgIleArgSerPheSerProLeuLysGluPro 820
Db 2866 TACAGCGGTCTCTTCGGCGCATTTGAAAGAAATTCGACAGCTTTAGCCCTCTCAAGAGCCC 2925
QY 821 LeuThrIleGlnValLeuThrValGlyAsnAlaLeuArgProLysIleLysTyrThrTyr 840
Db 2926 TTGACCATCCAGTCTTACTGTGGGCAATGCCCTTCGACCTAAAAATTAATACACCTAC 2985
QY 841 PheValLysLysLysLysGluSerPheAsnAlaIleProThrPheSerAlaTrpValIle 860
Db 2986 TTCGTAAGAAGAAGAAGAAATCTTTCAATGTCTATCCCACTTTTTCAGCATGGGTCAAT 3045
QY 861 GluGluTTPGlyCysSerLysSerCysGluLeuGlyTTPGlnArgArgLeuValGlu 880
Db 3046 GAAGAGTGGGGCAATGTTCTAAGTCATGTGAATGGGTGGCAGGAAGACTGTGTAGAA 3105
QY 881 CysArgAspIleAsnGlyGlnProAlaSerGluCysAlaLysGluValLysProAlaSer 900
Db 3106 TGCCGAGACATTAATGCACAGCTGCTCCGAGTGTGCAAGAAAGTGAAGCCAGCCAGC 3165
QY 901 ThrArgProCysAlaAspHisProCysProGlnTrpGlnIleuGlyGluTrpSerSerCys 920
Db 3166 ACCAGACCTTGTGCAGACCATCTCCCTCCCGCAGTGGCAGCTGGGGAGTGGTCAATCAT 3225
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QY 921 SerLysThrCysGlyLysGlyTyrLysLysThrSerLeuLysCysLeuSerHisAspGly 940
Db 3226 TCTAAGACTGTGGAGAGGTTACAAAAAGAAAGCTTGAAGTGTCTGCTCCCATGATGA 3285
QY 941 GlyValLeuSerHisAspSerCysAspProLeuLysLysProLysHisPheIleAspPhe 960
Db 3286 GGGGTGTATCTCATGAGAGCTGTGATCCTTTAAAGAAACCTTAAACATTTTCATAGACTTT 3345
QY 961 CysThrMetAlaGluCysSer 967
Db 3346 TGCACAATGGCAGAATGCAGT 3366

RESULT 5
US-10-105-929-1
; Sequence 1, Application US/10105929
; Publication No. US20020137142A1
; GENERAL INFORMATION:
; APPLICANT: Holtzman, Douglas A.
; APPLICANT: Goodearl, Andrew D.J.
; TITLE OF INVENTION: TANGO-71, TANGO-73, TANGO-74, TANGO-76, AND TANGO-83
; FILE REFERENCE: 09404/041001
; CURRENT APPLICATION NUMBER: US/10/105,929
; PRIOR FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/130,491
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-08-07
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/058,108
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-09-05
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/054,961
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-08-06
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 4676
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (460)...(3360)
US-10-105-929-1

Alignment Scores:
Pred. No.: 0 Length: 4676
Score: 5232.00 Matches: 957
Percent Similarity: 99.38% Conservative: 4
Best Local Similarity: 98.97% Mismatches: 6
Query Match: 98.96% Indels: 0
DB: 13 Gaps: 0

US-09-373-658c-126 (1-967) x US-10-105-929-1 (1-4676)
QY 1 MetGlnArgAlaValProGluGlyPheGlyArgAlaGlyLeuGlySerAspMetGlyAsn 20
Db 460 ATGCAGCAGCTGTGCTCCGAGGGGTTCCGAAAGCGCAAGCTGGCAGCAGCATGGGGAAC 519
QY 21 AlaGluArgAlaProGlySerArgSerPheGlyProValProThrLeuLeuLeuAla 40
Db 520 GCGAGGCGGCTCCGCGGTCTCGAGCTTTGGCGCGTACCCACAGCTGTCTGCTCGCC 579
QY 41 AlaAlaLeuLeuAlaValSerAspAlaLeuGlyArgProSerGluGluAspGluLeu 60
Db 580 GCGGCGCTACTGCGCGTGTGCGACGACTCGGCGCGCCCTCCGAGGAGACGAGGAGCTA 639
QY 61 ValValProGluLeuGluArgValProGlyHisGlyThrThrArgLeuArgLeuHisAla 80
Db 640 GTGGTGCCGAGCTGGAGCGCCCGGAGACCGGACCCCGCCCTCCGCTGACAGCC 699
QY 81 PheAspGlnGlnLeuAspLeuAspValProProAspSerSerPheLeuAlaProGlyPhe 100
Db 700 TTTGACACAGCAGCTGGATCTGGAGCTGCGGCCCGCAGCAGCTTTTGGCGCGCGCTTC 759
QY 101 ThrLeuGlnAsnValGlyArgLysSerGlySerAspThrProLeuProGluThrAspLeu 120
Db 760 ACGCTCCAGAACGTGGGGCGCAAAATCCGGGTCCGAGACGCGCTTCCGAAACCCGACCTG 819
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121 AlaHisCysPheTyrSerGlyThrValAsnGlyAspProSerSerAlaAlaLeuSer 140
122 |
820 GGCACGTGTTACTCCGGCACCGTGANTGGGATCCCGAGCTCGGCTCGCCCTCAGC 879
141 LeuCysGluGlyValArgGlyAlaPheTyrLeuLeuGlyGluAlaTyrPheLeuGlnPro 160
142 |
880 CTCTCGAGGGGTGCGCGCGCTTCTACTCTGCTGGGGAGGCGGTATTTTCATCCAGCGC 939
161 LeuProAlaAlaSerGluAlaGluAlaThrAlaAlaProGlyGluLysProProAlaPro 180
162 |
940 CTGCGCGCGCGCAGCGCGCTTCGCCACCGCGCGCCCGCGGAGGAGCGCGCGCACCA 999
181 LeuGlnPheHisLeuLeuArgArgAsnArgGlnGlyAspValGlyGlyThrCysGlyVal 200
182 |
1000 CTACAGTTCACCTCTCTGCGCGGANTCGCGAGGCGAGTAGCGCGCAGCTGCGGGGTC 1059
201 ValAspAspGluProArgProThrGlyLysAlaGluThrGluAspGluGlyThr 220
202 |
1060 GTGGACGACGAGCCCGCGCGACTGGGAAAGCGGAGACCGGAGCAGGAGCGAAGGACT 1119
221 GluGlyGluAspGluGlyProGlnTyrProGlnAspProAlaLeuGlnGlyValGly 240
222 |
1120 GAGGCGAGGACGAAGGGCTCAGTGGTGGCGGAGCCCGGCACTGCAAGGCGTAGGA 1179
241 GlnProThrGlyThrGlySerIleArgLysLysArgPheValSerSerHisArgTyrVal 260
242 |
1180 CAGCCACACGAGAACTGGAGCATAGAGAGCGATTTGTGTCCAGTCAACCGCTATGTG 1239
261 GluThrMetLeuValAlaAspGlnSerMetAlaGluPheHisGlySerGlyLeuLysHis 280
262 |
1240 GAAACCATGCTGTGGCAGACCACTGCATGGCAGAAATTCACGCGAGTGGTCTAAAGCAT 1299
281 TyrLeuLeuThrLeuPheSerValAlaAlaArgLeuTyrLysHisProSerIleArgAsn 300
282 |
1300 TACCTTTCTCAGTGTGTTTCGGTGGCAGCCAGATGTGTACAAACACCCCGCAGCATTCGTAAAT 1359
301 SerValSerLeuValValValLysIleLeuValIleHisAspGluGlnLysGlyProGlu 320
302 |
1360 TCAGTTAGCTGTGTGTGTGAAGATCTTGCTATCCACATGACAGAGGGGCGCGAA 1419
321 ValThrSerAsnAlaAlaLeuThrLeuArgAsnPheCysAsnTrpGlnLysGlnHisAsn 340
322 |
1420 GTGACCTCCAAATGCTGCCCTCACTCTGCGGAACTTTTGGCAACTGGCAGAGCAGCAAC 1479
341 ProProSerAspArgAspAlaGluHisTyrAspThrAlaIleLeuPheThrArgGlnAsp 360
342 |
1480 CCACCCAGTGCACCGGATGCAGAGCACTATGACACAGCAATTTCTTTCCACGACAGGAC 1539
361 LeuCysGlySerGlnThrCysAspThrLeuGlyMetAlaAspValGlyThrValCysAsp 380
362 |
1540 TTGTGTGGGTCACAGATGTGATCTCTTGGGATGCTGATGTTGGACTGTGTGTAT 1599
381 ProSerArgSerCysSerValIleGluAspAspGlyLeuGlnAlaAlaPheThrThrAla 400
382 |
1600 CCGAGCAGAGCTGCTCCGTCATAGAGATGATGTTTACAGCTGCTTCCACACAGCC 1659
401 HisGluLeuGlyHisValPheAsnMetProHisAspAlaLysGlnCysAlaSerLeu 420
402 |
1660 CATGAATTAGCCACGCTGTTTAAATGCCATGATGATGCAAGCAGTGTGCGAGCCTT 1719
421 AsnGlyValAsnGlnAspSerHisMetMetAlaSerMetLeuSerAsnLeuAspHisSer 440
422 |
1720 AATGGTGTGAACCAAGGATCCCATGATGGCTCAATGCTTTCCAACTTGGACCAACAGC 1779
441 GlnProTrpSerProCysSerGlyTyrMetIleThrSerPheLeuAspAsnGlyHisGly 460
442 |
1780 CAGCCTTGGTCTCTTGCATGGCTCATATGATTTACATCATTTCTGGATATGTCATGGG 1839
461 GluCysLeuMetAspLysProGlnAsnProIleGlnLeuProGlyAspLeuProGlyThr 480
462 |
1840 GAATGTTTGTGACAGGCTCAGAAATCCCATACAGCTCCCGAGCGAGTCTCCCTGGCACC 1899

481 SerTyrAspAlaAsnArgGlnCysGlnPheThrPheGlyGluAspSerLysHisCysPro 500
482 |
1900 TCGTACGATGCCAACCGGCGAGTCCAGTTTACATTTGGGGAGGACTCCAAACACTGCCCC 1959
501 AspAlaAlaSerThrCysSerThrLeuTyrCysThrGlyThrSerGlyGlyValLeuVal 520
502 |
1960 GATGCAGCCAGCACATGTAGCACTTGTGTGTATCCGGCACCTCTGTTGGTGGGTGCTGGTG 2019
521 CysGlnThrLysHisPheProTrpAlaAspGlyThrSerCysGlyGluGlyLysTrpCys 540
522 |
2020 TGTCAAAACCAACACTTCCGTGGGCGATGGCAGCTGTGCGAAGGGAATGGTGT 2079
541 IleAsnGlyCysValAsnLysAsnHisArgLysHisPheAspThrProPheHisGly 560
542 |
2080 ATCAACGGCAAGTGTGTGAACAAACCCGACAGAAAGCATTTGTATACGCCCTTTTCATGGA 2139
561 SerTyrGlyMetTyrProGlyAspCysSerArgThrCysGlyGlyGlyValGln 580
562 |
2140 AGCTGGGGAATGTGGGGGCTTGGGAGACTGTTCGAGAACCTGCGGTGGAGGAGTCCAG 2199
581 TyrThrMetArgGluCysAspAsnProValProLysAsnGlyGlyLysTyrCysGluGly 600
582 |
2200 TACACGATGAGGGAATGTGACAACCCAGTCCCAAGAAATGGAGGAAGTACTGTGAAGGC 2259
601 LysArgValArgTyrArgSerCysAsnLeuGluAspCysProAspAsnAsnGlnLysThr 620
602 |
2260 AAACGAGTGGCTTACAGATCTCTGTAACTTGGAGACTGTCCAGACATTAATGGAANAACC 2319
621 PheArgGluGluGlnCysGluAlaHisAsnGluPheSerLysAlaSerPheGlySerGly 640
622 |
2320 TTTAGAGAGGAACAAATGTGAAGCACACAGAGTTTTCAAAAGCTTCTTTGGAGATGGG 2379
641 ProAlaValGluTrpIleProLysTyrAlaGlyValSerProLysAspArgCysLysLeu 660
662 |
2380 CCTGCGGTGGATGGATTTCCCAAGTACGCTGGCGTCTCACCAGAGCAGAGTGTCAAGCTC 2439
661 IleCysGlnAlaLysGlyIleGlyTyrPhePheValLeuGlnProLysValValAspGly 680
682 |
2440 ATCTGCAAGCCAAAGGCATTTGGCTACTTCTCTGTTTGCAGCCCAAGGTTGTAGATGGT 2499
681 ThrProCysSerProAspSerThrSerValCysValGlnGlyGlnCysValLysAlaGly 700
682 |
2500 ACTCCATGTAGCCCAATTCACCTCTGTCTGTGTGCAAGACAGTGTGTAAAGCTTGGT 2559
701 CysAspArgIleIleAspSerLysLysPheAspLysCysGlyValCysGlyGlyAsn 720
722 |
2560 TGTGTATGCATCATAGACTCCAAAAGAGCTTTGATAAATGTGTGTTCGCGGGGAAT 2619
721 GlySerThrCysLysLysIleSerGlySerValThrSerAlaLysProGlyTyrHisAsp 740
742 |
2620 GGATCTACTTGTAAAAAATATCAGGATCAGTTACTAGTGCAAAACCTGGATATCATGAT 2679
741 IleIleThrIleProThrGlyAlaThrAsnIleGluValLysGlnArgAsnGlnArgGly 760
762 |
2680 ATCATCAAAATCCAACTGGAGCCACCAATCATGAAAGTGAACAGCGGAAACAGAGGGA 2739
761 SerArgAsnAsnGlySerPheLeuAlaIleLysAlaAlaAspGlyThrTyrIleLeuAsn 780
782 |
2740 TCCAGGAAACATGGCAGCTTCTTCCATCAAGCTGCTGATGGCACATATATCTTAAT 2799
781 GlyAspTyrThrLeuSerThrLeuGluGlnAspIleMetTyrLysGlyValValLeuArg 800
802 |
2800 GGTGACTTACTTGTCCACTTTAGAGCAAGACATTAATGATCAAAAGGTGTGTCTTGAGG 2859
801 TyrSerGlySerSerAlaAlaLeuGluArgIleArgSerPheSerProLeuLysGluPro 820
822 |
2860 TACAGCGGCTCTCTGCGGCAATTTGGAAGAAATTTGCGAGCTTTAGCCCTCTCTCAAGAGGCC 2919
821 LeuThrIleGlnValLeuThrValGlyAsnAlaLeuArgProLysIleLysTyrThrTyr 840
842 |
2920 TTGACCATTCAGGTTCTTACTGTGGGCAATGCCCTTCGACTAAATTAATATACACCTAC 2979
841 PheValLysLysLysGluSerPheAsnAlaIleProThrPheSerAlaTrpValIle 860

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Db 2980 TTCTGTAAGAGAGAGAGAACTTTTCATGCTATATCCCACTTTTTCAGCATGGGTCAAT 3039
Qy 861 GluGluTrpGlyGluCysSerLysSerCysGluLeuGlyTrpGlnArgArgLeuValGlu 880
Db 3040 GAAGAGTGGGGGGAATGTTCTAAGTCATGTGAATTTGGGTGGCAGAGAAGACTGGTAGAA 3099
Qy 881 CysArgAspIleAsnGlyGlnProAlaSerGluCysAlaLysGluValLysProAlaSer 900
Db 3100 TGCCGAGACATTAATGAGCAGCGCTGCTCCGAGTGTGCAAGAGAAAGTGAAGCCAGCCAGC 3159
Qy 901 ThrArgProCysAlaAspHisProCysProGlnTrpGlnLeuGlyGlnTrpSerCys 920
Db 3160 ACCAGACCTTGTGCAGACCATCCCTGCCCCAGTGGCAGCTGGGGAGTGGTCAATGT 3219
Qy 921 SerLysThrCysGlyLysGlyTrpLysLysThrSerLeuLysCysLeuSerHisAspGly 940
Db 3220 TCTAAGACCTGTGGGAAGGTTTACAAAAAGAAAGCTTGAAGTGTCTGTCCCATGATGA 3279
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Db 3280 GGGGTGTTATCTCATGAGAGCTGTGATCTTTTAAAGAAACCTTAAACATTTTCATGACTTT 3339
Qy 961 CysThrMetAlaGluCysSer 967
Db 3340 TGCACAAATGGCAGATGCAGT 3360

RESULT 6
US-10-667-281-1
; Sequence 1, Application US/10667281
; Publication No. US20050100916A1
; GENERAL INFORMATION:
; APPLICANT: Klonowski, Paul
; APPLICANT: Allard, John
; APPLICANT: Heller, Renu
; APPLICANT: Van Wart, Harold
; TITLE OF INVENTION: Human Aggreganase and Nucleic Acid
; FILE OF INVENTION: Compositions Encoding the Same
; FILE REFERENCE: ROCH-002
; CURRENT APPLICATION NUMBER: US/10/667,281
; PRIOR FILING DATE: 2003-09-17
; PRIOR APPLICATION NUMBER: US/09/568,559
; PRIOR FILING DATE: 2000-05-09
; PRIOR APPLICATION NUMBER: 60/133,343
; PRIOR FILING DATE: 1999-05-10
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 3889
; TYPE: DNA
; ORGANISM: human
US-10-667-281-1

Alignment Scores:
Pred. No.: 0 Length: 3889
Score: 5230.00 Matches: 956
Percent Similarity: 99.38% Conservative: 5
Best Local Similarity: 98.86% Mismatches: 6
Query Match: 98.92% Indels: 0
DB: 19 Gaps: 0

US-09-373-658C-126 (1-967) x US-10-667-281-1 (1-3889)
Qy 1 MetGlnArgAlaValProGluGlyPheGlyArgArgLysLeuGlySerAspMetGlyAsn 20
Db 8 ATGCAGCATCTGTGCCCCGAGGGGTTTCGGAAGGCGCAGCTGGCGCAGCAGCATGGGGAAC 67
Qy 21 AlaGluArgAlaProGlySerArgSerPheGlyProValProThrLeuLeuLeuAla 40
Db 68 GCGGAGCGGGCTCCGGGGGTCTCGAGCTTTGGGCGGTACCCACGCTGCTGCTGCTGCC 127
Qy 41 AlaAlaLeuLeuAlaValSerAspAlaLeuGlyArgProSerGluGluAspGluLeu 60
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Db 128 GCGGCGCTACTGGCGGTGTTCGAGCAGCACTCGGGCGCCCTCCGAGGAGACGAGGAGCTA 187
Qy 61 ValValProGluLeuGluArgValProGlyHisGlyThrThrArgLeuArgLeuHisAla 80
Db 188 GTGGTGGCGGAGCTCGAGCGGCCCGGACACGGGACACCGCGCTTCGCGCTCGACGCGC 247
Qy 81 PheAspGlnGlnLeuAspLeuAspValProProAspSerSerPheLeuAlaProGlyPhe 100
Db 248 TTTGACACGAGCAGCTGGATCTGGAGCTGGGCCCGGACAGCAGCTTTTGGCGCCCGGCTTC 307
Qy 101 ThrLeuGlnAsnValGlyArgLysSerGlySerAspThrProLeuProGluThrAspLeu 120
Db 308 ACGCTCCAGAAAGCTGGGGCGCAATCCGGGTCCGAGACGCGCTTCGGAACACCGACCTG 367
Qy 121 AlaHisCysPheThrSerGlyThrValAsnGlyAspProSerSerAlaAlaLeuSer 140
Db 368 GCGCATCTCTTACTCCGCGCACCGTGAATGGCGATCCAGCTCGGCTCGCCCTCCAGC 427
Qy 141 LeuCysGluGlyValArgGlyAlaPheTyrLeuLeuGlyGluAlaTyrPheIleGlnPro 160
Db 428 CTCCTCGAGGGGCTGCGCGCGCTTCTACCTGCTGGGGGAGCGGTATTTTCATCAGCGC 487
Qy 161 LeuProAlaAlaSerGluArgLeuAlaThrAlaAlaProGlyGluLysProProAlaPro 180
Db 488 CTGCGCGCGCGCAGCGAGCGCTCGCCACCGCGCCCGCCAGGGGAGAGCGCGCGCACA 547
Qy 181 LeuGlnPheHisLeuLeuArgArgAsnArgGlnGlyAspValGlyGlyThrCysGlyVal 200
Db 548 CTACAGTTTCCACTCTCGCGCGAATCGGAGGCGGACGCTCGCGCGGACGCTGCGGGGTC 607
Qy 201 ValAspAspGluProArgProThrGlyLysAlaGluThrGluAspGluAspGluGlyThr 220
Db 608 GTGGACGACGAGCCCGCGCGCTGCGGAGAGCGGAGACGGAAGACGAGGACGAGGACT 667
Qy 221 GluGlyGluAspGluGlyProGlnTrpSerProGlnAspProAlaLeuGlnGlyValGly 240
Db 668 GAGGGCGAGGACGAAAGGGGCTCAGTGTGTCGCGCAGGACCGCGCAGCTGCAAGGCGTAGA 727
Qy 241 GlnProThrGlyThrGlySerIleArgLysLysArgPheValSerSerHisArgTyrVal 260
Db 728 CAGCCACAGGAACCTGGAAAGCATAAGAAAGAGCATTTGTGTCCAGTCACGCTATGTG 787
Qy 261 GluThrMetLeuAlaAspGlnSerMetAlaGluPheHisGlySerGlyLeuLysHis 280
Db 788 GAAACCATGCTTGTGGCAGACCATCGATGGCAGATTTCCAGCGCAGTGTCTAAGCAT 847
Qy 281 TyrLeuLeuThrLeuPheSerValAlaAlaArgLeuTyrLysHisProSerIleArgAsn 300
Db 848 TACCTTCTCACGTTGTTTTCGGTGGCAGCCAGATTGTACAAACACCCAGCATTCGTAT 907
Qy 301 SerValSerLeuValValLysIleLeuValIleHisAspGluGlnLysGlyProGlu 320
Db 908 TCAGTTAGCCTGGTGGTGAAGATCTTGGTCATCCAGATGAACAGAGGGGGCGGAA 967
Qy 321 ValThrSerAsnAlaAlaLeuThrLeuArgAsnPheCysAsnTrpGlnLysGlnHisAsn 340
Db 968 GTGACCTCCATGCTGCCCTCACTCTGGGAACTTTTGCACTGGCAGAGCAGCAGCAAC 1027
Qy 341 ProProSerAspArgAspAlaGluHisTyrAspThrAlaIleLeuPheThrArgGlnAsp 360
Db 1028 CCACCCAGTGACCGGGATGCGAGCAGCTATGACACAGCAATTTCTTTTCCACAGACAGGAC 1087
Qy 361 LeuCysGlySerGlnThrCysAspThrLeuGlyMetAlaAspValGlyThrValCysAsp 380
Db 1088 TTGTGTGGTCCAGACATGTGATACTCTTGGGATGGCTGATGTGTGGAACTGTGTGTGAT 1147
Qy 381 ProSerArgSerCysSerValIleGluAspAspGlyLeuGlnAlaAlaPheThrThrAla 400
Db 1148 CGGACGAGAGCTGCTCCGTCATAGAAGATGATGTTTACAGCTGCCTTCCACAGCGC 1207
Qy 401 HisGluLeuGlyHisValPheAsnMetProHisAspAspAlaLysGlnCysAlaSerLeu 420
Db 1208 CATGAATTAGGCCACGCTGTTTAAACATGCACATGATGATGCAAGCAGTGTGCCAGCCTT 1267
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QY 421 AsnGlyValAsnGlnAspSerHisMetMetAlaSerMetLeuSerAsnLeuAspHisSer 440
DB 1268 AATGGTGTGACACGAGATCCCAATGATGGCTCAATGCTTTCCAAACCTGGACCAAGC 1327
QY 441 GlnProTrpSerProCysSerGlyTyrMetIleThrSerPheLeuAspAsnGlyHisGly 460
DB 1328 CAGCCTTGGTCTCTTGGCAGTGCTACATGATGATACATCAATTTCTGGATAATGTCATGGG 1387
QY 461 GluCysLeuMetAspLysProGlnAsnProIleGlnLeuProGlyAspLeuProGlyThr 480
DB 1388 GAATGTTTGTATGACACAGCTCCAGATCCCATACAGCTCCAGCGCATCTCCCTGGCACCC 1447
QY 481 SerTyrAsnAlaAsnArgGlnCysGlnPheThrPheGlyGluAspSerLysHisCysPro 500
DB 1448 TCGTAGATGCCAACCGCAGTGCAGGTTTACATTTTGGGAGAGCTCCAAACACTGCCCT 1507
QY 501 AspAlaAlaSerThrCysSerThrLeuTrpCysThrGlyThrSerGlyGlyValLeuVal 520
DB 1508 GATGAGCCAGCACATGTAGCACCTTGTGTGTACCGGCACCTCTGTGGGGTGTGGTG 1567
QY 521 CysGlnThrLysHisPheProTrpAlaAspGlyThrSerCysGlyGluGlyLysTrpCys 540
DB 1568 TGTCAAAACCAACACTTCCCGTGGCGGATGGCACCAAGCTGTGGAGAAAGGAAATGGTGT 1627
QY 541 IleAsnGlyLysCysValAsnLysAsnHisArgLysHisPheAspThrProPheHisGly 560
DB 1628 ATCAACGGCAAGTGTGTGAACAAACCCACAGAAAGCATTTTGTATCGCCTTTTTCATGGA 1687
QY 561 SerTrpGlyMetTrpGlyProTrpGlyAspCysSerArgThrCysGlyGlyGlyValGln 580
DB 1688 AGCTGGGAATGTGGGGCTTGGGAGACTGTTCAGAGACGTGGGTGGAGGATCCAG 1747
QY 581 TyrThrMetArgGluCysAspAsnProValProLysAsnGlyGlyLysTrpCysGlyGly 600
DB 1748 TACACGATGAGGAATGTGACAAACCCAGTCCCAAGAAATGGAGGAAAGTACTGTGAAGGC 1807
QY 601 LysArgValArgTyrArgSerCysAsnLeuGluAspCysProAspAsnAsnGlyLysThr 620
DB 1808 AAACGAGTGGCTACAGATCCTGTAACTTGTAGACTGTCCAGACATATATGAAANAACC 1867
QY 621 PheArgGluGlnCysGluAlaHisAsnGluPheSerLysAlaSerPheGlySerGly 640
DB 1868 TTTAGAGAGGACATGTGAGCACACACAGATTTTCAAAGCTTCTTTGGAGTGGG 1927
QY 641 ProAlaValGluTrpIleProLysTyrAlaGlyValSerProLysAspArgCysLysLeu 660
DB 1928 CCTGGGTGGAATGGATTCACAGTACGCTGGCTCTCACCAAGAGCACAGGTGCAAGCTC 1987
QY 661 IleCysGlnAlaLysGlyIleGlyTyrPhePheValLeuGlnProLysValValAspGly 680
DB 1988 ATCTGCCAAGCAAGGATGGCTACTTCTTCTGTGGAGCCCAAGTTGTAGATGGT 2047
QY 681 ThrProCysSerProAspSerThrSerValCysValGlnGlnCysValLysValAlaGly 700
DB 2048 ACTCCATGTAGCCAGATTCACCTCTGTCTGTGTGCAAGGACAGTGTGTAAGCTGGT 2107
QY 701 CysAspArgIleLeuAspSerLysLysPheAspLysCysGlyValCysGlyGlyAsn 720
DB 2108 TGTGATCGCATATAGACTCCAAAGAAAGTTTGTATAATGTGTGTGTGGGGGGAAT 2167
QY 721 GlySerThrCysLysLysIleSerGlySerValThrSerAlaLysProGlyTyrHisAsp 740
DB 2168 GGATCTACTTTGTAATAAATAATACAGATCACTAGTCAAGAACTGGATATCATGAT 2227
QY 741 IleIleThrIleProThrGlyValThrAsnIleGluValLysGlnArgAsnGlnArgGly 760
DB 2228 ATCATCAATTCATCTGGAGCCACCAACATCCAGTGAACACAGCGGACCAAGAGGGA 2287
QY 761 SerArgAsnAsnGlySerPheLeuAlaIleLysAlaAlaAspGlyThrTyrIleLeuAsn 780
DB 2288 TCCAGGAACAATGGCAGCTTCTTGGCCATCAAGCTGTGTGTCACATATATCTTTAAT 2347

QY 781 GlyAspTyrThrIleuSerThrLeuGluGlnAspIleMetTyrLysGlyValValLeuArg 800
DB 2348 GGTGACTACACTTTGTCCACCTTAGAGCAAGACATATGTACAAAGGTGTGTCTTGAGG 2407
QY 801 TyrSerGlySerSerAlaAlaLeuGluArgIleArgSerPheSerProLeuLysGluPro 820
DB 2408 TACAGCGGTCTCTCGCGCATTTGGAAGAATAATTCGACGCTTTAGCCCTCTCAAAGAGCCC 2467
QY 821 LeuThrIleGlnValLeuThrValGlyAsnAlaLeuArgProLysIleLysTyrThrTyr 840
DB 2468 TTGACCATCCAGGTTCTTACTGTGGCAATGCCCTTCGACCTAAATTAATACACCTAC 2527
QY 841 PheValLysLysLysLysGluSerPheAsnAlaIleProThrPheSerAlaTrpValIle 860
DB 2528 TTCGTAAGAAGAAGAAGGAATCTTTCAATGCTATCCCCACTTTTTCAGCATGGGTCAAT 2587
QY 861 GluGluTrpGlyCysSerLysSerCysGluLeuGlyTrpGlnArgArgLeuValGlu 880
DB 2588 GAAGAGTGGGGCGAATGTTCTTAAGTCATGTGAATGGGTTGGCAGAGAAGACTGGTAGAA 2647
QY 881 CysArgAspIleAsnGlyGlnProAlaSerGluCysAlaLysGluValLysProAlaSer 900
DB 2648 TGCCGAGACATTAATGACAGCCTGTCTCCAGTGTGCAAGAGAGTGAAGCCAGCCAGC 2707
QY 901 ThrArgProCysAlaAspHisProCysProGlnTrpGlnLeuGlyGluTrpSerSerCys 920
DB 2708 ACCAGACCTTGTGCAGACCATCTGCCCCAGTGGCAGCTGGGGAGTGTGCATCATGT 2767
QY 921 SerLysThrCysGlyLysGlyTyrLysLysThrSerLeuLysCysLeuSerHisAspGly 940
DB 2768 TCTAAGACCTGTGGGAAGGGTTACAAAAAAGAGCTTGAAGTGTCTGTCCCATGATGGA 2827
QY 941 GlyValLeuSerHisAspSerCysAspProLeuLysLysProLysHisPheIleAspPhe 960
DB 2828 GGGGTGTATCTCATGAGACTGTGATCCTTTAAGAAACCTTAAGAAACCTTAAGACTTT 2887
QY 961 CysThrMetAlaGluCysSer 967
DB 2888 TGCACAATGGCAGATGCACT 2908

RESULT 7
US-10-210-120-57
; Sequence 57, Application US/10210120
; Publication No. US20030175736A1
; GENERAL INFORMATION:
; APPLICANT: Chinnaiyan, Arul M.
; APPLICANT: Ruben, Mark A.
; APPLICANT: Sreekumar, Arun
; TITLE OF INVENTION: Expression Profile of Prostate Cancer
; FILE REFERENCE: UM-07221
; CURRENT APPLICATION NUMBER: US/10/210,120
; CURRENT FILING DATE: 2002-08-01
; PRIOR APPLICATION NUMBER: US 60/309,581
; PRIOR FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: US 60/334,468
; PRIOR FILING DATE: 2001-11-15
; NUMBER OF SEQ ID NOS: 123
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 57
; LENGTH: 4309
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-210-120-57

Alignment Scores:
Pred. No.: 0 Length: 4309
Score: 5224.00 Matches: 956
Percent Similarity: 99.28% Conservative: 4
Best Local Similarity: 98.86% Mismatches: 7
Query Match: 98.81% Indels: 0
DB: 16 Gaps: 0

US-09-373-658C-126 (1-967) x US-10-210-120-57 (1-4309)

QY 1 MetGlnArgAlaValProGluGlyPheGlyArgArgLysLeuGlySerAspMetGlyAsn 20
Db 116 ATGCAGCGAGCTGTGCCCCGAGGGTTTCGGAAGGCGCAAGCTGGCGAGCAGCATGGGGAAAC 175
QY 21 AlaGluArgAlaProGlySerArgSerPheGlyProValProThrLeuLeuLeuAla 40
Db 176 GCGGAGCGGGCTCCGGGGTCTCGGAGCTTTGGCCAGTACCCACGCTGCTGCTCGCC 235
QY 41 AlaAlaLeuLeuAlaValSerAspAlaLeuGlyArgProSerGluGluAspGluGluLeu 60
Db 236 GCGGGCTACTGGCGCTGTCGAGCGCACTCGGGCGCCCTCCGAGGAGCAGGAGGCTA 295
QY 61 ValValProGluLeuGluArgValProGlyHisGlyThrArgLeuArgLeuHisAla 80
Db 296 GTGGTGCCGGAGCTGAGCGCGCCCCGGGACACGGGACACCGCGCTCCGCGTGCACGCC 355
QY 81 PheAspGlnGlnLeuAspLeuAspValProProAspSerSerPheLeuAlaProGlyPhe 100
Db 356 TTTGACCAGAGCTGGATCTGGAGCTGCGGCCGCGACAGAGCTTTTGGCGGCCGCTTC 415
QY 101 ThrLeuGlnAsnValGlyArgLysSerGlySerAspThrProLeuProGluThrAspLeu 120
Db 416 ACGCTCCAGAACGTGGGGCGCAAACTCGGGTCCGAGACCGCTTCGCGAAACCGAGCTG 475
QY 121 AlaHisCysPheTyrSerGlyThrValAsnGlyAspProSerSerAlaAlaAlaLeuSer 140
Db 476 GGGCACTGCTTCTACTCCGGCACCGGTAATGGCGATCCCGAGCTCGCGCTCCGCGCTCAGC 535
QY 141 LeuCysGluGlyValArgGlyAlaPheTyrLeuLeuGlyGluAlaTyrPheIleGlnPro 160
Db 536 CTCGCGAGGGCGTGGCGCGCTTCTACTCTGCGGGAGGCGTATTTTCATCCAGCCG 595
QY 161 LeuProAlaAlaSerGluArgLeuAlaThrAlaAlaProGlyGluLysProProAlaPro 180
Db 596 CTGCGCGCGCGCAGCGAGCGCTCGCCACCGCGCGCCCGAGGAGAGCGCGCGCACCA 655
QY 181 LeuGlnPheHisLeuLeuArgArgAsnArgGlnGlyAspValGlyClyThrCysGlyVal 200
Db 656 CTACAGTCTCACCTCTCGCGGGGAATCGCGAGGGCGACGTGCGGGCGACGTGCGGGGTC 715
QY 201 ValAspAspGluProArgProThrGlyLysAlaGluThrGluAspGluAspGluGlyThr 220
Db 716 GTGGACGACGAGCCCGCGGCTGGGAAAGCGGAGACCGAGACGAGCAGCGAGGACT 775
QY 221 GluGlyGluAspGluGlyProGlnTrpSerProGlnAspProAlaLeuGlnGlyValGly 240
Db 776 GAGGGCGAGCGAAGGGGCTCAGTGGTCCGCGCGCAGGACCCGCGCACTGCAAGGCGTAGCA 835
QY 241 GlnProThrGlyThrGlySerIleArgLysLysArgPheValSerSerHisArgTyrVal 260
Db 836 CAGCCACAGGAACCTGGAAGCATAGAAAGACCGAATTTGTGTCAGTCACCGCTATGTG 895
QY 261 GluThrMetLeuValAlaAspGlnSerMetAlaGluPheHisGlySerGlyLeuLysHis 280
Db 896 GAAACCATCTTGTGSCAGACCACTGATGGCAGAAATCCACGGCAGTGTCTAAAGCAT 955
QY 281 TyrLeuLeuThrLeuPheSerValAlaAlaArgLeuTyrLysHisProSerIleArgAsn 300
Db 956 TACCTTCTCACGTGTGTTCGGTGGCGAGCAGATTGTACAAACACCCCGAGCATTCGTAAAT 1015
QY 301 SerValSerLeuValValLysIleLeuValIleHisAspGluGlnLysGlyProGlu 320
Db 1016 TCAGTTAGCTGTGGTGGTGAAGATCTTGGTCAATCCAGCATGAACAGAAAGGGCCGGAA 1075
QY 321 ValThrSerAsnAlaAlaLeuThrLeuArgAsnPheCysAsnTrpGlnLysGlnHisAsn 340
Db 1076 GTGACCTCCAATGCTGCCCTCACTCTGCGGAACTTTTGGCAACTGGCGAGAGCAGCACAAAC 1135
QY 341 ProProSerAspArgAspAlaGluHisTyrAspThrAlaIleLeuPheThrArgGlnAsp 360
Db 1136 CCACCCAGTGACCGGGATGACAGGACACTATGACACAGCAATTCCTTTCCACGACAGGAC 1195

QY 361 LeuCysGlySerGlnThrCysAspThrLeuGlyMetAlaAspValGlyThrValCysAsp 380
Db 1196 TTGTGTGGGTCCAGACATGTGATACTCTTGGATGGCTGATGTGTGAACTGTGTGTGAT 1255
QY 381 ProSerArgSerCysSerValIleGluAspAspGlyLeuGlnAlaAlaPheThrThrAla 400
Db 1256 CCGAGCAGAGCTGCTCGCTCATAGAAGATGATGTTTACAAGCTGCCTTCACCACAGCC 1315
QY 401 HisGluLeuGlyHisValPheAsnMetProHisAspAspAlaLysGlnCysAlaSerLeu 420
Db 1316 CATGAATTAGGCCACGCTGTTTAACATGCCACATGATGATGCAAAAGCAGTGTGTGCAGCCTT 1375
QY 421 AsnGlyValAsnGlnAspSerHisMetMetAlaSerMetLeuSerAsnLeuAspHisSer 440
Db 1376 AATGGTGTGAACAGGATTTCCACATGATGGCGTCAATGCTTTCCAACTGGACACAGC 1435
QY 441 GlnProTrpSerProCysSerGlyTyrMetIleThrSerPheLeuAspAsnGlyHisGly 460
Db 1436 CAGCCTTGTCTCTCTTCAGTGCCTACATGATTACATCATTTCTGGATAATGTCATGGG 1495
QY 461 GluCysLeuMetAspLysProGlnAsnProIleGlnLeuProGlyAspLeuProGlyThr 480
Db 1496 GAATGTTTGAATGGACAAGCCTCAGAAATCCATACAGCTCCCGAGCGATCTCCCTGGCACC 1555
QY 481 SerTyrAspAlaAsnArgGlnCysGlnPheThrPheGlyGluAspSerLysHisCysPro 500
Db 1556 TGTACGATGCCAACCGGCGAGTCCAGTTTCAATTTGGGGAGGACTCCAAACACTGCCCCC 1615
QY 501 AspAlaAlaSerThrCysSerThrLeuTrpCysThrGlyThrSerGlyGlyValLeuVal 520
Db 1616 GATGCAGCCAGCACATGTAGCACCTTGTGGTGTACCGGCACCTCTGTTGGGTGGTGGTG 1675
QY 521 CysGlnThrLysHisPheProTrpAlaAspGlyThrSerCysGlyGluClyLysTrpCys 540
Db 1676 TGTCAAAACAAACACTCCCGTGGCGGATGGCACCGAGCTGTGGAGAGGGAATGGTGT 1735
QY 541 IleAsnGlyLysCysValAsnLysAsnHisArgLysHisPheAspThrProPheHisGly 560
Db 1736 ATCAACGGCAGTGTGTGNACAAAACCCGACAGAAAGCATTTTGTATACGCTTTTCATGGA 1795
QY 561 SerTrpGlyMetTrpGlyProTrpGlyAspCysSerArgThrCysGlyGlyValGln 580
Db 1796 AGCTGGGAATGTGGGGCTTGGCGAGACTGTTCCAGAACCTGCGGTGGAGAGTCCAG 1855
QY 581 TyrThrMetArgGluCysAspAsnProValProLysAsnGlyGlyLysTrpCysGluGly 600
Db 1856 TACACGATGAGGAATGTGACAAACCCAGTCCCAAGAAATGGAGGGAAGTACTGTGAAGGC 1915
QY 601 LysArgValArgTyrArgSerCysAsnLeuGluAspCysProAspAsnAsnGlyLysThr 620
Db 1916 AAACGAGTGGCTACAGATCCTGTAACTTGAGGACTGTCCAGACATATATGGAAAAACC 1975
QY 621 PheArgGluGluGlnCysGluAlaHisAsnGluPheSerLysAlaSerPheGlySerGly 640
Db 1976 TTTTAGAGAGAAACAATGTGAACACACACAGAGTTTCAAAAGCTTCTTTTGGAGTGGG 2035
QY 641 ProAlaValGluTrpIleProLysTyrAlaGlyValSerProLysAspArgCysLysLeu 660
Db 2036 CTGCGGGTGAATGATTTCCCAAGTACGCTGGCGTCTCAACAAAGACAGGTGCAAGCTC 2095
QY 661 IleCysGlnAlaLysGlyIleGlyTyrPhePheValLeuGlnProLysValValAspGly 680
Db 2096 ATCTGCCAAGCCAAAGGCATTGGCTACTTCTCGTTTTTGCAGCCCCAAGTGTGTAGTGT 2155
QY 681 ThrProCysSerProAspSerThrSerValCysValGlnGlnCysValLysAlaGly 700
Db 2156 ACTCCATGTAGCCAGATTCCACCTCTGTCTGTGTGCAAGGACAGTGTGTAAAGTGTGT 2215
QY 701 CysAspArgIleIleAspSerLysLysPheAspLysCysGlyValCysGlyGlyAsn 720
Db 2216 TGTGATCGCATAGACTCCAAAGAAAGATTGATAAATGTGGTGTTCGGGGGAAT 2275
QY 721 GlySerThrCysLysLysIleSerGlySerValThrSerAlaLysProGlyTyrHisAsp 740

Db 2276 GGATCTACTTGTAAATAATATCAGGATCAGTTACTAGTGCAGAACTCGATATCATGAT 2335
Qy 741 IleIleThrIleProThrGlyAlaThrAsnIleGluValysGlnArgAsnGlnArgGly 760
Db 2336 ATCATCACAAATTCACATGAGGAGCCACCAATCATGAAAGTGAACAGCGGACCAAGGGGA 2395
Qy 761 SerArgAsnAsnGlySerPheLeuAlaIleValAlaAlaAspGlyThrTyrIleLeuAsn 780
Db 2396 TCAGAGAACAAATGGCAGCTTCTTGCATCAAGCTGCTGATGGCACATATATCTTAAAT 2455
Qy 781 GlyAspTyrThrLeuSerThrLeuGluGlnAspIleMetTyrIysGlyValValLeuArg 800
Db 2456 GGTGACTACATTTGTCCACTTAGAGCAAGACATTATGATACAAAGTGTTGTCTTGAGG 2515
Qy 801 TyrSerGlySerSerAlaAlaLeuGluArgIleArgSerPheSerProLeuIysGluPro 820
Db 2516 TACAGCGGCTCTCTGCGGCATTTGGAAAGAAATTCGACGCTTTTAGCCCTCTCAAGAGGCC 2575
Qy 821 LeuThrIleGlnValLeuThrValGlyAsnAlaLeuArgProIysIleIysTyrThrTyr 840
Db 2576 TTGACCAATCCAGGTTCTTACTGTGGCAATGCCCTTCGACCTAAATTAATATACCTAC 2635
Qy 841 PheValIysIysIysGlySerPheAsnAlaIleProThrPheSerAlaIleValIle 860
Db 2636 TTCGTAAGAAGAAGAGGAATCTTTCAATGCTATCCCACTTTTTCAGCATGGGTCAAT 2695
Qy 861 GluGluTrpGlyGluCysSerIysSerCysGluLeuGlyTrpGlnArgArgLeuValGlu 880
Db 2696 GAAGAGTGGGGCGAATGTTCTAAGTCTATGTGAATTTGGGTGGCAGAGAAGACTGGTAGAA 2755
Qy 881 CysArgAspIleAsnGlyGlnProAlaSerGluCysAlaIysGluValIysProAlaSer 900
Db 2756 TGGCAGACATTAATGACAGCCTGCTTCGAGTGTGCAAGAGAGTGAAGCCAGCCAGC 2815
Qy 901 ThrArgProCysAlaAspHisProCysProGlnTrpGlnLeuGlyGluTrpSerSerCys 920
Db 2816 ACCAGACTTGTGCAGACCATCTCTGCCCCAGTGGCGAGTGGTGCATCATGT 2875
Qy 921 SerIysThrCysGlyIysGlyTyrIysIysThrSerLeuIysCysLeuSerHisAspGly 940
Db 2876 TCTAAGACCTGTGGAGGGGTACAAAAAAGAAAGCTTGAAGTGTCTGTCCCATGATGGA 2935
Qy 941 GlyValIleSerHisAspSerCysAspProLeuIysIysProIysHisPheIleAspPhe 960
Db 2936 GGGGTGTATCTCATGAGAGCTGTGATCCCTTTAAAGAAACCTAAACATTTTCATAGACTTT 2995
Qy 961 CysThrMetAlaGluCysSer 967
Db 2996 TGCACAAATGGCAGAAATGCAGT 3016

RESULT 8

US-10-755-889-133
; Sequence 133, Application US/10755889
; Publication No. US20040171823A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: PATHWAY
; FILE REFERENCE: D0284 NP
; CURRENT APPLICATION NUMBER: US/10755,889
; CURRENT FILING DATE: 2004-01-13
; PRIOR APPLICATION NUMBER: U.S. 60/440,068
; PRIOR FILING DATE: 2003-01-14
; PRIOR APPLICATION NUMBER: U.S. 60/469,757
; PRIOR FILING DATE: 2003-05-12
; NUMBER OF SEQ ID NOS: 823
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 133
; LENGTH: 4447
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-755-889-133

Alignment Scores:
Pred. No.: 0 Length: 4447
Score: 5224.00 Matches: 955
Percent Similarity: 99.28% Conservatives: 5
Best Local Similarity: 98.76% Mismatches: 7
Query Match: 98.81% Indels: 0
DB: 18 Gaps: 0
US-09-373-658c-126 (1-967) x US-10-755-889-133 (1-4447)

Qy 1 MetGlnArgAlaValProGluGlyPheGlyArgArgIysLeuGlySerAspMetGlyAsn 20
Db 243 ATGCAGCAGCTGTGCGCGAGGGGTTTCGGAAGCGCAAGCTGGCGACGACATGGGGAAC 302
Qy 21 AlaGluArgAlaProGlySerArgSerPheGlyProValProThrLeuLeuLeuAla 40
Db 303 GCGAGCGGGCTCCGGGGTCTCGAGCTTTGGGCGGCTATCCCAAGCTGTCTGTCTGCC 362
Qy 41 AlaAlaLeuAlaValSerAspAlaLeuGlyArgProSerGluGluAspGluLeu 60
Db 363 GCGCGCTACTGCGCGCTGTGCGACGCACTCGGGCGCCCTCCGAGGAGGACGAGGAGCTA 422
Qy 61 ValValProGluLeuGluArgValProGlyHisGlyThrThrArgLeuArgLeuHisAla 80
Db 423 GTGGTCCGAGCTGGAGCGCGCCCGGGACACCGGACACACGCGCCCTCCGCTGCACGCC 482
Qy 81 PheAspGlnGlnLeuAspLeuValProProAspSerSerPheLeuAlaProGlyPhe 100
Db 483 TTTGACCCAGCAGCTGGATCTGGAGCTGCGGCGCCGACAGCAGCTTTTGGCGCCGGCTTC 542
Qy 101 ThrLeuGlnAsnValGlyArgIysSerGlySerAspThrProLeuProGluThrAspLeu 120
Db 543 ACCTCCAGAACCTGGGGCGCAATCCGGGTCCGAGACGCGCTCCGGAACCGACCTG 602
Qy 121 AlaHisCysPheTyrSerGlyThrValAsnGlyAspProSerSerAlaAlaLeuSer 140
Db 603 GCGCACTGCTTCTACTCCGCGACCGTGAATGGCGATCCCACTCGGCTCGCGCTCCAGC 662
Qy 141 LeuCysGluGlyValArgGlyAlaPheTyrLeuLeuGlyGluAlaTyrPheIleGlnPro 160
Db 663 CTCTGGAGGGCGTGGCGCGCTTCTACTCTGCGGGAGGCGGTATTTTCATCCAGCCG 722
Qy 161 LeuProAlaAlaSerGluArgLeuAlaThrAlaAlaProGlyGluIysProProAlaPro 180
Db 723 CTGCGCGCGCCACGAGCGCTTCGCCACGCGCGCCCGGAGGAGGAGCGCGGACCA 782
Qy 181 LeuGlnPheHisLeuLeuArgArgAsnArgGlnGlyAspValGlyThrCysGlyVal 200
Db 783 CTACAGTTCCACTCTCTGCGCGGAATCGGCGAGCGACCTAGCGCGGACGCTGCGGGGTC 842
Qy 201 ValAspAspGluProArgProThrGlyIysAlaGluThrGluAspGluAspGlyThr 220
Db 843 GTGGACGACGAGCGCGCGCGCTGCGGAAAGCGGAGACCGCAAGACGAGGAGGAGACT 902
Qy 221 GluGlyGluAspGluGlyProGlnTrpSerProGlnAspProAlaLeuGlnGlyValGly 240
Db 903 GAGGGCGAGGACGAGGGCTCTAGTGGTCCCGCAGGACCGCGCACTGCAAGGCGTAGGA 962
Qy 241 GlnProThrGlyThrGlySerIleArgIysIysArgPheValSerSerHisArgTyrVal 260
Db 963 CAGCCCAACAGAACTGGAGCAATAAGAAAGCGATTTGTCTCAGTCCAGTCCCGCTATGT 1022
Qy 261 GluThrMetLeuValAlaAspGlnSerMetAlaGluPheHisGlySerGlyLeuIysHis 280
Db 1023 GAAACCACTGTTGTGGCAGACCACTGATCGATGCGAGATTCCACGCGCATGTGTAAAGCAT 1082
Qy 281 TyrLeuLeuThrLeuPheSerValAlaAlaArgLeuTyrIysHisProSerIleArgAsn 300
Db 1083 TACCTTCTCAGTGTGTTTTCGGTGGCAGCCAGATTGTACAAACACCCAGCATTCGTAAAT 1142
Qy 301 SerValSerLeuValValIysIleLeuValIleHisAspGluGlnIysGlyProGlu 320

Db 1143 TCAGTTAGCCTGGTGGTGAAGATCTTTGGTCATCCACGATGAACAGAGGGCGCGAA 1202
Qy 321 ValThrSerAsnAlaLeuThrLeuArgAsnPheCysAsnTrpGlnLysGlnHisLeu 340
Db 1203 GTGACCTCCAAATGCTGCCCTCACTCTGGCGAACTTTTGGCAATGGCAGAGCAGCAAC 1262
Qy 341 ProProSerAspArgAspAlaGluHisTyrAspThrAlaIleLeuPheThrArgGlnAsp 360
Db 1263 CCACCCAGTGACCGGGATGCAGAGCACTATGACACAGCAATTCCTTTCCACAGACAGGAC 1322
Qy 361 LeuCysGlySerGlnThrCysAspThrLeuGlyMetAlaAspValGlyThrValCysAsp 380
Db 1323 TTGTGTGGTCCACAGCATGTATCTCTTGGATGGCTGATGTGGAACTGTGTGTGAT 1382
Qy 381 ProSerArgSerCysSerValIleGluAspGlyLeuGlnAlaAlaPheThrAla 400
Db 1383 CCGAGCAGAAGCTGCTCCGTCATAGAAGATGATGTTTACAAGCTGCCTTCCACAGCC 1442
Qy 401 HisGluLeuGlyHisValPheAsnMetProHisAspAspAlaLysGlnCysAlaSerLeu 420
Db 1443 CATGAATTAGGCCACGCTGTTTAACATGCCACATGATGATGCAAGAGCTGTCAGCCCT 1502
Qy 421 AsnGlyValAsnGlnAspSerHisMetMetAlaSerMetLeuSerAsnLeuAspHisSer 440
Db 1503 AATGGTGTGAACACAGGATTCACCATGATGGCGTCAATGCTTTTCCAACCTGGACACACAGC 1562
Qy 441 GlnProTrpSerProCysSerGlyTyrMetIleThrSerPheLeuAspAsnGlyHisGly 460
Db 1563 CAGCCTTGGTCTCCCTTGGCAGTCCCTACATGATATCATCATTTCTGGATAATGGTCATGG 1622
Qy 461 GluCysLeuMetAspLysProGlnAsnProIleGlnLeuProGlyAspLeuProGlyThr 480
Db 1623 GAATGTTTGTATGGACAGCTCATATCCATACAGCTCCAGGGCACTCCCTGGCACC 1682
Qy 481 SerTyrAspAlaAsnArgGlnCysGlnPheThrPheGlyGluAspSerLysHisCysPro 500
Db 1683 TCGTACGATGCCCAACCGGCAGTGCCAGTTTACATTTGGGGAGGACTCCAAAACACTGCCCT 1742
Qy 501 AspAlaAlaSerThrCysSerThrLeuTrpCysThrGlyThrSerGlyGlyValLeuVal 520
Db 1743 GATGACGCAGCAGCATGTAGACACCTTGTGGTGATCCGGCACTCTGGTGGGGTGCTGGTG 1802
Qy 521 CysGlnThrLysHisPheProTrpAlaAspGlyThrSerCysGlyGluGlyLysTrpCys 540
Db 1803 TGTCAAAACCAACACTTCCCGTGGCGGATGCCACAGCTGTGGAGAGGAAATGGTGT 1862
Qy 541 IleAsnGlyLysCysValAsnLysAsnHisArgLysHisPheAspThrProPheHisGly 560
Db 1863 ATCAACGGCAAGTGTGTGAACAAACCCGACAGAAAGCAATTTTGATACGCTTTTCATGGA 1922
Qy 561 SerTrpGlyMetTrpGlyProTrpGlyAspCysSerArgThrCysGlyGlyValGln 580
Db 1923 AACTGGGGAATGTGGGGCTTGGGAGACTGTTCGAGAACGTGGCGTGAGAGTCCAG 1982
Qy 581 TyrThrMetArgGluCysAspAsnProValProLysAsnGlyLysTyrCysGluGly 600
Db 1983 TACACGATGAGGGATGTGACACCCAGCTCCCAAGAGATGGAGGAGTACTGTGAAGC 2042
Qy 601 LysArgValArgTyrArgSerCysAsnLeuGluAspCysProAspAsnAsnGlyLysThr 620
Db 2043 AAACGAGTGGCTACAGATCTCTGAACCTTGAGGACTGTCCAGACATAATGGAAGAAACC 2102
Qy 621 PheArgGluGlnCysGluAlaHisAsnGluPheSerLysAlaSerPheGlySerGly 640
Db 2103 TTTAGAGAGGAACAATGTGAAGCACACACAGAGTTTTCAGAAAGCTTCTTTGGGAGTGGG 2162
Qy 641 ProAlaValGluTrpIleProLysTyrAlaGlyValSerProLysAspArgCysLysLeu 660
Db 2163 CTGCGGTGGATGGATTTCCCAAGTACGTGGCGTCTCACCAAGAGCAGGTGCAAGCTC 2222
Qy 661 IleCysGlnAlaLysGlyIleGlyTyrPhePheValLeuGlnProLysValValAspGly 680
Db 2223 ATCTGCCAAGCCAAAGGCATTTGGTACTTCTTCGTTTTTGCAGCCCAAGGTTGTAGATGT 2282

Qy 681 ThrProCysSerProAspSerThrSerValCysValGlnGlnCysValLysAlaGly 700
Db 2283 ACTCATGTAGCCAGATTCACCTCTCTGTGTGTGAGGACAGTGTGTAAAGCTGGT 2342
Qy 701 CysAspArgIleIleAspSerLysLysPheAspLysCysGlyValCysGlyGlyAsn 720
Db 2343 TGTGATCGCATCATAGACTCCAAAAGAAAGTTTGATAAATGTGGTGTTCGGGGGAAA 2402
Qy 721 GlySerThrCysLysLysLysLysSerGlySerValThrSerAlaLysProGlyTyrHisLeu 740
Db 2403 GGATCTACTTGTAAAAAAATATCAGGATCAGTTACTAGTGCAAAAACCTGGATATCATGAT 2462
Qy 741 IleIleThrIleProThrGlyValaThrAsnIleGluValLysGlnArgAsnGlnArgGly 760
Db 2463 ATCATCANTTCCAACTGGAGCCACCAACATCGAAGTGAACAGCGGACACAGAGGGA 2522
Qy 761 SerArgAsnAsnGlySerPheLeuAlaIleLysAlaAlaAspGlyThrTyrIleLeuAsn 780
Db 2523 TCCAGGAACAATGGCAGCTTTCTTGCATCAAGCTGCTGATGGCACATATATTTCTTAAT 2582
Qy 781 GlyAspTyrThrLeuSerThrLeuGluGlnAspIleMetTyrLysGlyValValLeuArg 800
Db 2583 GGTGACTACACTTTGTCCACCTTAGAGCAAGACATATGTACAAAGGTGTTCTCTTGAGG 2642
Qy 801 TyrSerGlySerSerAlaAlaLeuGluArgIleArgSerPheSerProLeuLysGluPro 820
Db 2643 TACAGCGCTCTCTCGCGCATTTGAAAGAAATTCGACGCTTTAGCCCTCTCAAGAGCCC 2702
Qy 821 LeuThrIleGlnValLeuThrValGlyAsnAlaLeuArgProLysIleLysTyrThrTyr 840
Db 2703 TTGACCATCCAGTCTTACTGTGGGCAATGCCCTTCGACCTTAAATTTAAATACACCTAC 2762
Qy 841 PheValLysLysLysLysGluSerPheAsnAlaIleProThrPheSerAlaTrpValIle 860
Db 2763 TTCGTAAGAAGAAAGAAAGAAATCTTTCAATGCTATCCCCACTTTTTCAGCATGGGTCA 2822
Qy 861 GluGluTrpGlyGluCysSerLysSerCysGluLeuGlyTrpGlnArgArgLeuValGlu 880
Db 2823 GAAGATGGGGCGAATGTTCTAAGTCATGTGAATGGGTGGCAGAGAAGACTGGTAGAA 2882
Qy 881 CysArgAspIleAsnGlyGlnProAlaSerGluCysAlaLysGlyValLysProAlaSer 900
Db 2883 TGCCGAGACATTAATGAGCAGCTCTTCCGAGTGTGCAAGGAAAGTGAAGCAGCAGC 2942
Qy 901 ThrArgProCysAlaAspHisProCysProGlnTrpGlnLeuGlyGluTrpSerSerCys 920
Db 2943 ACCAGACCTTGTGCAGACCATCCCTGCCCCAGTGGCAGCTGGGGAGTGGTCATCATGT 3002
Qy 921 SerLysThrCysGlyLysGlyTyrLysLysThrSerLeuLysCysLeuSerHisAspGly 940
Db 3003 TCTAAGACTGTGGAGAGGTTACAAAAAGAAAGCTTGAAGTGTCTGCCCATGTGGA 3062
Qy 941 GlyValLeuSerHisAspSerCysAspProLeuLysLysProLysHisPheIleAspPhe 960
Db 3063 GGGGTGTTATCTCATGAGAGCTGTGATCTTTAAAGAAACCTTAAACATTTTCATAGACTTT 3122
Qy 961 CysThrMetAlaGluCysSer 967
Db 3123 TGCACAAATGGCAGAATGCAGT 3143

RESULT 9

US-10-159-563-192
; Sequence 192, Application US/10159563
; Publication NO. US20040009154A1
; GENERAL INFORMATION:
; APPLICANT: Khan, Javed
; APPLICANT: Ringner, Markus
; APPLICANT: Peterson, Carsten
; APPLICANT: Meltzer, Paul
; TITLE OF INVENTION: SELECTIONS OF GENES AND METHODS OF USING THE SAME FOR
; TITLE OF INVENTION: DIAGNOSIS AND FOR TARGETING THE THERAPY OF SELECT CANCERS
; FILE REFERENCE: 11613.56US11

CURRENT APPLICATION NUMBER: US/10/159,563
CURRENT FILING DATE: 2002-12-09
PRIOR APPLICATION NUMBER: US 10/133,937
PRIOR FILING DATE: 2002-04-25
NUMBER OF SEQ ID NOS: 444
SOFTWARE: Patent in version 3.1
SEQ ID NO 192
LENGTH: 4459
TYPE: DNA
ORGANISM: Homo sapiens
US-10-159-563-192

Alignment Scores:
Pred. No.: 0 Length: 4459
Score: 5294.00 Matches: 956
Percent Similarity: 99.28% Conservative: 4
Best Local Similarity: 98.86% Mismatches: 7
Query Match: 98.81% Indels: 0
DB: 17 Gaps: 0

US-09-373-658c-126 (1-967) x US-10-159-563-192 (1-4459)

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Db	243	ATGCAGCGAGCTGTGCCGAGGGGTTTCGGAAGCGCAAGCTGGGCGACGATGGGGAC	302
Qy	21	AlaGluArgAlaProGlySerArgSerPheGlyProValProThrLeuLeuLeuAla	40
Db	303	GCGAGCGGGCTCCGGGGTCTCGAGCTTTGGGCCCGTACCCAGCTGCTGCTCGCC	362
Qy	41	AlaAlaLeuLeuAlaValSerAspAlaLeuGlyArgProSerGluGluAspGluGluLeu	60
Db	363	GCGGCGCTACTGGCCGTCTCGAGCGACTCGGGCGCCCTCCGAGGAGGACGAGGACTA	422
Qy	61	ValValProGluLeuGluArgValProGlyHisGlyThrThrArgLeuArgLeuHisAla	80
Db	423	GTGGTCCGAGCTGGAGCGGCCCGCGGACACGCGGACACGCGCCCTCCGCTCGACGCC	482
Qy	81	PheAspGlnGlnLeuAspLeuAspValProProAspSerSerPheLeuAlaProGlyPhe	100
Db	483	TTTGACGAGCGCTGGATCTGGAGCTCGGCCCGCCGACGAGCTTTTGGCGCCGGCTTC	542
Qy	101	ThrLeuGlnAsnValGlyArgGlySerGlySerAspThrProLeuProGluThrAspLeu	120
Db	543	ACGCTCCAGAACGTGGGGCGCAATCCGGGTCCGAGACCGCTTCGCGAAACCGACCTG	602
Qy	121	AlaHisCysPheTyrSerGlyThrValAsnGlyAspProSerSerAlaAlaLeuSer	140
Db	603	GCGCACTGCTTACTCCGCGCACCGTGAATGGCGATCCAGCTCGGCTGCGCCCTCAGC	662
Qy	141	LeuGlyGluGlyValArgGlyAlaPheTyrLeuLeuGlyGluAlaTyrPheLeuGlnPro	160
Db	663	CTCTGCGAGGCGGTGCGCGCGCTTCTACTCTGGGGGAGGGGTATTTTCATCCAGCCG	722
Qy	161	LeuProAlaAlaSerGluArgLeuAlaThrAlaAlaProGlyGluLysProProAlaPro	180
Db	723	CTGCCCGCGCCAGCAGCGCTCGCCACCGCCCGCCCGGAGGAGAGCCCGCGCACCA	782
Qy	181	LeuGlnPheHisLeuLeuArgArgAsnArgGlnGlyAspValGlyThrCysGlyVal	200
Db	783	CTACAGTTCCACTCTCTGCGCGGAAATCGGCGGGCGACGTCGCGCGCGACGTGCGGGTC	842
Qy	201	ValAspAspGluProArgProThrGlyValAlaGluThrGluAspGluAspGlyThr	220
Db	843	GTGGACACGAGCCCGCGCGACTTGGGAAAGCGGAGACCGAAGACGAGGAGGACT	902
Qy	221	GluGlyGluAspGluGlyProGlnTrpSerProGlnAspProAlaLeuGlnGlyValGly	240
Db	903	GAGGCGGAGGACGAGGGGCTCACTGTGCGCCGAGGACCGCGACTTCGAGGCGTAGGA	962
Qy	241	GlnProThrGlyThrGlySerIleArgLysLysArgPheValSerSerHisArgTyrVal	260
Db	963	CAGCCCAACAGACTGGAAGCATAAAGAGCGATTTGTGTCCAGTCAACCGCTATGTG	1022

Qy	261	GluThrMetLeuValAlaAspGlnSerMetAlaGluPheHisGlySerGlyLeuLysHis	280
Db	1023	GAAACCATCTTGTGGCAGACCATCGATGGCAGAAATTCACGGCAGTGTCTTAAAGCAT	1082
Qy	281	TyrLeuLeuThrLeuPheSerValAlaAlaArgLeuTyrLysHisProSerIleArgAsn	300
Db	1083	TACCTTTCTCACGTGTGTTCGGTGGCAGCCAGATGTACAAACACCCACGATTCGTAAT	1142
Qy	301	SerValSerLeuValValLysIleLeuValIleHisAspGluGlnLysGlyProGlu	320
Db	1143	TCAGTTAGCTGTGTGTGTGAAGATCTTGTTCATCCACGATGACAGAGGGGCGGAA	1202
Qy	321	ValThrSerAsnAlaAlaLeuThrLeuArgAsnPheCysAsnTrpGlnLysGlnHisAsn	340
Db	1203	GTGACCTCCAAATGCTGCTCCTCACTTCGCGAACTTTTGCACCTGGCAGAGCAGCAAC	1262
Qy	341	ProProSerAspArgAspAlaGluHisTyrAspThrAlaIleLeuPheThrArgGlnAsp	360
Db	1263	CCACCCAGTGACCGGGATGCGAGCAGCTATGACACAGCAATCTTTTCCACGACGAGAC	1322
Qy	361	LeuCysGlySerGlnThrCysAspThrLeuGlyMetAlaAspValGlyThrValCysAsp	380
Db	1323	TTGTGTGGTCCACAGACATGTGATCTCTTGGATGGCTGATCTTGGAACTGTGTGAT	1382
Qy	381	ProSerArgSerCysSerValIleGluAspAspGlyLeuGlnAlaAlaPheThrAla	400
Db	1383	CCGAGCAGAAAGCTGCTCCGCTCATAGAAGATGATGGTTTACAGCTGCTTCCACACAGCC	1442
Qy	401	HisGluLeuGlyHisValPheAsnMetProHisAspAspAlaLysGlnCysAlaSerLeu	420
Db	1443	CATGAATTAGGCCACCGTGTAAACATGCCACATGATGATGATGATGATGATGATGAT	1502
Qy	421	AsnGlyValAsnGlnAspSerHisMetMetAlaSerMetLeuSerAsnLeuAspHisSer	440
Db	1503	AATGGTGTGAACAGGATTTCCACATGATGGCGTCAATGCTTTCCAACTTGGACACAGC	1562
Qy	441	GlnProTrpSerProCysSerGlyTyrMetIleThrSerPheLeuAspAsnGlyHisGly	460
Db	1563	CAGCTTGTGCTCTCTTGCAGTGCCTACATGATTTACATCATTTCTGGATATGTCATGGG	1622
Qy	461	GluCysLeuMetAspLysProGlnAsnProIleGlnLeuProGlyAspLeuProGlyThr	480
Db	1623	GAATGTTGATGACAAAGCCTCAGAAATCCCATACAGCTCCAGCGCGATCTCCCTGGCACC	1682
Qy	481	SerTyrAspAlaAsnArgGlnCysGlnPheThrPheGlyGluAspSerLysHisCysPro	500
Db	1683	TCGTACGATGCCAACCGCGAGTCCAGTTTACATTTGGGAGGAGACTCCAAACACTGCCCC	1742
Qy	501	AspAlaAlaSerThrCysSerThrLeuTrpCysThrGlyThrSerGlyGlyValLeuVal	520
Db	1743	GATGACGACGACATGATGACCTTGTGTGTGTACCGGACCTCTGTGGGGTGTCTGGTG	1802
Qy	521	CysGlnThrLysHisPheProTrpAlaAspGlyThrSerCysGlyGluGlyLysTrpCys	540
Db	1803	TGTCAAAACCAACACTTCCGTTGGCGGATGGCAGCAGCTGTGGAGAGGAAATGTGT	1862
Qy	541	IleAsnGlyLysCysValLeuLysAsnHisArgLysHisPheAspThrProPheHisGly	560
Db	1863	ATCAACGGCAAGTGTGTGAACAAACCGACAGAAAGCATTTTGTATAGCCCTTTTCATGGA	1922
Qy	561	SerTrpGlyMetTrpGlyProTrpGlyAspCysSerArgThrCysGlyGlyValGln	580
Db	1923	AGCTGGGAATGTGGGGCTTGGGAGACTGTTCGAGAACGTCGCGTGGAGGAGTCCAG	1982
Qy	581	TyrThrMetArgGluCysAspAsnProValProLysAsnGlyGlyLysTrpCysGluGly	600
Db	1983	TACACGATGAGGGAATGTGCAACCCAGCTCCCAAGAAATGGAGGGAATGTGTGAAGGC	2042
Qy	601	LysArgValArgTyrArgSerCysAsnLeuGluAspCysProAspAsnAsnGlyLysThr	620
Db	2043	AAACGAGTGGCTACAGATCTTGTAACTTGTGAGACTGTCCAGACAATATATGAAAAACC	2102

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QY 621 PheArgGluGluGlnCysGluAlaHisAenGluPheSerLysAlaSerPheGlySerGly 640
Db 2103 TTTAGAGAGGAACAATGTGACACACACACAGTTTTCAAAAGCTTCTTTGGAGTGGG 2162
QY 641 ProAlaValGluTrpIleProLysTyrAlaGlyValSerProLysAspArgCysLysLeu 660
Db 2163 CCTGGCGTGAATGGAATCCCAAGTACGTCGCGTCTCACCAAGACACAGGTGCAAGCTC 2222
QY 661 IleCysGlnAlaLysGlyIleGlyTyrPheValLeuGlnProLysValValAspGly 680
Db 2223 ATCTGCAAGCAAGGCAATGGCTACTTCTTCGTTTCGACCCCAAGGTTTGAATGT 2282
QY 681 ThrProCysSerProAspSerThrSerValCysValGlnGlnCysValLysAlaGly 700
Db 2283 ACTCCATGTAGCCAGATTCACCTCTGCTGTGTGCAAGGACAGTGTGTAAAGCTGT 2342
QY 701 CysAspArgIleIleAspSerLysLysLysPheAspLysCysGlyValCysGlyGlyAen 720
Db 2343 TGTGATCGCATCATAGACTCCAAAAGAAAGTTTGATAAATGTGTGTGTCGGGGGAAAT 2402
QY 721 GlySerThrCysLysLysLysSerGlySerValThrSerAlaLysProGlyTyrHisasp 740
Db 2403 GGATCTACTTGTAAAAAAATATCAGATCAGTTACTAGTGCAAAACCTTGATATCATGAT 2462
QY 741 IleIleThrIleProThrGlyAlaThrAenIleGluValLysGlnArgAenGlnArgGly 760
Db 2463 ATCATCACAAATTCACCTGAGCCACCAATCGAAGTGAACAGCGGAACAGAGGGA 2522
QY 761 SerArgAsnAsnGlySerPheLeuAlaLysLysAlaAlaAspGlyThrTyrIleLeuAen 780
Db 2523 TCCAGGAACAATGGCAGCTTCTTGCATCAAAAGCTGTGTGATGCACATATATTTCTTAAT 2582
QY 781 GlyAspTyrThrLeuSerThrLeuGlnGlnAspIleMetTyrLysGlyValValLeuArg 800
Db 2583 GGTGACTACACTTGTGCCACTTAGAGCAAGACATATATGACAAAGTGTGTCTTGAGG 2642
QY 801 TyrSerGlySerSerAlaAlaLeuGluArgIleArgSerPheSerProLeuLysGluPro 820
Db 2643 TACAGCGGCTCTCTGCGCAATTGAAAGAAATTCGACGCTTTAGCCCTCTCAAGAGCC 2702
QY 821 LeuThrIleGlnValLeuThrValGlyAenAlaLeuArgProLysIleLysTyrThrTyr 840
Db 2703 TTGACCATCCAGGTTCTTACTGTGGCAATGCCCTTCGACCTAAAAATTAATACACCTAC 2762
QY 841 PheValLysLysLysLysGluSerPheAenAlaIleProThrPheSerAlaTrpValIle 860
Db 2763 TTCGTAAGAAGAAGAAGAAATCTTTCAATGCTATCCCCACTTTTTCAGCATGGGTCAAT 2822
QY 861 GluGluTrpGlyGluCysSerLysSerCysGluLeuGlyTrpGlnArgArgLeuValGlu 880
Db 2823 GAAGAGTGGGGCGAATGTTCTAAGTCACTGTAATGGGTGGCAGAGAAGACTGGTAGAA 2882
QY 881 CysArgAspIleAsnGlyGlnProAlaSerGluCysAlaLysGluValLysProAlaSer 900
Db 2883 TGCCGAGACATTAATGACAGCCTGCTCCGAGTGTGCAAGAAAGTGAAGCAGCAGCAGC 2942
QY 901 ThrArgProCysAlaAspHisProCysProGlnTrpGlnLeuGlyGluTrpSerCys 920
Db 2943 ACCAGACCTTGTGCAGACCATCTCTGCCCCAGTGGCAGCTGGGGAGTGGTCATCATGT 3002
QY 921 SerLysThrCysGlyLysGlyTyrLysLysThrSerLeuLysCysLeuSerHisaspGly 940
Db 3003 TCTAAGACCTGTGGGAAGGTTTACAAAAAAGAAAGCTTCAAGTGTCTGTCCTCATGATGA 3062
QY 941 GlyValLeuSerHisaspSerCysAspProLeuLysLysProLysHisPheIleaspPhe 960
Db 3063 GGGGTGTATCATGAGAGCTGTGATCTCTTTAAAGAAACCTAAACATTTTCATAGACTTT 3122
QY 961 CysThrMetAlaGluCysSer 967
Db 3123 TGCACATATGGCAGATGCAGT 3143
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RESULT 10

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US-10-159-563-308
; Sequence 308, Application US/10159563
; Publication No. US20040009154A1
; GENERAL INFORMATION:
; APPLICANT: Khan, Javed
; APPLICANT: Ringner, Markus
; APPLICANT: Peterson, Carsten
; APPLICANT: Meltzer, Paul
; TITLE OF INVENTION: SELECTIONS OF GENES AND METHODS OF USING THE SAME FOR
; FILE REFERENCE: 11613.56US11
; CURRENT APPLICATION NUMBER: US/10/159,563
; PRIOR FILING DATE: 2002-12-09
; PRIOR APPLICATION NUMBER: US 10/133,937
; PRIOR FILING DATE: 2002-04-25
; NUMBER OF SEQ ID NOS: 444
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 308
; LENGTH: 4459
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-159-563-308

Alignment Scores:
Pred. No.: 0 Length: 4459
Score: 5224.00 Matches: 956
Percent Similarity: 99.28% Conservative: 4
Best Local Similarity: 98.88% Mismatches: 7
Query Match: 99.81% Indels: 0
DB: 17 Gaps: 0

US-09-373-658c-126 (1-967) x US-10-159-563-308 (1-4459)
QY 1 MetGlnArgAlaValProGluGlyPheGlyArgArgLysLeuGlySerAspMetGlyAen 20
Db 243 ATGCAGCAGCTGTCTCCGAGGGGTTCGGAAGCCCAAGCTGGCAGCGACATGGGGAAC 302
QY 21 AlaGluArgAlaProGlySerArgSerPheGlyProValProThrLeuLeuLeuAla 40
Db 303 GCGGAGCGGGCTCCGGGGTCTCGAGCTTTGGGCCGTACCCACCGTGTCTGTCTCGCC 362
QY 41 AlaAlaLeuLeuAlaValSerAspAlaLeuGlyArgProSerGluGluAspGluLeu 60
Db 363 GCGGCGCTACTGGCGGTGTGCGACGCACTCGGGGCGCCCTCCGAGGAGACGAGAGCTA 422
QY 61 ValValProGluLeuGluArgValProGlyHisGlyThrArgLeuArgLeuHisAla 80
Db 423 GTGGTCCCGAGCTGGAGCGGCCGCCGAGACACAGGACCCAGCGCTCTCGCTGCACGCC 482
QY 81 PheAspGlnGlnLeuAspLeuAspValProProAspSerSerPheLeuAlaProGlyPhe 100
Db 483 TTTGACCAAGCAGCTGGATCTGGAGCTGGCGGCCGACAGCAGCTTTTGGCGCCCGCTTC 542
QY 101 ThrLeuGlnAsnValGlyArgLysSerGlySerAspThrProLeuProGluThrAspLeu 120
Db 543 ACGCTCCAGAACGTCGGGGCGAAATCCGGGTCCGAGACGCCCTTCGGAACACCGACCTG 602
QY 121 AlaHisCysPheTyrSerGlyThrValAsnGlyAspProSerSerAlaAlaAlaLeuSer 140
Db 603 GCGCACTGCTTCTACTCCGGCACCCGTGAATGCGATCCAGCTCGGCTCGGCCCTTCAGC 662
QY 141 LeuCysGluGlyValArgGlyAlaPheTyrLeuLeuGlyGluAlaTyrPheIleGlnPro 160
Db 663 CTCCTCGAGGGGTGGCGGGCGCTTCTACCTGTCTGGGGAGGCGGTATTTTCATCCAGCG 722
QY 161 LeuProAlaAlaSerGluArgLeuAlaThrAlaAlaProGlyGluLysProAlaPro 180
Db 723 CTGCCCGCGCCAGCAGCGCTTCGCCACCGCCGCCCGCCAGGGGAGAGCCGCCGCCACA 782
QY 181 LeuGlnPheHisLeuLeuArgAsnArgGlnGlyAspValGlyGlyThrCysGlyVal 200
Db 783 CTACAGTTCCACTCTCTCGGGCGGAATCGGCGAGGCGGACGTCGCGGCGACGTCGCGGGTIC 842
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Qy	201	ValAspAspGluProArgProThrGlyLysAlaGluThrGluAspGluAspGluGlyThr	220
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Qy	221	GluGlyGluAspGluGlyProGlnTTPSerProGlnAspProAlaLeuGlnGlyValGly	240
Db	903	GAGGGCGAGACCAAGGGGCTCAGTGTGTCGCCGAGACC CGGACATGCAAGCGGTAGGA	962
Qy	241	GlnProThrGlyThrGlySerIleArgLysLysArgPheValSerSerHisArgTyrVal	260
Db	963	CAGCCACACGAACTGGAGACATAAGAAAGAGGATTGTGTCCAGTCACCGCTATGTG	1022
Qy	261	GluThrMetLeuValAlaAspGlnSerMetAlaGluPheHisGlySerGlyLeuLysHis	280
Db	1023	GAAAACCATGCTTGTGGCAGACCAAGTCGATGGCAGAAATCCACGGCAGTGTCTAAAGCAT	1082
Qy	281	TyrLeuLeuThrIleuPheSerValAlaAlaArgLeuTyrIlyShiProSerIleArgAsn	300
Db	1083	TACCTTCTCAGTGTGTTCGTGGTGAGCAGATTGTACAAACACCCAGCATTCGTAAAT	1142
Qy	301	SerValSerLeuValValLysIleLeuValIleHisAspGluGlnLysGlyProGlu	320
Db	1143	TCAGTTAGCCTGGTGGTGGTGAAGACTCTTGTCATCCACGATGAACGAGAGGCGCGAA	1202
Qy	321	ValThrSerAsnAlaAlaLeuThrLeuArgAsnPheCysAsnTTPGlnLysGlnHisAsn	340
Db	1203	GTGACCTCCAATGTCGCCCTCACTCTCGGAACTTTTGCACACTGGCAGACGACGACAC	1262
Qy	341	ProProSerAspArgAspAlaGluHisTyrAspThrAlaIleLeuPheThrArgGlnAsp	360
Db	1263	CCACCCAGTGACCGGATGAGACACTATGACACAGCAATCTTTTCCACGACGAGGAC	1322
Qy	361	LeuCysGlySerGlnThrCysAspThrLeuGlyMetAlaAspValGlyThrValCysAsp	380
Db	1323	TTGTGTGGGTCCCAGACATGTGATACTCTTGGGATGGCTGATGTGGAACTGTGTGTGAT	1382
Qy	381	ProSerArgSerCysSerValIleGluAspAspGlyLeuGlnAlaAlaPheThrThrAla	400
Db	1383	CCGAGCAGAAAGCTGCTCCGTATAGAAAGATGATGGTTTACAAGTGCCTTTCCACGAGCC	1442
Qy	401	HisGluLeuGlyHisValPheAsnMetProHisAspAspAlaLysGlnCysAlaSerLeu	420
Db	1443	CATGAATTAGGCCACGTGTTTAAACATGCCACATGATGATCAAGACAGTGTCCAGCGCTT	1502
Qy	421	AsnGlyValAsnGlnAspSerHisMetMetAlaSerMetLeuSerAsnLeuAspHisSer	440
Db	1503	AATGGTGTGAACACGAGATTTCCACATGATGGCGTCATGTCTTCCAACTGGACCAAGC	1562
Qy	441	GlnProTTPSerProCysSerGlyTyrMetIleThrSerPheLeuAspAsnGlyHisGly	460
Db	1563	CAGCCTTTGGTCTCCTTGCAGTGCCCTCATCATGATTACATCAATTTCTGGATAATGGTCATGGG	1622
Qy	461	GluCysLeuMetAspLysProGlnAsnProIleGlnLeuProGlyAspLeuProGlyThr	480
Db	1623	GAATGTTTGTATGGACAAGCCTCAGAAATCCCATACAGCTCCAGCGCATCTCCCTGGCACC	1682
Qy	481	SerTyrAspAlaAsnArgGlnCysGlnPheThrPheGlyGluAspSerLysHisCysPro	500
Db	1683	TCGTACGATGCCAACCGGCACTGCAGTTTACATTTGGGGAGGACTCCAAACACTGCCCC	1742
Qy	501	AspAlaAlaSerThrCysSerThrLeuTTPCysThrGlyThrSerGlyGlyValLeuVal	520
Db	1743	GATGCAGCAGCACATGTAGCACCTTGTGGTGTACCGGCACCTCTGGTGGGTGCTGGTG	1802
Qy	521	CysGlnThrLysHisPheProTTPAlaAspGlyThrSerCysGlyGluGlyLysTTPCys	540
Db	1803	TGTCAAACCAACAACCTTCCCGTGGCGGATGGCACCAAGCTGTGGAGAAGGGAATGTGTGT	1862
Qy	541	IleAsnGlyLysCysValAsnLysAsnHisArgLysHisPheAspThrProPheHisGly	560
Db	1863	ATCAACGGCAAGTGTGTGAAACAAACCGACAGAAAGCAATTTTGATACGCCCTTTTCATGGA	1922
Qy	561	SerTTPGlyMetTTPGlyProTTPGlyAspCysSerArgThrCysGlyGlyGlyValGln	580

Db	1923	AGCTGGGGAAATGGGGGGCCCTTGGGGAGACTGTTCCAGAAACGTGCCGTGGAGAGTCCAG	1982
Qy	581	TyrThrMetArgGluCysAspAsnProValProLyAsnGlyGlyLysTyrCysGluGly	600
Db	1983	TACACGATGAGGGAATGTGACAAACCCAGTCCCAAAAGATGGAGGGAAGTACTGTGAAGGC	2042
Qy	601	LysArgValArgTyrArgSerCysAsnLeuGluAspCysProAspAsnAsnGlyLysThr	620
Db	2043	AAACGAGTGGCTACAGATCTCTGTAACTTTGAGGACTGTCCACACAATATATGAAAAC	2102
Qy	621	PheArgGluGluGlnCysGluAlaHisAsnGluPheSerLysAlaSerPheGlySerGly	640
Db	2103	TTTAGAGAGGAAACAATGTGAAGCACACAACGAGTTTTCAAAAGCTTCCTTTGGAGTGGG	2162
Qy	641	ProAlaValGluTrpIleProLysTyrAlaGlyValSerProLysAspArgCysLysLeu	660
Db	2163	CCTGCGGTGGATGGATTCCCAAGTAGCTGGCGTCTCACAAAGGACAGGTGCAAGCTC	2222
Qy	661	IleCysGlnAlaLysGlyIleGlyTyrPhePheValLeuGlnProLysValValAspGly	680
Db	2223	ATCTGCCAAGCCAAAGGCATTTGGCTACTTCTTCGTTTTGACGGCCAAAGGTTGTAGATGGT	2282
Qy	681	ThrProCysSerProAspSerThrSerValCysValGlnGlyGlnCysValLysAlaGly	700
Db	2283	ACTCCATGTAGCCAGATTCACCTCTGTCTGTGTGACAGACAGTGTGTAAAGCTGGT	2342
Qy	701	CysAspArgIleIleAspSerLysLysPheAspLysCysGlyValCysGlyGlyAsn	720
Db	2343	TGTGATCGCATCATAGATCCCAAAAGAACTTTGATAAATGTGGTGTTCGCGGGGAAAT	2402
Qy	721	GlySerThrCysLysLysIleSerGlySerValThrSerAlaLysProGlyTyrHisAsp	740
Db	2403	GGATCTACTTGTAAAAAATATCAGGATCATCTAGTGTGTCACAAACCTGGATATCATGAT	2462
Qy	741	IleIleThrIleProThrGlyAlaThrAsnIleGluValLysGlnArgAsnGlnArgGly	760
Db	2463	ATCATCACAATCCAACTGGAGCCACCAATCGAGTGAAACACGCGAACCCAGAGGGGA	2522
Qy	761	SerArgAsnAsnGlySerPheLeuAlaIleLysAlaAlaAspGlyThrTyrIleLeuAsn	780
Db	2523	TCCAGGACAAATGGCAGCTTCTTGCCATCAAAAGCTGCTGATGGCACATATATCTTAAT	2582
Qy	781	GlyAspTyrThrLeuSerThrLeuGluGlnAspIleMetTyrLysGlyValValLeuArg	800
Db	2583	GGTGACTACACTTTGTCCACTTAGACCAAGACATATGTACAAAGTGTTGTCTTGAGG	2642
Qy	801	TyrSerGlySerSerAlaAlaLeuGluArgIleArgSerPheSerProLeuLysGluPro	820
Db	2643	TACAGCGGCTTCCTGCGCAATTTGGAAAGAAATTCGCGAGCTTTAGCCCTCTCAAGAGCCC	2702
Qy	821	LeuThrIleGlnValLeuThrValGlyAsnAlaLeuArgProLysIleLysTyrThrTyr	840
Db	2703	TTGACCATCAGGTTCTTACTGTGGGCAATGCCCTTCGACCTTAAATATAATACACCTAC	2762
Qy	841	PheValLysLysLysLysGluSerPheAsnAlaIleProThrPheSerAlaTrpValIle	860
Db	2763	TTCTGTAAGAAGAAGAGGAATCTTTCAATGCTATCCCTCATCCCACTTTTTCAGCATGGGTCA	2822
Qy	861	GluGluTrpGlyGluCysSerLysSerCysGluLeuGlyTrpGlnArgArgLeuValGlu	880
Db	2823	GAGAGTGGGGCGAATGTTCTAAGTCAATGAAATTTGGGTGGCCAGAGAACTGGTAGAA	2882
Qy	881	CysArgAspIleAsnGlyGlnProAlaSerGluCysAlaLysGluValLysProAlaSer	900
Db	2883	TGCCGAGACATTAATGACGACCTGCTTCGAGGTGTCMAAGGAAGTGAAGCCAGCCAGC	2942
Qy	901	ThrArgProCysAlaAspHisProCysProGlnTrpGlnLeuGlyGluTrpSerSerCys	920
Db	2943	ACCAGACTTGTGCAGACCATCCCTGCGCCAGTGGGAGCTGGGGGAGTGTGTCATCATGT	3002
Qy	921	SerLysThrCysGlyLysGlyTyrLysLysThrSerLeuLysCysLeuSerHisAspGly	940

Db 3003 TCTAAGACCTGTGGGAAGGTTTACAAAAAGAAAGCTTGAAGTGTCTGTCCCATGATGGA 3062
QY 941 GlyValLeuSerHisAspSerCysAspProLeuLeuLysLysProLysHisPheIleAspPhe 960
Db 3063 GGGGTGTATCTCATGAGAGCTGTGATCTTTTAAAGAAACCTTAAACATTTTCATAGACTTT 3122
QY 961 CysThrMetAlaGluCysSer 967
Db 3123 TGCACATGGCAGATGCAGT 3143

RESULT 11
US-09-971-429B-17
; Sequence 17, Application US/09971429B
; Publication No. US20030175704A1
; GENERAL INFORMATION:
; APPLICANT: Lasek, Amy K. W.
; APPLICANT: Shyjan, Andrew W.
; APPLICANT: Turner, Christopher M.
; TITLE OF INVENTION: GENES EXPRESSED IN LUNG CANCER
; FILE REFERENCE: PA-0040 US
; CURRENT APPLICATION NUMBER: US/09/971,429B
; CURRENT FILING DATE: 2001-10-04
; PRIOR APPLICATION NUMBER: 60/239,024
; PRIOR FILING DATE: 2000-04-10
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: PERL Program
; SEQ ID NO 17
; LENGTH: 4760
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: incyte ID No. US20030175704A1 007074.13
; NAME/KEY: unsure
; LOCATION: 118
; OTHER INFORMATION: a, t, c, g, or other
US-09-971-429B-17

Alignment Scores:
Pred. No.: 0 Length: 4760
Score: 5224.00 Matches: 956
Percent Similarity: 99.28% Conservative: 4
Best Local Similarity: 98.86% Mismatches: 7
Query Match: 98.81% Indels: 0
DB: 10 Gaps: 0

US-09-373-658C-126 (1-967) x US-09-971-429B-17 (1-4760)

QY 1 MetGlnArgAlaValProGluGlyPheGlyArgArgLysLeuGlySerAspMetGlyAen 20
Db 561 ATGCAGCAGCTGTGCCCGAGGGGTTCCGAAGGCGCAAGCTGGCGAGCAGATCGGGGAAC 620
QY 21 AlaGluArgAlaProGlySerArgSerPheGlyProValProThrLeuLeuLeuAla 40
Db 621 GCGGAGCGGGCTCCGGGGTCTCGAGCTTTGGGCCAGTACCCACGCTGCTGCTCGCC 680
QY 41 AlaLeuLeuAlaValSerAspAlaLeuGlyArgProSerGluGluAspGluGluLeu 60
Db 681 GCGGGCGCTACTGGCGCTGTCCGACGCACTCGGGCGCCCTCCGAGGAGCAGGAGCTTA 740
QY 61 ValValProGluLeuGluArgValProGlyHisGlyThrArgLeuArgLeuHisAla 80
Db 741 GTGGTGGCGAGCTGAGCGCGCCCGGACACGGGACCCACGCGCTCCGCTGCACGCC 800
QY 81 PheAspGlnGlnLeuAspLeuAspValProProAspSerSerPheLeuAlaProGlyPhe 100
Db 801 TTGTACCAGCAGCTGGATCTGGAGCTGCGGCCGCGACAGAGCTTTTGGCGCCCGGCTTC 860
QY 101 ThrLeuGlnAsnValGlyArgLysSerGlySerAspThrProLeuProGluThrAspLeu 120
Db 861 ACCTCCAGACGTTGGGGCGCAATCCGGGTCCGAGACGCGCTTCGGGAAACCGACCTG 920

QY 121 AlaHisCysPheTyrSerGlyThrValAsnGlyAspProSerSerAlaAlaAlaLeuSer 140
Db 921 GGCACACTGTTCTACTCCGGCACCGTGATGGCGATCCAGCTCGGCTGCCGCCCTCAGC 980
QY 141 LeuCysGluGlyValArgGlyAlaPheTyrLeuLeuGlyGluAlaTyrPheIleGlnPro 160
Db 981 CTCTCGGAGGGCGTCCGCGCGCTTCTACCTGCTGGGGAGGCGTATTTTCATCCAGCG 1040
QY 161 LeuProAlaAlaSerGluArgLeuAlaThrAlaAlaProGlyGluLysProAlaPro 180
Db 1041 CTGCCCGCGCGAGCGAGCGCTCCGCCCGCGCGCGAGGAGCGCGCGCACCA 1100
QY 181 LeuGlnPheHisLeuLeuArgArgAsnArgGlnGlyAspValGlyGlyThrCysGlyVal 200
Db 1101 CTACAGTTCCACTCTCTCGGGCGGAATCGCACGGCGAGCTAGCGGCGACGTCGGGGT 1160
QY 201 ValAspAspGluProArgProThrGlyLysAlaGluThrGluAspGluAspGluGlyThr 220
Db 1161 GTGGACGACGAGCCCGCGCGACTCGGAAAGCGGAGACCGAAGACGAGGACGAGGACT 1220
QY 221 GluGlyGluAspGluGlyProGlnTrpSerProGlnAspProAlaLeuGlnGlyValGly 240
Db 1221 GAGGGCGAGGACGAAAGGGGCTCAGTGGTGGCGCGAGGACCCGCGACTGCAAGCGCTAGGA 1280
QY 241 GlnProThrGlyThrGlySerIleArgLysLysArgPheValSerSerHisArgTyrVal 260
Db 1281 CAGCCCAACGNACTGGAGACATAAGAAAGAACGATTTGTGTCCAGTCACCGCTATGTG 1340
QY 261 GluThrMetLeuValAlaAspGlnSerMetAlaGluPheHisGlySerGlyLeuLysHis 280
Db 1341 GAAACCATGCTTGTGGCAGACCCAGTCGATGGCAGAAATCCACGGCAGTGGTCTTAAAGCAT 1400
QY 281 TyrLeuLeuThrLeuPheSerValAlaAlaArgLeuTyrLysHisProSerIleArgAsn 300
Db 1401 TACCTTCTCACGTGTTTTTGGTGGCAGCCAGATTTGTATCAAAACACCCAGCATTCGTAT 1460
QY 301 SerValSerLeuValValLysIleLeuValIleHisAspGluGlnLysGlyProGlu 320
Db 1461 TCAGTTAGCTGGTGGTGGTGAAGATCTTGGTCATCCAGATGAACAGAGGGGCGGNA 1520
QY 321 ValThrSerAsnAlaAlaLeuThrLeuArgAsnPheCysAsnTrpGlnLysGlnHisAsn 340
Db 1521 GTGACCTCCAATGCTGCCCTCACTCTCGCGAACTTTTGCNACTGGCAGAGCAGCACAC 1580
QY 341 ProProSerAspArgAspAlaGluHisTyrAspThrAlaIleLeuPheThrArgGlnAsp 360
Db 1581 CCACCCAGTGACCCGGGATGCAGAGCAGCATATGACACAGCAATTCCTTCCACAGAGGAC 1640
QY 361 LeuCysGlySerGlnThrCysAspThrLeuGlyMetAlaAspValGlyThrValCysAsp 380
Db 1641 TTGTGTGGGTCCAGACATGTATCTTTGGGATGGCTGATGTTGGAACTGTGTGTGAT 1700
QY 381 ProSerArgSerCysSerValIleGluAspAspGlyLeuGlnAlaAlaPheThrThrAla 400
Db 1701 CCGAGCAGAGCTGCTCCGTATAGATGATGTTTACAAGCTGCCTTCCACACAGCC 1760
QY 401 HisGluLeuGlyHisValPheAsnMetProHisAspAspAlaLysGlnCysAlaSerLeu 420
Db 1761 CATGAATTAGCCACGCTGTTTAAACATGCCACATGATGATGCAAGAGCGATGTCAGCCCT 1820
QY 421 AsnGlyValAsnGlnAspSerHisMetMetAlaSerMetLeuSerAsnLeuAspHisSer 440
Db 1821 AATGTGTGAACACAGATTTCCACATGATGGCTCAATGCTTTCCAACTGGACCCACAGC 1880
QY 441 GlnProTrpSerProCysSerGlyTyrMetIleThrSerPheLeuAspAsnGlyHisGly 460
Db 1881 CAGCCTTGCTCTCTTCAGTGCCTTACATGATTAATCATCTCTGATAATGCTCATGGG 1940
QY 461 GluCysLeuMetAspLysProGlnAsnProIleGlnLeuProGlyAspLeuProGlyThr 480
Db 1941 GAATGTTTGTAGTGAACAGCCTCAGAAATCCATACAGTCCCGAGGCGATCTCCCTGGCAC 2000
QY 481 SerTyrAspAlaAsnArgGlnCysGlnPheThrPheGlyGluAspSerLysHisCysPro 500

Db 642 GTGGTCCGGAGCTGGAGCGCGCCCGGACACGRGACCACCGCTCCGCTCCGACGCC 701
Qy 81 PheAspGlnLeuAspLeuValProProAspSerPheLeuAlaProGlyPhe 100
Db 702 TTGTGACACAGCTGGATCTGGAGCTCGGCCGACAGCAGCTTTTGGCGCCCGCTTC 761
Qy 101 ThrLeuGlnAsnValGlyArgLysSerGlySerAspThrProLeuProGluThrAspLeu 120
Db 762 ACGCTCCAGACGTTGGGGCGAAATCCGGTCCGAGACGCCGCTTCGGGAAACCGACCTG 821
Qy 121 AlaHisCysPheThrSerGlyThrValAsnGlyAspProSerSerAlaAlaLeuSer 140
Db 822 GCGCATGCTTCTACTCCGCGCACCGTGAATGCGGATCCAGCTCGCGCTCGCCCTCAGC 881
Qy 141 LeuCysGluGlyValArgGlyAlaPheTyrLeuLeuGlyGluAlaTyrPheileGlnPro 160
Db 882 CTCTCGAGGGGCTGCGCGCGCCCTTCTACCTGCTGGGGGAGCGGTATTTCATCCAGCGG 941
Qy 161 LeuProAlaAlaSerGluArgLeuAlaThrAlaAlaProGlyGluLysProProAlaPro 180
Db 942 CTGCGCGCGCCAGCGAGCGCTCGCCACCGCGCGCCCGCCAGGGGAGAGCGCGCGACCA 1001
Qy 181 LeuGlnPheHisLeuLeuArgAsnArgGlnGlyAspValGlyGlyThrCysGlyVal 200
Db 1002 CTACAGTTCCACTCTCTGCGCGGAATCGGCAGGCGCAGCTMGCGGCGCACGTGCGGGGTS 1061
Qy 201 ValAspAspGluProArgProThrGlyLysAlaGluThrGluAspGluAspGluGlyThr 220
Db 1062 GTGGACGACGAGCCCGCGCGACTGGAAAGCGGAGACCGAAAGCAGGACGAGCGAGGACT 1121
Qy 221 GluGlyGluAspGluGlyProGlnTrpSerProGlnAspProAlaLeuGlnGlyValGly 240
Db 1122 GAGGCGGAGGACGAGGGGCTCAGTGTGCGCGCAGGACCCCGCACTGCAAGCGCTAGGA 1181
Qy 241 GlnProThrGlyThrGlySerIleArgLysLysArgPheValSerSerHisArgTyrVal 260
Db 1182 CAGCCACAGGAACCTGGAAGCATAGAAAGAGCGATTTGTGTCCAGTCACCGCTATGTG 1241
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Db 1242 GAAACCATGCTTGTGGCAGACCGCTGATGGGAGCAATTCACGCGCAGTGGTCTAAAGCAT 1301
Qy 281 TyrLeuLeuThrLeuPheSerValAlaAlaArgLeuTyrLysHisProSerIleArgAsn 300
Db 1302 TACCTTCTCACGTTGTTTGGTGGCAGCCAGCATTTGTACAAACACCCCGCAGCATTCGTAAT 1361
Qy 301 SerValSerLeuValValLysIleLeuValIleHisAspGluGlnLysGlyProGlu 320
Db 1362 TCAGTTAGCTGTGGTGGTGAAGATCTTGGTCTATCCACGATGAACAGAGGGGCGGAA 1421
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Db 1422 GTGACTCCAAATGTGCTCCCTCACTCTGGCGAACTTTTGGCACTGGCAGAGCAGCACAC 1481
Qy 341 ProProSerAspArgAspAlaGluHisTyrAspThrAlaIleLeuPheThrArgGlnAsp 360
Db 1482 CCACCCAGTGACCGGGATGACAGCAGCTATGACACAGCAATTTCTTTCCACGACAGGAC 1541
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Db 1542 TTGTGTGGGTCCACAGCATGTATCTCTTGGGATGGCTGATGTGGAACTGTGTGTGAT 1601
Qy 381 ProSerArgSerCysSerValIleGluAspAspGlyLeuGlnAlaAlaPheThrThrAla 400
Db 1602 CCGACGAGAGCTGCTCCGTCTAGAAGATGATGGTTTACAAGCTGCTTCACACAGGCC 1661
Qy 401 HisGluLeuGlyHisValPheAsnMetProHisAspAspAlaLysGlnCysAlaSerLeu 420
Db 1662 CATGAATTAGGCCACGCTGTTTAACATGCCACATGATGATGCAAGCAGTGTGCCAGCCTT 1721
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Db 1722 AATGGTGTGAACAGGATTTCCACATGATGGGCTCAATGCTTTTCCAACCTGGACACAGC 1781

Qy 441 GlnProTrpSerProCysSerGlyTyrMetIleThrSerPheLeuAspAsnGlyHisGly 460
Db 1782 CAGCCCTTGGTCTCTCTGAGTGCCTCATGATATTACATTCTTGGATAATGGTCATGGG 1841
Qy 461 GluCysLeuMetAspLysProGlnAsnProIleGlnLeuProGlyAspLeuProGlyThr 480
Db 1842 GAAATGTTTGGTGGACAAGCCTCAGAAATCCCATACAGCTCCAGGCGATCTCCCTGGCACC 1901
Qy 481 SerTyrAspAlaAsnArgGlnCysGlnPheThrPheGlyGluAspSerLysHisCysPro 500
Db 1902 TGTACAGATGCCAACCGCAGTGCAGTTTACATTGGGGAGGACTCCAAACACACTGCCCY 1961
Qy 501 AspAlaAlaSerThrCysSerThrLeuTrpCysThrGlyThrSerGlyGlyValLeuVal 520
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Qy 521 CysGlnThrLysHisPheProTrpAlaAspGlyThrSerCysGlyGluGlyLysTrpCys 540
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Qy 541 IleAsnGlyLysCysValAsnLysAsnHisArgLysHisPheAspThrProPheHisGly 560
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Qy 561 SerTrpGlyMetTrpGlyProTrpGlyAspCysSerArgThrCysGlyGlyValGln 580
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Db 2262 AAACGAGTGCCTACAGATCTCTTAACCTTGAGGACTGTCCAGACAAATAATGGAAAAACC 2321
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Db 2442 ATCTGCCAAGCCAAAGGCAATTGGCTACTTCTTGTGTTTGCAGCCCAAGGTTGTAGTGT 2501
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Db 2502 ACTCATGTAGCCCGATTTCCCTCTGTCTGTGTGCAAGGACAGTGTGTAAAAAGCTGGT 2561
Qy 701 CysAspArgIleIleAspSerLysLysPheAspLysCysGlyValCysGlyGlyAsn 720
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Qy 721 GlySerThrCysLysLysIleSerGlySerValThrSerAlaLysProGlyTyrHisAsp 740
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Qy 761 SerArgAsnAsnGlySerPheLeuAlaIleLysAlaAlaAspGlyThrTyrIleLeuAsn 780
Db 2742 TCCAGGAACAATGGCAGCTTTCTTCCCATCAAGCTGCTGATGGCACATATATTTCTTAAT 2801
Qy 781 GlyAspTyrThrLeuSerThrLeuGluGlnAspIleMetTyrLysGlyValValLeuArg 800
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QY 821 LeuThrIleGlnValLeuThrValGlyAsnAlaLeuArgProLysIleLysIleThrTyr 840
DB 2922 TTGACCATCCAGGTCTTACTGTGGGCAATGCTTCCGACCTAAATTTAAATACACCTAC 2981
QY 841 PheValLysLysLysLysGluSerPheAsnAlaIleProThrPheSerAlaTrpValIle 860
DB 2982 TTGCTAAAGAAAGAGAGGAATCTTCAATGCTATCCCCACTTTTTCAGCATGGGTCAAT 3041
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DB 3102 TGCCGAGACATTAATGACAGCCTGCTTCCGAGTGTGCAAGGAAGTGAAGCCAGCCAGC 3161
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DB 3162 ACCAGACTTGTGTCAGACACCATCCCTGCCCCAGTGGCAGCTGGGGAGTGGTCATCATGT 3221
QY 921 SerLysThrCysGlyLysGlyTyrLysLysThrSerLeuLysCysLeuSerHisAspGly 940
DB 3222 TCTAAGACCTGTGGGAAGGGTTACAAAAGAAAGCTTGAAGTGTCTGTCCCATGATGGA 3281
QY 941 GlyValLeuSerHisAspSerCysAspProLeuLysLysProLysHisPheIleAspPhe 960
DB 3282 GGGGTGTATCTCATGAGAGCTGTGATCCCTTAAAGAAACCTTAAACATTTTCATAGACTT 3341
QY 961 CysThrMetAlaGluCysSer 967
DB 3342 TGCACAATGGCAGAATGCAGT 3362

RESULT 13
US-10-741-600-777
; Sequence 777, Application US/10741600
; Publication No. US20050026169A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; FILE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001499
; CURRENT APPLICATION NUMBER: US/10/741.600
; CURRENT FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 73997
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 777
; LENGTH: 4459
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(4459)
; OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables 1-
US-10-741-600-777

Alignment Scores:
Pred. No.: 0 Length: 4459
Score: 5202.00 Matches: 953
Percent Similarity: 98.97% Conservative: 4
Best Local Similarity: 98.55% Mismatches: 10
Query Match: 98.39% Indels: 0
DB: 19 Gaps: 0

US-09-373-658C-126 (1-967) x US-10-741-600-777 (1-4459)

QY 1 MetGlnArgAlaValProGluGlyPheGlyArgArgLysLeuLysGlySerAspMetGlyAsn 20
DB 243 ATGCAGCAGCTGTGCCCCGAGGGGTTCGAGAGCGCAAGCTGGGCAGGCAGCATGGGGAAC 302
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QY 21 AlaGluArgAlaProGlySerArgSerPheGlyProValProThrLeuLeuLeuLeuAla 40
DB 303 GCGGAGCGGGCTCCGCGGTCTCGAGCTTTGGGCGMGTATCCACAGCTGTGTCTGCTCGCC 362
QY 41 AlaAlaLeuLeuAlaValSerAspAlaLeuGlyArgProSerClnuAspGluGluLeu 60
DB 363 GCGGCGCTACTGCGCGTGTTCGACGCACTCGGGCGCCCTTCGAGGAGGACGAGGAGCTA 422
QY 61 ValValProGluLeuGluArgValProGlyHisGlyThrThrArgLeuArgLeuHisAla 80
DB 423 GTGGTCCCGAGCTGGAGCGCGCCCGGACACGRCACCGCGCTCCGCGCTGCACGCC 482
QY 81 PheAspGlnGlnLeuAspLeuAspValProProAspSerSerPheLeuAlaProGlyPhe 100
DB 483 TTTGACCAGCAGCTGGATCTGGAGCTCGCGCCCGCAGCAGCAGCTTTTGGCGCGCGCTTC 542
QY 101 ThrLeuGlnAsnValGlyArgLysSerGlySerAspThrProLeuProGluThrAspLeu 120
DB 543 ACCTCTCAAGACGTGGGGCGCAAAATCCGGGTCCGAGACGCCGCTTCCGHAACCGACCTG 602
QY 121 AlaHisCysPheTyrSerGlyThrValAsnGlyAspProSerSerAlaAlaLeuSer 140
DB 603 GCGCATGCTTCTACTCCGGCACCGTGAATGGGATCCAGCTCGGCTCGCGCTCAGC 662
QY 141 LeuCysGluGlyValArgGlyAlaPheTyrLeuLeuGlyGluAlaTyrPheIleGlnPro 160
DB 663 CTCTGCGAGGCGTGC CGCGCGCTTCTACTCTGGGGGAGCGCTATTTTCATCCAGCG 722
QY 161 LeuProAlaAlaSerGluArgLeuAlaThrAlaAlaProGlyGluLysProAlaPro 180
DB 723 CTGCCCGCGCACGAGCGCTTCGCCACCGCGCCCGCAGGGAGAAAGCCCGCGCACCA 782
QY 181 LeuGlnPheHisLeuLeuArgArgAsnArgGlnGlyAspValGlyGlyThrCysGlyVal 200
DB 783 CTACAGTTTCCACCTCTCTGCGCGGAATTCGACAGGGCAGCTMGCGGCGCACGTGCGGGTS 842
QY 201 ValAspAspGluProArgProThrGlyLysAlaGluThrGluAspGluAspGluGlyThr 220
DB 843 GTGACGACGAGCGCGCGCGCTGGGAAAGCGAGACCGAAGACGAGGACGAGAGGACT 902
QY 221 GluGlyGluAspGluGlyProGlnTrpSerProGlnAspProAlaLeuGlnGlyValGly 240
DB 903 GAGGCGCAGACGAGCGGCTCAGTGTGTCCCGCAGGACCGCGCAGCTGCAAGGCGTAGGA 962
QY 241 GlnProThrGlyThrGlySerIleArgLysArgPheValSerSerHisArgTyrVal 260
DB 963 CAGCCCAACAGAACTGGAAGCATAAAGAAAGAGCGATTTGTTCAGTCCCGCTATGTG 1022
QY 261 GluThrMetLeuValAlaAspGlnSerMetAlaGluPheHisGlySerGlyLeuLysHis 280
DB 1023 GAAACCATGCTTGTGGCAGACCATGTCGATGGCAGAAATTCACGCGCAGTGGTCTAAAGCAT 1082
QY 281 TyrLeuLeuThrLeuPheSerValAlaAlaArgLeuTyrLysHisProSerIleArgAsn 300
DB 1083 TACCTTCTCAGTGTGTTCGTGGCAGCCAGATTTGACAAACACCCCGAGCATTTCTGTAAT 1142
QY 301 SerValSerLeuValValValLysIleLeuValIleHisAspGluGlnLysGlyProGlu 320
DB 1143 TCAGTTAGCTGTGGTGGTGAAGATCTTGTGTCTCCACGATGAACAGAGGGGCGCGAA 1202
QY 321 ValThrSerAsnAlaAlaLeuThrLeuArgAsnPheCysAsnTrpGlnLysGlnHisAsn 340
DB 1203 GTGACCTTCAATGCTGCCCTCAGCTTCGCGGAACCTTTTGCACATGGCAGAACGAGCACAAC 1262
QY 341 ProProSerAspArgAspAlaGluHisTyrAspThrAlaIleLeuPheThrArgGlnAsp 360
DB 1263 CCACCCAGTACCAGGATGCAGAGCACTATGACACAGCAATTTCTTTTCCAGCAGAGAC 1322
QY 361 LeuCysGlySerGlnThrCysAspThrLeuGlyMetAlaAspValGlyThrValCysAsp 380
DB 1323 TTGTGTGGTCCCCAGACATGTGATCTCTGGGATGGCTGTATTTGGACATGTGTGTGAT 1382
QY 381 ProSerArgSerCysSerValIleGluAspAspGlyLeuGlnAlaAlaPheThrThrAla 400
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Best Local Similarity: 98.55%		Mismatches: 10	
Query Match: 98.39%		Indels: 0	
DB: 19		Gaps: 0	
US-09-373-658C-126 (1-967) x US-10-741-600-775 (1-4658)			
QY	1	MetGlnArgAlaValProGluGlyPheGlyArgArgLysLeuGlySerAspMetGlyAsn	20
DB	462	ATGCAGCGAGCTGTGCCGAGGGGTTCGGAAGCGCAAGCTGGCGACGACATGGGGGAAC	521
QY	21	AlaGluArgAlaProGlySerArgSerPheGlyProValProThrLeuLeuLeuAla	40
DB	522	GCGGAGCGGGCTCCGGGGTCTCGAGACTTTGGGCGMTACTCCACGCTGCTGCTCGCC	581
QY	41	AlaAlaLeuLeuAlaValSerAspAlaLeuGlyArgProSerGluGluAspGluGluLeu	60
DB	582	GCGGCGCTACTGGCGGTTCGAGCGACTTCGGGCGCCCTCCGAGGAGGACGAGGAGCTA	641
QY	61	ValValProGluLeuGluArgValProGlyHisGlyThrThrArgLeuArgLeuHisAla	80
DB	642	GTGGTCCCGAGCTGGAGCGCGCCCGGAGACACRGACACCGCGCTCCGCCCTGCGACGCC	701
QY	81	PheAspGlnGlnLeuAspLeuAspValProProAspSerSerPheLeuAlaProGlyPhe	100
DB	702	TTTGACCGAGCAGCTGGATCTGGAGCTGCGGCCCGCACAGCAGCTTTTGGCGCCCGCTTC	761
QY	101	ThrLeuGlnAsnValGlyArgLysSerGlySerAspThrProLeuProGluThrAspLeu	120
DB	762	ACGCTCCAGAACGTGGGGCGCAATCCGGTCCGAGACGCGCTTCGGGAAACCGACCTG	821
QY	121	AlaHisCysPheThrSerGlyThrValAsnGlyAspProSerSerAlaAlaLeuSer	140
DB	822	GCGCACTGCTTCTACTCCGCGCACGTCGAATGGCGATCCAGCTCGGCTCGCGCCCTCAGC	881
QY	141	LeuCysGluGlyValArgGlyAlaPheThrLeuLeuGlyGluAlaThrPheIleGlnPro	160
DB	882	CTCTGCCAGGGCGTGGCGCGCTTCTACTCTCTGGGGAGGCGTATTTTCATCCAGCCG	941
QY	161	LeuProAlaAlaSerGluArgLeuAlaThrAlaAlaProGlyLysProProAlaPro	180
DB	942	CTGCCCGCCGACGAGCGCTCGCCACCGCGCCCGAGGAGAGCGCGCGCACCA	1001
QY	181	LeuGlnPheHisLeuLeuArgArgAsnArgGlnGlyAspValGlyGlyThrCysGlyVal	200
DB	1002	CTACAGTTCCACCTCTCGCGCGGAATCGGCAGGCGCACGTGCGCGCACGTCGCGGGTS	1061
QY	201	ValAspAspGluProArgProThrGlyLysAlaGluThrGluAspGluAspGluGlyThr	220
DB	1062	GTGGACGACGAGCCCGCGCGCTGAGTGGTTCGCGAGGACCGGACCTGCAAGCGGTAGGA	1121
QY	221	GluGlyGluAspGluGlyProGlnTrpSerProGlnAspProAlaLeuGlnGlyValGly	240
DB	1122	GAGGGCGAGGACGAGGGGCTCAGTGTCTCGCGCAGGACCGCGCACCTGCAAGGGGTAGGA	1181
QY	241	GlnProThrGlyThrGlySerIleArgLysLysArgPheValSerSerHisArgGlyVal	260
DB	1182	CAGCCCAACAGAACTGGAAGCATTAAGAAAGAGCGATTTGTCTCAGTCCACCGCTATGTG	1241
QY	261	GluThrMetLeuValAlaAspGlnSerMetAlaGluPheHisGlySerGlyLeuLysHis	280
DB	1242	GAACACCATGCTTGTGGCAGACCACTCGATGGCAGAAATTCACCGGCACTGGTGTAAAGCAT	1301
QY	281	TyrLeuLeuThrLeuPheSerValAlaAlaArgLeuThrLysHisProSerIleArgAsn	300
DB	1302	TACCTTCTCAGTGTGTTTTCGGTGGCAGCCAGATTTGACAAACACCCACCATTCGTAT	1361
QY	301	SerValSerLeuValValLysIleLeuValIleHisAspGluGlnLysGlyProGlu	320
DB	1362	TCAGTTAGCTGTGTGTGTAAGATCTTGTCTATCCAGCATGAACAGAGGGCGCGGAA	1421
QY	321	ValThrSerAsnAlaAlaLeuThrLeuArgAsnPheCysAsnTrpGlnLysGlnHisAsn	340
DB	1422	GTGACCTCCAATGTGCCCTCACTCTCGGAACTTTTGGCACTGGCAGAGCAGCACAC	1481

QY	341	ProProSerAspArgAspAlaGluHisTyrAspThrAlaIleLeuPheThrArgGlnAsp	360
DB	1482	CCACCAGTGACCGGGATGCAGAGCACTATGACACAGCAATTCCTTTCCACGACAGGAC	1541
QY	361	LeuCysGlySerGlnThrCysAspThrLeuGlyMetAlaAspValGlyThrValCysAsp	380
DB	1542	TTGTGTGGGTCCACAGCATGTGATCTCTTGGATGGCTGATGTTGGAACTGTGTGTGAT	1601
QY	381	ProSerArgSerCysSerValIleGluAspAspGlyLeuGlnAlaAlaPheThrAla	400
DB	1602	CCGAGCAGAGCTGCTCCGTCATAGAGATGATGTTTACAAGTCGCTTCCACACAGCC	1661
QY	401	HisGluLeuGlyHisValPheAsnMetProHisAspAspAlaLysGlnCysAlaSerLeu	420
DB	1662	CATGAATTAGCGCCGCTGTTTAAACATGCCACATGATGATGCAAGCAGTGTGCCAGCCTT	1721
QY	421	AsnGlyValAsnGlnAspSerHisMetMetAlaSerMetLeuSerAsnLeuAspHisSer	440
DB	1722	AATGGTGTGAACAGGATTCACACATGATGGGTCAATGCTTTCCAACTGGACACAGC	1781
QY	441	GlnProTrpSerProCysSerGlyTyrMetIleThrSerPheLeuAspAsnGlyHisGly	460
DB	1782	CAGCCTTGCTCTCTTGCAGTGCCTACATGATTTACATCATTTCTGATATATGTCATGGG	1841
QY	461	GluCysLeuMetAspLysProGlnAsnProIleGlnLeuProGlyAspLeuProGlyThr	480
DB	1842	GAATGTTTATGGACAAAGCTCCAGATCCACATCAGCTCCACAGCGCATCTCCCTGGCAC	1901
QY	481	SerTyrAspAlaAsnArgGlnCysGlnPheThrPheGlyGluAspSerLysHisCysPro	500
DB	1902	TGCTAGTAGTCCAAACCGGAGTCCAGTTTACATTTGGGGAGGACTCCAAACACTGCCCY	1961
QY	501	AspAlaAlaSerThrCysSerThrLeuTrpCysThrGlyThrSerGlyGlyValLeuVal	520
DB	1962	GATGCAGCCAGCACATGTAGCACCCTTGTGTGTACCGCACCTCTGTGTGGTGTGGTG	2021
QY	521	CysGlnThrLysHisPheProTrpAlaAspGlyThrSerCysGlyGluGlyLysTrpCys	540
DB	2022	TGTCAAACCAACACCTCCGTCGGCGGATGGCACCGCTGTGGAGAGGAAATGGTGT	2081
QY	541	IleAsnGlyLysCysValAsnLysAsnHisArgLysHisPheAspThrProPheHisGly	560
DB	2082	ATCAACGGCAAGTGTGTGAACAAACCGACAGAAAGCAATTTTGTATAGCCTTTTCATGGA	2141
QY	561	SerTrpGlyMetTrpGlyProTrpGlyAspCysSerArgThrCysGlyGlyValGln	580
DB	2142	AGCTGGGGATGTGGGGCTTGGGGAGACTGTTCCAGAACGTCGTCGAGGAGTCCAG	2201
QY	581	TyrThrMetArgGluCysAspAsnProValProLysAsnGlyGlyLysTrpCysGluGly	600
DB	2202	TACACGATGAGGAAATGTGACAAACCCAGTCCCAAGAAATGGAGGAAGTACTGTGAAGGC	2261
QY	601	LysArgValArgTyrArgSerCysAsnLeuGluAspCysProAspAsnAsnGlyLysThr	620
DB	2262	AAACGAGTGGCTTACAGATCTGTAACTTGGAGACTGTCCAGACATATATGGAAGAAC	2321
QY	621	PheArgGluGlnCysGluAlaHisAsnGluPheSerLysAlaSerPheGlySerGly	640
DB	2322	TTTAGAGAGAACATGTGAGCAGACACACAGCTTTTCAAAAGCTTCTTTGGAGTGGG	2381
QY	641	ProAlaValGlnTrpIleProLysTyrAlaGlyValSerProLysAspArgCysLysLeu	660
DB	2382	CCTGCGGTGGAATGGATTCCAAGTACGCTGGCGTCTCCAAAGGACAGGTGCAAGCTC	2441
QY	661	IleCysGlnAlaLysGlyIleGlyTyrPhePheValIleGlnProLysValValAspGly	680
DB	2442	ATCTGCCAAGCCAAAGGCATTTGCTACTTCTGTTTGGAGCCCAAGGTTGTAGATGGT	2501
QY	681	ThrProCysSerProAspSerThrSerValCysValGlnGlyGlnCysValLysAlaGly	700
DB	2502	ACTCCATGTAGCCAGATTCACCTCTGTCGTGTGCAAGGACAGTGTGTATAAGCTGGT	2561

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QY 701 CysAspArgIleileaspSerLysLysLysPheAspLysCysGlyValCysGlyGlyAen 720
Db 2562 TGTGATCGCATCATAGACTCCAAAAGAAGTTTGATAAATGGTGGTTCGGGGGAAT 2621
QY 721 GlySerThrCysLysLysLysSerGlySerValThrSerAlaLysProGlyTyrHisAsp 740
Db 2622 CGATCTACTTGTAAAAAATATCAGGATCAGTTACTAGTGCAGAAACCTGGATATCATGAT 2681
QY 741 IleIleThrIleProThrGlyAlaThrAsnIleGluValLysGlnArgAsnGlnArgGly 760
Db 2692 ATCATCACAAATTCACATGGAGCCCAACATCGAAGTGAAACAGCGGAACAGAGGGGA 2741
QY 761 SerArgAsnAsnGlySerPheLeuAlaIleLysAlaAlaAspGlyThrTyrIleLeuAsn 780
Db 2742 TCAGAGAACATGGCAGCTTCTTCCATCAAGCTGCTGATGGCACATATATTTTAAAT 2801
QY 781 GlyAspTyrThrLeuSerThrLeuGluGlnAspIleMetTyrLysGlyValValLeuArg 800
Db 2802 CGTGNCTACACTTGTCCACCTTAGAGCAAGACATTTATGTACAAAGGTGTGTCTTGAGG 2861
QY 801 TyrSerGlySerSerAlaAlaLeuGluArgIleArgSerPheSerProLeuLysGluPro 820
Db 2862 TACAGCGGCTCTCTGCGCATTTGAAAGAAATTCGACGCTTTAGCCCTCTCAAGAGGCC 2921
QY 821 LeuThrIleGlnValLeuThrValGlyAsnAlaLeuArgProLysIleLysTyrThrTyr 840
Db 2922 TTGACCATCCAGTTCTTACTGTGGCAATGCCCTTCGACCTAAATTAATACACCTAC 2981
QY 841 PheValLysLysLysGlySerPheAsnAlaIleProThrPheSerAlaTrpValIle 860
Db 2982 TTCTGTAAAGAGAGAAAGAAATCTTTCAATGCTATCCCCACTTTTTCAGCATGGTCAAT 3041
QY 861 GluGluTrpGlyGluCysSerLysSerCysGluLeuGlyTrpGlnArgArgLeuValGlu 880
Db 3042 GAAGAGTGGGGGAATGTCTTAAGTCATGTGAATTTGGGTGGCAGAGAAGCTGTGTAGAA 3101
QY 881 CysArgAspIleAsnGlyGlnProAlaSerGluCysAlaLysGluValLysProAlaSer 900
Db 3102 TGCCGAGACATTAATGGACAGCTGCTTCCGAGTGTGCAGAGAAATGAGCCAGCCAGC 3161
QY 901 ThrArgProCysAlaAspHisProCysProGlnTrpGlnLeuGlyGluTrpSerSerCys 920
Db 3162 ACCAGACCTTGTGCAGACCATCCCTGCCCCAGTGGCAGCTGGGGAGTGGTTCATCATGT 3221
QY 921 SerLysThrCysGlyLysGlyTyrLysLysThrSerLeuLysCysLeuSerHisAspGly 940
Db 3222 TCTAAGACTGTGGGAAGGGTTACAAAAAAGAAAGCTTGAAGTGTCTGTCCCATGATGGA 3281
QY 941 GlyValLeuSerHisAspSerCysAspProLeuLysLysProLysHisPheIleAspPhe 960
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QY 961 CysThrMetAlaGluCysSer 967
Db 3342 TGCACAAATGGCAGAAATGCAGT 3362
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RESULT 15

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US-09-373-658-1
; Sequence 1, Application US/09373658
; Publication No. US20030092900A1
; GENERAL INFORMATION:
; APPLICANT: Iruela-Arispe, Luisa
; APPLICANT: Hastings, Gregg A.
; APPLICANT: Ruben, Steven M.
; APPLICANT: Jonak, Zdenka L.
; APPLICANT: Trulli, Stephen H.
; APPLICANT: Fronwald, James A.
; APPLICANT: Terrett, Jonathan A.
; TITLE OF INVENTION: Meth1 and Meth2 Polynucleotides and Polypeptides
; FILE REFERENCE: 1488.1070006
; CURRENT APPLICATION NUMBER: US/09/373,658
; NUMBER OF SEQ ID NOS: 125
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; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 3261
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(2853)
; NAME/KEY: UNSURE
; LOCATION: (3095)
; OTHER INFORMATION: May be any nucleic acid
; NAME/KEY: UNSURE
; LOCATION: (3248)
; OTHER INFORMATION: May be any nucleic acid
; NAME/KEY: UNSURE
; LOCATION: (3255)
; OTHER INFORMATION: May be any nucleic acid
; NAME/KEY: UNSURE
; LOCATION: (3261)
; OTHER INFORMATION: May be any nucleic acid
US-09-373-658-1

Alignment Scores:
Pred. No.: 0 Length: 3261
Score: 5144.00 Matches: 940
Percent Similarity: 99.37% Conservative: 4
Best Local Similarity: 98.95% Mismatches: 6
Query Match: 97.30% Indels: 0
DB: 10 Gaps: 0

US-09-373-658C-126 (1-967) x US-09-373-658-1 (1-3261)

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QY 38 LeuLeuAlaAlaLeuLeuAlaValSerAspAlaLeuGlyArgProSerGluGluAsp 57
Db 61 CTGCTCGCGGGGGCTACTGGCGGTGTCGACGCACTCGGGGCGCCCTCCGAGAGGAC 120
QY 58 GluGluLeuValProGluLeuGluArgValProGlyHisGlyThrArgLeuArg 77
Db 121 GAGGAGCTAGTGTGTCCGAGCTGGAGCGCGCCCGGACACGCGCCGCTCCGCTCCGC 180
QY 78 LeuHisAlaPheAspGlnGlnLeuAspLeuAspValProProAspSerSerPheLeuAla 97
Db 181 CTGACGCTTTTGACACGACGCTGGATCTGGAGCTCGCGCGCCGACGACGAGCTTTTGGCG 240
QY 98 ProGlyPheThrLeuGlnAsnValGlyArgLysSerGlySerAspThrProLeuProGlu 117
Db 241 CCGGGCTTCAGCTCCAGAACGTGGGGGCGAAATCCGGGTCCGAGACGCGCTTCGGNA 300
QY 118 ThrAspLeuAlaHisCysPheTyrSerGlyThrValAsnGlyAspProSerSerAlaAla 137
Db 301 ACCGACCTGGGCGACTGCTTCTACTCCGCGCACCGTGAATGGCGATCCACGCTCGGCTGCC 360
QY 138 AlaLeuSerLeuCysGluGlyValArgGlyAlaPheTyrLeuLeuGlyGluAlaTyrPhe 157
Db 361 GCCCTCAGCCCTTCGAGGGGGTGGCGCGCGCTTCTACCTGCTGGGGGAGCGGTATTC 420
QY 158 IleGlnProLeuProAlaAlaSerGluArgLeuAlaThrAlaAlaProGlyLysPro 177
Db 421 ATCCAGCGCGCTGCCCGCGCGCAGCGAGCGCTCCGCCACCGCGCCCGCCAGGAGAGCG 480
QY 178 ProAlaProLeuGlnPheHisLeuLeuArgArgAsnArgGlnGlyAspValGlyThr 197
Db 481 CCGGCACCACTACAGTTCCACTCCTCGCGGGGAATCCGCGAGGGGCGACGTAGCGCGCAG 540
QY 198 CysGlyValValAspAspGluProArgProThrGlyLysAlaGluThrGluAspGluAsp 217
Db 541 TCGGGGTGTGGAGCAGCAGCGCCCGCGGCTGCTGGAAGCGGAGACCGAGACGAGGAC 600
QY 218 GluGlyThrGluGlyGluAspGluGlyProGlnTrpSerProGlnAspProAlaLeuGln 237
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601	Db	GAAGGGCACTGAGGGCCAGGACGAAAGGGCTTCACTGGTGC CGCAGAGCCGGCACTGC	CAA	660
238	Qy	GlyValGlyGlnProThrGlyThrGlySerIleArgIleValSerHis	257	
661	Db	GGCGTAGGACAGCCCAAGGACATGGAAGCATAAGAAAGAGGATTTGGTCCATGCAC	720	
258	Qy	ArgTyrValGluThrMetLeuValAlaAspGlnSerMetAlaGluPheHisGlySerGly	277	
721	Db	CGCTATGTGGAAACCATGCTTTGGCAGACCACTCGATGSCAGAAATTCACAGCGCAGTGGT	780	
278	Qy	LeuLysHisTyrIleuLeuThrLeuPheSerValAlaAlaArgLeuTyrLysHisProSer	297	
781	Db	CTAAAGCATTTACCTTCTCAGTGTGTTTCCGTGGCAGCCAGATTTGTACAAACACCCGACG	840	
298	Qy	IleArgAsnSerValSerLeuValValValLysIleuValLysIleHisAspGluGlnLys	317	
841	Db	ATTTCGTAATTCAGTTAGCTGGTGGTGGTGAAGATCTTGGTCAATCACAGATGAACAGAAG	900	
318	Qy	GlyProGluValThrSerAsnAlaAlaLeuThrLeuArgAsnPheCysAsnTrpGlnLys	337	
901	Db	GGCGCGGAAGTGAACCTCCATGCTGCCCTCACTCTGGGAACCTTTGCACCTGGCAGAAG	960	
338	Qy	GlnHisAsnProProSerAspArgAspAlaGluHisTyrAspThrAlaIleLeuPheThr	357	
961	Db	CAGCACAAACCCACCCAGTGAACCGGATGCAGAGCACTATGACACAGCAATTTCTTTCAACC	1020	
358	Qy	ArgGlnAspLeuCysGlySerGlnThrCysAspThrLeuGlyMetAlaAspValGlyThr	377	
1021	Db	AGACAGACTTGTGTGGTCCCAACATGTGTATCTCTGGAGTGGTGAATTTGGAACT	1080	
378	Qy	ValCysAspProSerArgSerCysSerValIleGluAspAspGlyLeuGlnAlaAlaPhe	397	
1081	Db	GTGTGTGATCCGACGACGAACTGCTCGTCAATAGAGATGATGGTTTACAGCTGCCTTC	1140	
398	Qy	ThrThrAlaHisGluLeuGlyHisValPheAsnMetProHisAspAspAlaLysGlnCys	417	
1141	Db	ACCACAGCCCATGAATTAGGCCACGCTGTTTAAATGACATGCACATGATGATGCAGGACAGTGT	1200	
418	Qy	AlaSerLeuAsnGlyValAsnGlnAspSerHisMetMetAlaSerMetLeuSerAsnLeu	437	
1201	Db	GCCAGCCTTAATGGTGTGAACACGAGATTCACACATGATGGCGTCAATGCTTTTCCAACTG	1260	
438	Qy	AspHisSerGlnProTrpSerProCysSerGlyTyrMetIleThrSerPheLeuAspAsn	457	
1261	Db	GACCACAGCAGCCCTTGCTTCCCTTGAGTGCCTACATGATTAATCATCTTCTTGGATTAAT	1320	
458	Qy	GlyHisGlyGlyCysLeuMetAspLysPheProGlnAsnProIleGlnLeuProGlyAspLeu	477	
1321	Db	GGTCATGGGAAATGTTTGGTGGACAAGCCCTCAGAAATCCATACAGTCCCGAGGCGATCTC	1380	
478	Qy	ProGlyThrSerTyrAspAlaAsnArgGlnCysGlnPheThrPheGlyGluAspSerLys	497	
1381	Db	CCTGGCACCTCGTACGATGCGCAACCGGCAGTGCCTTTCATTTGGGGAGGACTCCAAA	1440	
498	Qy	HisCysProAspAlaAlaSerThrCysSerThrLeuTrpCysThrGlyThrSerGlyGly	517	
1441	Db	CAC TGCCCTGATGACGACGACATGATGACACTTGTGGTGTACCGGCACTCTGGTGGG	1500	
518	Qy	ValLeuValCysGlnThrLysHisPheProTrpAlaAspGlyThrSerCysGlyGluGly	537	
1501	Db	GTGCTGGTGTGCACAAACCAACTTCCCGTGGCGGATGGCACCACTGTGGAGAGGG	1560	
538	Qy	LysTrpCysIleAsnGlyLysCysValAsnLysAsnHisArgLysHisPheAspThrPro	557	
1561	Db	AAATGGTGTATCAACGGCAAGTGTGTGAACAAAAACCGACAGAAAGCAATTTTGATACGCCT	1620	
558	Qy	PheHisGlySerTrpGlyMetTrpGlyProTrpGlyAspCysSerArgThrCysGlyGly	577	
1621	Db	TTTTCATGGAGCTGGGGAATGTGGGGCTTGTGGGGAGACTGTTTCAGAACCTGGCGGTGA	1680	
578	Qy	GlyValGlnTyrThrMetArgGluCysAspAsnProValProLysAsnGlyGlyLysTyr	597	

1681	Db	GGAGTCCAGTACACGATGAGGGATGTGACACCCAGTCCCAAGAAGTAATGGAGGAAGTAC	1740
598	Qy	CysGluGlyLysArgValArgTyrAraSerCysAsnLeuGluAspCysProAspAsnAsn	617
1741	Db	TGTGAAGGCAACGAGTGGCTACAGATCTGTAACTTTGAGGACTGTCCAGACAATAAT	1800
618	Qy	GlyLysThrPheArgGluGluGlnCysGluAlaHisAsnGluPheSerLysAlaSerPhe	637
1801	Db	GGAAAAACCTTTAGAGAGGAACAATGTGAAGCAACAACGAGTTTTCAAAAGCTTCCTTT	1860
638	Qy	GlySerGlyProAlaValGluTrrPileProLysTyrAlaGlyValSerProLysAspArg	657
1861	Db	GGGAGTGGCGCTCGGTGGATGGATTCACAGTAGCTGGCGCTCTCACCAAGAGCAGG	1920
658	Qy	CysLysLeuIleCysGlnAlaLysGlyIleGlyTyrPhePheValLeuGlnProLysVal	677
1921	Db	TGCAAGCTCATCTGCCAAGCCAAAGCATTTGGCTACTTCTTCCTTTTGCAGCCCAAGTT	1980
678	Qy	ValAspGlyThrProCysSerProAspSerThrSerValCysValGlnGlyGlnCysVal	697
1981	Db	GTAGATGGTACTCCATGTAGCCAGATTCACACTCTGTCTGTGTGAAGGACAGTGTGA	2040
698	Qy	LysAlaGlyCysAspArgIleIleAspSerLysLysLysPheAspLysCysGlyValCys	717
2041	Db	AAAGCTGGTTGTGATCGCATCATAGACTCCAAAAGAAGTTTGATAAATGTGGTGTTCG	2100
718	Qy	GlyGlyAsnGlySerThrCysLysLysIleSerGlySerValThrSerAlaLysProGly	737
2101	Db	GGGGAAATGCATCTACTTGTAAAAAAATATCAGGATCAGTTACTAGTCAAAACCTGGA	2160
738	Qy	TyrHisAspIleIleThrIleProThrGlyAlaThrAsnIleGluValLysGlnArgAsn	757
2161	Db	TATCATGATATCATCAATTCCAACTCGAGGCCACCACAACATCGAAGTGAACAGCGAAC	2220
758	Qy	GlnArgGlySerArgAsnGlySerPheLeuAlaIleLysAlaAlaAspGlyThrTyr	777
2221	Db	CAGAGGGGATCCAGGAACAATGGCAGCTTTCTTGCCATCAAGCTGCTGATGGCACATAT	2280
778	Qy	IleLeuAsnGlyAspTyrThrLeuSerThrLeuGluGlnAspIleMetTyrLysGlyVal	797
2281	Db	ATTTCTTAATGGTGACTACACTTTGTCCACCTTAGAGCAAGACATATATGACAAAGGTGTT	2340
798	Qy	ValLeuArgTyrSerGlySerSerAlaAlaLeuGluArgIleArgSerPheSerProLeu	817
2341	Db	GTCTTGAGGTACAGCGGCTCCTCTCGCGCATTCGAAAGAATTCGCAGCTTTAGCCCTCTC	2400
818	Qy	LysGluProLeuThrIleGlnValLeuThrValGlyAsnAlaLeuArgProLysLysLys	837
2401	Db	AAAGAGCCCTTGACCATTCAGAGTCTTACTGTGGGCAATGCCCTTCGACCTTAAATAATAA	2460
838	Qy	TyrThrTyrPheValLysLysLysGluSerPheAsnAlaIleProThrPheSerAla	857
2461	Db	TACACCTACTTCGTAAAGAGAGAGAGGAATCTTTCAATGCTATCCCACTTTTTCAGCA	2520
858	Qy	TrpValIleGluGluTrrPglyGlyCysSerLysSerCysGluLeuGlyTrrPglNArgArg	877
2521	Db	TGGGTCAATGAAGAGTGGCGGCAATGTTCTAAGTCAATGTGAATGGGTTGGCAGAGAAGA	2580
878	Qy	LeuValGluCysArgAspIleAsnGlyGlnProAlaSerGluCysAlaLysGluValLys	897
2581	Db	CTGTGTAGAATGCCGAGACATTAATGGACAGCGCTCTTCCGAGTGTGCAAAAGGAAGTGAAG	2640
898	Qy	ProAlaSerThrArgProCysAlaAspHisProCysProGlnTrrPglNLeuGlyGluTrrP	917
2641	Db	CCAGCCAGCACCAACCTTGTGCAGACATCCCTTGCCCCCAGTGGCAGCTGGGGGAGTGG	2700
918	Qy	SerSerCysSerLysThrCysGlyLysGlyTrrLysLysThrSerLeuLysCysLeuSer	937
2701	Db	TCATCATGTTCTAAGACTGTGGGGAAGGGTTACAAAAAAGAAGCTTTGAAGTGTCTGTCC	2760
938	Qy	HisAspGlyGlyValLeuSerHisAspSerCysAspProLeuLysLysProLysHisPhe	957
2761	Db	CATCATGGAGGGGTATCTCTCATGAGAGCTGTGATCTTTTAAAGAAACCTTAAACATTTTC	2820

Qy 958 IleaspPheCysThrMetAlaGluCysSer 967
Db 2821 ATAGACTTTTGCAATGGCAGATGCAGT 2850

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